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Chapter 21

New Emerging Viruses

Chapter Outline

21.1 Epidemiology 289
21.2 Newly Emerging Viruses 290
  21.2.1 Ebola Virus 291
  21.2.2 West Nile Virus 291
  21.2.3 Sin Nombre Virus 293
  21.2.4 Nipah Virus 294
  21.2.5 SARS-Coronavirus (SARS) 294
21.2.6 MERS-Coronavirus 296
21.2.7 Why Do New Viruses Emerge? 297
21.3 Reemerging Viruses 297
21.4 New Epidemic of Existing Viruses 299
21.5 Perspectives 301
21.6 Summary 301

Study Questions 302

Newly emerging viruses such as the Ebola virus, severe acute respiratory syndrome (SARS)-, Middle East respiratory syndrome (MERS)-coronavirus, and the avian influenza virus are serious threats to public health and have become a global concern. In this chapter, we will learn the basic terminology of the epidemiology of infection and the outbreaks caused by newly emerging viruses.

21.1 EPIDEMIOLOGY

To define the causes and the patterns of an infection, epidemiologic studies are conducted. Epidemiology\(^1\) is the study of patterns, causes, and effects of disease conditions in defined populations. Viral infections can be classified depending on their epidemiologic features (Table 21.1). Epidemic infection (or epidemics\(^2\)) is a type of infection in which the infection is extensive and not limited to a certain region but only lasts transiently (Fig. 21.1). The seasonal flu is an example of an epidemic infection. In the case of the seasonal flu, although the affected region is extensive, the epidemics in different regions are linked because the same strain of influenza virus is often responsible for a season. Endemic infection is a type of infection in which the infection persists for a longer period of time in a certain region but the infection is typically limited to only a subset of the population. Hepatitis B viral infection in China and in Korea is an example of endemic infection. A subset of the population (~4–8%) is chronically infected. Sporadic infection is a type of infection in which the infection is limited to the affected persons and regions. It lasts transiently. In this case, there are no links between outbreaks\(^3\) occurring in different regions. Pandemics refer to epidemics occurring across multiple continents.

Surveillance to monitor the emergence of new viruses and their transmission is an important goal of public health authorities. In particular, the explosive expansion of international trade and travel has made it difficult to control viral transmission between countries and continents. Quarantine\(^4\) at airports and seaports has become increasingly important for surveillance (Fig. 21.2).

1. Epidemiology It is derived from Greek ἐπί, meaning “upon,” δῆμος, meaning “people,” and λόγος, meaning “study.”
2. Epidemics It refers to the rapid spread of infectious disease to a large number of people in a given population within a short period of time. The period is usually 2 weeks or less.
3. Outbreak In epidemiology, an outbreak is an occurrence of disease greater than expected at a particular time and place. Outbreaks may also refer to epidemics which affect a particular region in a country or a group of countries.
4. Quarantine Quarantine is used to separate and restrict the movement of people who may have been exposed to a communicable disease in order to monitor their health. The word comes from the Italian (17th-century Venetian) word “quarantana,” which is the number of days ships were required to be isolated (quarantined) before coming ashore during the black death.
21.2 NEWLY EMERGING VIRUSES

Since the 1970s, newly emerging viruses of unknown origins have been continuously discovered (Fig. 21.3). The first outbreak of the Ebola virus occurred in 1976 in Zaire and Sudan. AIDS was first described as acquired immunodeficiency syndrome among homosexual males in 1981 and its culprit was soon identified in 1983 as HIV (see Box 17.3). SARS, a respiratory disease caused by SARS-CoV, was first reported in Hong Kong in 2003. More recently, a novel coronavirus, Middle East respiratory syndrome-coronavirus (MERS-CoV), was discovered in 2012 in Saudi Arabia. Newly emerging

### TABLE 21.1 Epidemiologic Patterns of Viral Transmission

| Infection Pattern | Scale in Population | Region    | Linked | Period     | Persistency |
|-------------------|---------------------|-----------|--------|------------|-------------|
| Endemic          | Small to large       | Local     | Yes    | Long (>yr) | Yes         |
| Epidemic         | Small to large       | Local     | Yes    | Short (<yr)| No          |
| Sporadic         | Small               | Multilocal| No     | Short (<yr)| No          |
| Pandemic         | Large               | Multicontinents | Yes | Short (<yr) | No          |

**FIGURE 21.1** Epidemic versus endemic infection. Infection period and the infection scale are depicted to contrast epidemic versus endemic infection. A virus infection pattern can be changed from epidemic to endemic. For instance, WNV infection is now considered to be endemic in the United States (see Fig. 21.8).

**FIGURE 21.2** Quarantine at the airport. A quarantine official (left) checks people arriving at South Korea’s Incheon International Airport for signs of fever during MERS outbreak in 2015.
viruses, such as the Ebola virus, the WNV, Nipah virus, and SARS-CoV, will be described in this chapter. HIV will be covered in a separate chapter due to its huge impact on the global community (see chapter: HIV and AIDS).

21.2.1 Ebola Virus

Since the first Ebola outbreak in 1976, Ebola outbreaks have continued to be reported. The fatality rate of Ebola fever is extremely high (~90%). Fortunately, Ebola outbreaks have been mainly restricted to Africa. The potential for Ebola to become a widespread epidemic is low due to the high case-fatality rate and the rapid demise of patients. The Ebola virus came up in the Hollywood movie, “Outbreak,” starring Dustin Hoffman. While a monkey served as the reservoir of the virus in the movie, in reality, bats are the reservoir (Fig. 21.4). Bats and primates are sold in markets and consumed as bush meat in some areas of Africa. In a viral perspective, the host change from bats to humans is a bit challenging as it imposes a selective pressure for mutations. It is thought a variant highly virulent in humans is generated during the adaptation of the virus in a new host. The Ebola virus is a good example of a new emerging virus which originates from the rainforest in Africa.

The recent 2013–14 Ebola outbreak in Western Africa set a record death toll (ie, 11,295 deaths on July 31, 2015) (Fig. 21.5). It has been the most widespread Ebola epidemic in history. It began in Guinea in December 2013 and then spread to Liberia and Sierra Leone. International organizations from around the world have responded to help stop the ongoing Ebola epidemic in West Africa. In July 2014, the World Health Organization (WHO) declared the outbreak as an international public health emergency. In September 2014, the United Nations Security Council declared the Ebola outbreak in the West African region “a threat to international peace and security” and unanimously adopted a resolution urging its member states to provide more resources to fight the outbreak. As of August 2015, the outbreak is almost contained. