Introduction

With the emergence of the second wave of the 2009 influenza A (H1N1) virus, there have been concerns that this pandemic may rival those of 1957, 1968, and even 1918 in which not thousands, but millions of people around the world died from the disease (Table 113.1). WHO is advising the countries of the northern and southern hemisphere to prepare for a second wave of H1N1 pandemic in which large numbers of severely ill patients requiring more and more intensive care infrastructure are likely to be seen, creating pressures that could overwhelm in hospitals and intensive care units, and possibly disrupt the provision of care of other diseases. The newly developed H1N1 vaccine is expected to reduce the impact of the second wave of H1N1 influenza pandemic in the population, especially, on high risk groups, with diminished complications, hospitalization rates, and mortality. On the other hand, previous H1N1 strains have developed antiviral resistance, and this, as well as mutation to greater virulence, remain concerns for the future. Past pandemics were characterized by several features that have been seen since March 2009: the rapid spread of a virus with novel antigenic determinants, a change in pathogenicity with high death rates in younger age groups, successive pandemic waves, apparent higher transmissibility than that of the seasonal influenza, and differences in impact in different geographic region. The overall mortality in the previous century’s three pandemics ranged from 1 million to more than 45 million deaths. In the three previous influenza pandemics, vaccines were not produced in time to have any substantial impact. Even though the technology of vaccine manufacture, produced in embryonated eggs, has changed little since the 1930s, there is some hope that vaccines will be available to mitigate the force of later waves of the current epidemic. In addition, several clinically useful antiviral drugs are now available, although there are still concerns about development of resistance.

Influenza Virus: Back to Basics

The viruses that cause influenza are influenza A, B, and C belonging to the family Orthomyxoviridae, which is characterized by segmented minus-strand RNA genome. Influenza A and B viruses’ genomes consist of eight separate segments. These include the following: three transcriptases (PB1, PB2, and PA); two surface glycoproteins, the hemagglutinin (H or HA) and neuraminidase (N & NA); two matrix proteins (M1 and M2); and one nucleocapsid protein (NP). Epidemic disease is caused by influenza virus type A and B. Influenza C viruses cause sporadic mild influenza-like illness in children. The focus of this chapter will be on influenza A virus, which may infect humans and birds, and most importantly has the capability of developing into pandemic virus. Influenza A virus has been divided into multiple subtypes, and the natural host for most of these is various avian species. In addition, influenza A viruses of a few distinct subtypes have been isolated from pigs, horses, seals, whales, and human beings, and the genome of the virus codes for two important surface glycoproteins, the hemagglutinin (H or HA) and the neuraminidase (N or NA), have been identified. Based on both sequence and antigenic analysis, 16 distinct H (H1-H16) and 9 distinct N (N1-N9) subtypes are now recognized in animal and avian influenza viruses, but only 3 H subtypes (H1, H2, and H3) and 2 N subtypes (N1, N2) have caused extensive outbreaks in human beings. The influenza virus has a poor ability to proofread its genetic material while replicating, which results in frequent errors in progeny genes, and thus frequent mutations. When such minor changes occur in the H and N proteins, they result in “antigenic drift,” the slow but significant change in antigenicity that occurs over time in both influenza A and influenza B, and that requires periodic changes in the yearly vaccine. An example of such drift occurred during the 2003/2004 influenza season when the H3N2 circulating virus developed over 80% drift from the virus that was used to make one of the three major vaccine components that year (Table 113.2). Further, marked changes in H, with or without similar changes in N, termed “antigenic shift” occur when new H or N gene segments are acquired by a process known as “reassortment.” This may take place by the mixing of genetic segments during dual infection of cells by a human and an animal virus. When such viruses containing reassorted gene segments are introduced into
a population that has no pre-existing immunity, they may lead to a pandemic. This happened in 1957 and 1968.

Devastating pandemics take place when populations are exposed to a new viral subtype in the absence of pre-existing immunity. The infectious capabilities of a new virus that emerges in this way through reassortment are likely to be acquired from one or more of the human influenza gene segments. Conditions favorable for the emergence of an antigenic shift (reassortment) involve humans living in close proximity to domestic poultry and pigs. Pigs play an important role in interspecies transmission of influenza virus. Susceptible pig cells process receptors for both avian and human influenza strains, which allow the pigs to serve as mixing vessels for the exchange of genetic material between human and avian viruses, resulting in the appearance of novel subtypes. Analysis of the 1957 H2N2 pandemic strain found that the emergent virus resulted from the acquisition by previously circulating human H1N1 of three new gene segments of avian origin (the H2 gene, the N2 gene, and one other). Similarly, the 1968 pandemic H3N2 virus acquired two new genes from an avian virus closely related to viruses isolated from ducks in Asia in 1963. In contrast, the 1918 H1N1 virus appears to have been an avian-like influenza virus derived from an unknown source. The currently circulating novel influenza H1N1 viruses that have been isolated around the globe during 2009 appear to have originated from two unrelated swine viruses, one of them a derivative of the 1918 human virus (Table 113.3).

Table 113.1
Influenza pandemic of the twentieth century

| Date           | Strain | Estimate number of worldwide deaths | Comments |
|----------------|--------|-------------------------------------|----------|
| 1918–1919 (Spanish Flu) | H1N1   | Over 50 million                     | ● Three waves: A first, mild wave in the spring of 1918 was replaced by a second wave in September to November, 1918 that resulted in a mortality rate over 2.5%. A third wave with equally high mortality rates swept around the world in 1919 ● The virus probably originated from the United States and then spread to Europe |
| 1957–1958 (Asian Flu) | H2N2   | 1–1.5 million                       | Two waves: The virus originated in Southern China in February 1957 and spread over 3 months to Singapore, Hong Kong, and Japan and in October 1957 reached United Kingdom and United States. A second wave was detected in January 1958 |
| 1968–1969 (Hong Kong Flu) | H3N2   | 3/4 million                         | Two waves in winters of 1968–1969 and 1969–1970. The virus originated from Hong Kong in July 1968 |

Table 113.2
Antigenic drift and shift

| Drift                                      | Shift                                      |
|--------------------------------------------|--------------------------------------------|
| Minor change within subtype                | Major change, new subtype                  |
| Point mutations                            | Exchange of gene segments                  |
| Occurs in A and B subtypes                 | Occurs in A subtypes only                  |
| May cause epidemics                        | May cause pandemic                         |
| Example: A/Fujian (H3N2) replaced A/Panama (H3N2) in 2003–2004 | Example: H3N2 replaced H2N2 in 1968 |

Evolution, Zoonotic Transmission, and Possible Origin of 2009 H1N1 (Swine Influenza)

The 1918 H1N1 pandemic is believed to have also affected swine at that time. Its descendents have been enzootic in pigs up ever since. The first influenza A isolated from diseased pigs in United States (USA) was in 1930. These H1N1 swine viruses are called the classical swine H1N1 viruses and have continued to circulate in pigs in the Americas, Asia, and, until 1980, also in Europe, and they remain relatively antigenically stable. This swine H1N1 subtype has crossed over to
humans periodically, including the Fort Dix outbreak in 1976, resulting in infections that have been occasionally fatal, particularly in pregnant or immunocompromised persons, but not producing human epidemics. Moreover, following the human pandemic of the H3N2 subtype in 1968, H3N2 influenza virus infected pigs, although such porcine strains have shown less antigenic drift in swine than in humans. In 1998, H3N2 viruses with genes derived from human, swine, and avian genes of North America (“Triple reassortant viruses”) were first isolated from pigs in the USA. The triple reassortant H3N2 viruses also continue to acquire other virus genes via reassortment to generate triple reassortant H1N2 or H1N1 viruses. Swine viruses of subtypes H1N1, H1N2, and H3N2 have been reported to cause occasional human infection during this time. Between 1958 and 2005, 37 human swine-origin influenzas were reported. Twenty-two (51%) of these cases reported recent exposure to pigs. The overall fatality rate was 17%. Prior to the current pandemic, but after December 2005, 11 sporadic cases of triple reassortment swine viruses were reported. Twenty-nine (51%) of these cases reported recent exposure to pigs. The overall fatality rate was 17%. Prior to the current pandemic, but after December 2005, 11 sporadic cases of triple reassortment H1 viruses were reported to the Centers for Disease Control and Prevention (CDC) in the USA, 10 carrying H1N1 genes and 1 carrying H1N2 genes. Some of the patients had close exposure to pigs. Possible limited human-to-human transmission was reported in several situations. Genetic analysis of 2009 H1N1 viruses isolated in North America, Europe, and Asia revealed quadruple reassortant swine influenza A viruses that have not been recognized previously in pigs or human.

The virus resulted from the reassortment of North American H3N2 and H1N2 swine viruses (triple reassortment viruses: avian/swine/human with Eurasian swine viruses). Sequence analysis also suggests that PB2 and PA genes originated from American H3N2 avian virus; a PB1 originated from H3N2; HA, NP, and NS genes originated from classical swine virus; and NA and M genes originated from Eurasian swine virus (Fig. 113.1). One of the swine genes of this new virus has been derived from the 1918 human virus, so the strain causing the 2009 pandemic is a fourth generation descendant of the 1918 virus. The 2009 H1N1 viruses are more pathogenic in mammalian models than seasonal H1N1 viruses, showing the ability to replicate and cause appreciable pathology in the lungs of mice, ferrets, and non-human primates. The pathologic changes seen were similar to those found in the lungs of animals infected with the highly pathogenic H5N1 avian influenza virus.

Epidemiology and Impact

Epidemiological data now indicate that 2009 H1N1 influenza virus pandemic started as an outbreak of influenza-like illness in the Mexican town of La Gloria, Veracruse in mid-February 2009. In mid-April, the Center of Disease Control (CDC) identified swine origin H1N1 influenza virus in two specimens, independently collected in southern California. By the end of April, international spread and human-to-human transmission prompted the WHO to increase the pandemic alert from Phase 3 to Phase 4 and shortly after to Phase 5. On June 11, 2009, the WHO raised its pandemic to the highest level, Phase 6, indicating widespread community transmission on at least two continents (Table 113.4). As of December 6, 2009, more than 208 countries and overseas territories/communities have each reported at least one laboratory-confirmed case of pandemic H1N1 influenza, with a total of more than 622,000 laboratory confirmed cases and at least 9,596 deaths. However, the number of cases reported vastly underestimates the real number of cases; the WHO ceased regular reporting of case counts on July 16, 2009, because many countries were having difficulty tracking their numbers, and the WHO judged that their time would be better spent on investigating severe cases and other exceptional events. Most patients in the world with 2009 H1N1 have been teenagers and young adults, with rates of hospitalization highest in very young children. Between 1% and 10% with clinical illness require hospitalization. Overall, 7% to 10% of all hospitalized patients are pregnant.
women in their second or third trimester. Of the hospitalized patients, 10% to 25% have required admission to intensive care, and 2–9% have died. Little is known about the level of pre-existing immunity to the 2009 H1N1 virus. Recent studies suggest that persons under the age of 30 years have little evidence of protective antibodies. However, a portion of older adults have pre-existing cross-reactive antibodies, presumably as a result of exposure to H1N1 strains circulating before 1957.

Transmission of 2009 H1N1 virus from person to person is similar to that of other influenza viruses. The main route of transmission is respiratory through inhalation of large-particle respiratory droplets, and possibly via droplet nuclei. Transmission via large-particle droplets requires close contact because these droplets do not remain suspended in the air and generally travel only short distances (less than 2 m). Contact with contaminated surfaces is another possible source of transmission. All respiratory secretions and bodily fluids (e.g., fomites, diarrheal stool) of infected person should be considered potentially infectious. The secondary attack rates in households were estimated to be 27.3%, and in school settings, an infected school child was estimated to infect 2.4 other children within the school. The estimated incubation period could range from 1 to 7 days, but is most likely 1–4 days. Infected persons can be assumed to be shedding virus from 1 day prior to illness-onset until resolution of symptoms (up to 7 days following illness-onset). Children and immunocompromised or immunosuppressed persons may be contagious for longer periods. The amount of virus shed is greatest during the first 2–3 days of infection and appears to correlate directly with the height of fever. The 2009 pandemic H1N1 virus is expected to come in waves, and the middle of the second
wave is going on. This wave may continue during winter, or there may be a third wave. As of today no increase of severity has been seen, and genetic mutations have been minimal.

**Clinical Features**

The clinical manifestations can vary from asymptomatic infection to serious fatal illness that may include exacerbation of other underlying conditions or severe viral pneumonia with multi-organ failure. The Centers for Disease Control and Prevention (CDC) defines cases as influenza-like illness (ILI), if there is a fever of $>37.8^\circ C$ (>$100^\circ F$) plus cough and/or sore throat in the absence of a known cause other than influenza. In the outbreak of 2009 H1N1 influenza pandemic in New York City, 95% of virologically proven cases satisfied the ILI definition. Fever has been absent in some outpatients and in, up to one in six surviving hospitalized patients. Vomiting and diarrhea have occurred in up to 38% of outpatients in United States. Young children may have atypical influenza illness with the absence of fever and cough.

Among 89 children with confirmed H1N1 who required hospitalization in Birmingham, United Kingdom, the most common symptoms were fever (81%), cough (73%), and diarrhea (62%). Infant may present with fever and lethargy. The CDC case definitions for confirmed, probable, and suspected cases are in Table 113.5.

Three categories of clinical presentations have been seen during the current pandemic:

1. Mild illness is characterized by fever (some patients had no fever), cough, sore throat, diarrhea, myalgias, and headache. Other frequent findings have included chills and malaise. Vomiting and diarrhea have been reported in some patients, but no shortness of breath, dyspnea, or severe dehydration.

2. Progressive illness is characterized by mild illness in addition to signs or symptoms suggesting a progressive illness which include (Table 113.6):
   - Chest pain, tachypnea, or labored breathing in children
   - Hypotension
   - Confusion or altered mental status
   - Severe dehydration or exacerbations of chronic conditions (e.g. asthma, cardiovascular conditions)

3. Severe illness characterized by the following:
   - Profound hypoxemia, abnormal chest radiograph, and mechanical ventilation
   - Encephalitis or encephalopathy
   - Shock, multisystem organ failure
   - Myocarditis and rhabdomyolysis
   - Invasive secondary bacterial infection (e.g. pneumococcal disease)

### Table 113.4

**World Health Organization pandemic levels**

| Phase 1 – No viruses circulating among animals have been reported to cause infections in humans |
| Phase 2 – An animal influenza virus circulating among domesticated or wild animals is known to have caused infection in humans, and is therefore considered a potential pandemic threat |
| Phase 3 – An animal or human-animal influenza reassortant virus has caused sporadic cases or small clusters of disease in people, but has not resulted in human-to-human transmission sufficient to sustain community-level outbreaks. Limited human-to-human transmission may occur when there is close contact between an infected person and an unprotected caregiver, but the virus is not widely transmitted among humans |
| Phase 4 – Verified human-to-human transmission of an animal or human-animal influenza reassortant virus able to cause “community-level outbreaks.” The risk of pandemic is significantly raised |
| Phase 5 – Human-to-human spread of the virus into at least two countries in one WHO region. The declaration of Phase 5 is a strong signal that a pandemic is imminent |
| Phase 6 – The pandemic phase is characterized by community level outbreaks in at least one other country in a different WHO region in addition to the criteria defined in Phase 5. A global pandemic is under way |

### Table 113.5

**CDC: case definition for 2009 H1N1 Influenza virus**

| Confirmed case | An individual with an acute febrile respiratory illness with laboratory confirmed 2009 H1N1 infection by one or more of the following tests: ● Real time reverse-transcription polymerase (rRT-PCR) or ● Viral culture |
| Probable case | An individual with influenza like illness (i.e., an illness with a fever and cough or sore throat ) who is positive for influenza A, but negative for H1 and H3 by rRT-PCR |
| Suspected case | An individual who does not meet the definitions of confirmed or probable pandemic H1N1 influenza A, but has ILI an epidemiologic link (e.g., likely exposure to a confirmed or probable case within the past 7 days) |
Complications

Most patients appear to have mild illness and recover spontaneously. Approximately 2–5% of laboratory-confirmed 2009 A (H1N1) influenza in Canada, and in the United States, as well as 8% in Mexico have required hospitalization. Nearly three quarters of cases in the USA requiring hospitalization, as well as 21 (46%) of 45 fatal cases in Mexico, involved one or more underlying conditions including asthma, diabetes, heart or lung disease, neurologic disease, pregnancy, morbid obesity, autoimmune disorders, and associated immunosuppressive therapies. Forty-five percent of patients admitted to intensive care units in the USA were children under the age of 18 years, and 5% were 65 years of age or older. Surveillance of pediatric deaths reported by CDC indicated that, of 36 children who died, 7 (19%) were aged <5 years, and 24 (67%) had one or more high-risk medical conditions. Twenty-two (92%) of the twenty-four children with high-risk medical condition had neuro-developmental disabilities which included cerebral palsy, developmental delay, autism, congenital neurological disorders, and other central nervous system disorders. Pneumonia is the most common and serious complication of the 2009 H1N1 pandemic influenza. The clinical course of 45 fatal cases in Mexico was characterized by severe pneumonia, hypoxemia with multifocal infiltrates including nodular alveolar, or basilar opacities on chest X-ray, and rapid progression to acute respiratory distress syndrome (ARDS) and renal or multi-organ failure. A similar experience was reported from Canada, Australia, and New Zealand. Some patients who required intensive care required advanced mechanical ventilation with high-frequency oscillatory bi-level ventilation and mean airway pressures of 32–55 cm/H₂O or veno-venous extracorporeal membrane oxygenation (ECMO) support. Bacterial co-infections likely played a role in almost one third of fatal cases of 2009 pandemic influenza A (H1N1) in the USA. The CDC investigators found evidence of concurrent bacterial infection in lung specimens from 22 of 77 patients (29%) with fatal pandemic H1N1 infection. A total of ten cases were co-infections with Streptococcus pneumoniae, six with Streptococcus pyogenes, seven with Staphylococcus aureus, two with Streptococcus mitis, and one with Haemophilus influenzae. Four of the fatal cases involved multiple pathogens. The age of patients ranged from 2 months to 56 years, with a median of 31 years. Among other complications of pandemic H1N1 are acute neurologic syndromes reported in four patients aged 7–17 years who were admitted with signs of ILI, and findings that included seizures or altered mental status in two children, encephalitis in two, and ataxia in one. Three of the four patients had abnormal electroencephalogram (EEG). In all patients, pandemic H1N1 viral RNA was detected in nasopharyngeal specimen, but not in cerebrospinal fluids (CSF). All were recovered without sequelae. The overall case-fatality rate was 0.4% (compared with 2.4% for the 1918–1919 influenza pandemic) based on surveillance data from Mexico and mathematical modeling. There was a documented underlying medical condition in at least 49% of global documented fatal case.

Diagnosis

When influenza viruses are known to be circulating in the community, patients presenting with mild influenza can be diagnosed on clinical and epidemiological grounds alone. All patients should be instructed to return for follow-up should they develop any signs or symptoms of progressive disease (Table 113.6) or fail to improve within 72 h of the onset of symptoms. Under no

| Table 113.6 | Clinical signs indicating rapid progression and need for urgent medical care |
|-------------|--------------------------------------------------------------------------------|
| In adults   | In children                                                                      |
| ● Difficult breathing or shortness of breath | ● Tachypnea or labored breathing |
| ● Pain or pressure in the chest or abdomen    | ● Skin color change, gray or blue |
| ● Episodes of sudden dizziness                 | ● Inadequate intake of oral fluids |
| ● Severe or continuous vomiting                | ● Severe or continuous vomiting |
| ● Influenza-like illness that improves but then returns with fever and cough | ● Influenza-like illness that improves but then returns with fever and cough |
| ● Confusion                                     | ● Irritable or not waking up |

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| ● Confusion                                     | ● Irritable or not waking up |
circumstances should influenza diagnostic tests delay initiation of infection control practices or antiviral treatment, if 2009 H1N1 pandemic disease is suspected. Laboratory testing should be prioritized to include hospitalized patients; patients where a diagnosis of influenza will inform decisions regarding clinical care, infection control or management of close contacts; and patients who have died of an acute illness in which influenza was suspected.

The gold standard for laboratory diagnosis of the 2009 H1N1 influenza is the real-time reverse transcriptase polymerase chain reaction (rRT-PCR) test, using primer and detector sequences tailored to the specific detection of this virus. A number of other diagnostic tests are available to detect the presence of 2009 H1N1 influenza in clinical specimens, but they differ in their sensitivity and specificity. Rapid influenza diagnostic tests (RIDTs) are based on various forms of antigen detection and have high specificity (>95%), but variable sensitivity (10–70%). Preferred respiratory specimens include a nasopharyngeal swab with a synthetic tip (e.g., polyester or dacron), nasal wash, bronchoalveolar lavage (BAL) or endotracheal aspirate. Lower respiratory tract specimens have a higher yield in patients with pneumonia due to viral replication in the lower respiratory tract. Many experts advise the use of a combination of nasopharyngeal swab with oropharyngeal swab. Isolation of H1N1 virus in cell culture or embryonated eggs is a diagnostic for infection but it may not yield timely result for clinical management; in addition, a negative viral culture does not exclude infection. All diagnostic laboratory work on clinical sample from patients, who are suspected cases of influenza H1N1 virus infection, should be done in a biosafety level (BSL) laboratory. Growth of H1N1 virus in cell culture or embryonated eggs should be performed in a BSL-2 laboratory using BSL-3 practices.

Management of 2009 H1N1 Influenza

The majority of individuals infected with the pandemic H1N1 influenza A virus can be treated with simple supportive care at home using antipyretics (e.g., acetaminophen or ibuprofen). Aspirin (acetylsalicylic acid) or aspirin-containing products (e.g., bismuth, subsalicylate-PepoBismo) should not be used in children <18 years due to the risk of Reye’s syndrome.

Empiric antiviral therapy should be started as soon as possible for persons with suspected, probable, or confirmed influenza and for:

1. Illness requiring hospitalization
2. Progressive, severe, or complicated illness regardless of previous health status and/or
3. High risk for severe disease (Table 113.7)

Recent reports have shown that 21–25% of hospitalized patients with confirmed 2009 H1N1 infections have not received antivirals or have delay in receiving antivirals. Among 27 fatal cases in Mexico, the median time from the appearance of symptoms to treatment with antivirals was 8 days (range: 1–26 days).

### Table 113.7

| High risk groups for severe illness |
|------------------------------------|
| 1. Children younger than 2 years old |
| 2. Pregnant woman up to 2 weeks post partum (regardless how the pregnancy ended) |
| 3. Adult, 65 years of age or older |
| 4. Persons younger than 19 years who are receiving long-term aspirin therapy |
| 5. Persons with medical condition including asthma, neurological and neurodevelopmental conditions (including disorder of the brain, spinal cord, peripheral nerve and muscle such as cerebral palsy), chronic obstructive lung disease, cardiac disease, diabetes mellitus, and immunosuppressive conditions (including HIV/AIDS and cancer) |

Antiviral Drugs for Treatment of 2009 H1N1 Influenza

The neuraminidase inhibitors, oseltamivir (Tamiflu<sup>®</sup>) and zanamivir (Relenza<sup>®</sup>) are the drugs of choice for treatment and while the vast majority of pandemic H1N1 circulating strains are sensitive to these medications, all strains tested are resistant to amantadine and rimantadine (Table 113.8).

Oseltamivir and zanamivir are generally well-tolerated. Nausea and vomiting were reported with moderate frequency among adults receiving oseltamivir for treatment (nausea without vomiting, 10%; vomiting 9%). In children treated with oseltamivir, 14% reported vomiting. Oseltamivir suspension is formulated with sorbitol, which may be associated with diarrhea, and abdominal pain in patients who are fructose-intolerant. Zanamivir is formulated for oral inhalation and is contraindicated in patients with asthma or chronic obstructive disease. As of November 18, 2009, 39 isolates (among more than 1,000 tested) of pandemic H1N1 were resistant to oseltamivir. Among
the 32 cases for which detailed information were available, 16 were associated with antiviral prophylaxis, and 3 had no history of exposure to oseltamivir. Resistance was associated with the common H275Y mutation, with retention of zanamivir susceptibility. Antiviral therapy is most effective when started within 48 h after the onset of symptoms; however, evidence suggests that treatment may benefit patients with prolonged or severe illness, even when started more than 48 h after the onset of illness. The recommended duration of treatment is 5 days. Hospitalized patients with severe infection might require longer antiviral courses. Some experts have advocated use of double doses of oseltamivir in critically ill patient, despite lack of published dates about efficacy. Zanamivir-inhaled formulation is not designed to be used in any nebulizer or mechanical ventilator as there is a risk that lactose drug carrier can obstruct ventilator equipment. For patients who are unable to take oral medication or in whom oral medication appears to be ineffective, peramivir, which is an investigational neuraminidase inhibitor formulated for intravenous administration, can be requested from the CDC under Food and Drug Administration (FDA) and emergency use authorization, although studies on efficacy and safety are limited.

Symptomatic patients who have highly suspected or documented oseltamivir resistance should not be treated with peramivir, because strains with the H275Y mutation have demonstrated reduced in vitro susceptibility to peramivir. These patients should be treated with intravenous zanamivir, which is an investigational drug that can be requested from the FDA for compassionate use. The CDC suggests limiting the use of antiviral chemoprophylaxis to specific groups. Antiviral doses recommended for treatment and prophylaxis of 2009 H1N1 influenza in adult and children are listed in Table 113.8. Clinicians should consider empiric treatment with antibacterial drugs if bacterial co-infection is suspected during or after influenza. Antibiotics selection should take into consideration, local data regarding frequency of pathogen causing secondary infection and pattern of drug resistance. When pneumonia is present, treatment with antibiotics should follow evidence-based guidelines for community acquired pneumonia.

The use of corticosteroids for H1N1 influenza is controversial. High-dose systemic steroid are not recommended for use in viral pneumonitis outside clinical trials. However, low-dose steroids may be considered in patient with septic shock who require vasopressors.

### Isolation of the Hospitalized Patient with 2009 H1N1 Infection

CDC recommends standard, droplet, and contact precautions for care of patients with suspected or confirmed 2009 H1N1 influenza infection. Health care workers should use

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**Table 113.8**

Antiviral treatment and chemoprophylaxis of 2009 H1N1 influenza

| Medication/age groups | Treatment (5 days) | Chemoprophylaxis (10 days) |
|-----------------------|-------------------|--------------------------|
| Oseltamivir          |                   |                          |
| Adults               | 75 mg twice daily | 75 mg once per day       |
| Children (age ≥12 months), weight | | |
| ≤15 kg               | 30 mg twice daily | 30 mg once per day       |
| 15–23 kg             | 45 mg twice daily | 30 mg once per day       |
| 24–40 kg             | 60 mg twice daily | 60 mg once per day       |
| >40 kg               | 75 mg twice daily | 75 mg once per day       |
| Children (age 3 months to <12 months) | 3 mg/kg/dose twice daily | 3 mg/kg/dose once per day |
| Children (0–<3 months) | 3 mg/kg/dose twice daily | Not recommended, unless situation judged critical (limited data) |
| Zanamivir            |                   |                          |
| Adults               | Two 5-mg inhalations (10 mg total) twice daily | Two 5-mg inhalations (10 mg total) daily |
| Children             |                   |                          |
| ≥7 years or older for treatment | Two 5-mg inhalations (10 mg total) twice daily | Two 5-mg inhalations (10 mg total) daily |
| ≥5 years for chemoprophylaxis |                   |                          |
surgical masks for routine non-aerosolizing patient care and N95-respirators for aerosol-generating procedures. Isolation precautions should continue for 7 days after illness-onset or until 24 h after the resolution of fever and respiratory symptoms. A longer period of isolation may be considered in the case of young children and severely immunocompromised patients.

2009 H1N1 Vaccine

An effective vaccine is the best tool to prevent the unpredictable spread of the current influenza pandemic. The 2009 H1N1 virus has the potential to cause severe disease, deaths, and potential socioeconomic dysfunction, and mathematical modeling suggests that the effect of the virus can be reduced by immunization. Two types of H1N1 vaccines have been prepared and have received approval from the FDA or the European Medicine Agency (EMEA) for use in the prevention of influenza caused by the 2009 pandemic influenza A (H1N1) virus. Both “adjuvanted” and “unadjuvanted” vaccine formulations are available. An adjuvant is a substance that boosts the immune response. It is made up of naturally occurring oil, water, and vitamin E. The “unadjuvanted” vaccine does not include this material. Vaccination campaigns are currently underway to protect populations from pandemic H1N1. Preliminary data indicate that both vaccines are safe and immunogenic. The Advisory Committee on Immunization Practice (ACIP) recommends that vaccination efforts should focus initially on persons in five target groups at high risk for influenza related complications (Table 113.9).

On November 19, 2009, the WHO estimated that around 80 million doses of pandemic vaccine had been distributed globally and around 65 million people had been vaccinated. The side-effect profile of the H1N1 vaccine (“adjuvanted” and “unadjuvanted”), particularly the frequency and severity of solicited adverse events, is consistent with previous experience from seasonal influenza vaccine. To date, less than ten suspected cases of Guillain-Barre syndrome have been reported in people who have received vaccines. These numbers are in line with normal background rates of this illness as recently reported. All such cases are being investigated to determine whether these are randomly occurring events or whether they might be associated with vaccination. WHO has received no reports of fatal outcome or confirmed cases of Guillain-Barre syndrome, since the H1N1 vaccination campaigns began. All cases have recovered. Intense active monitoring for rare adverse reactions of H1N1 vaccine is ongoing, but all data compiled to date indicate that pandemic H1N1 vaccines match the excellent safety profile of the seasonal influenza vaccines which has been used for more than 60 years.

### Table 113.9

| ACIP priority target groups for H1N1 influenza vaccine |
|-------------------------------------------------------|
| ● Pregnant woman                                       |
| ● Household contact and caregivers for infant younger than 6 months of age |
| ● All people from 6 months through 24 years of age     |
| ● Persons aged 25 through 64 years who have health conditions associated with high risk of medical complications from influenza (table) |

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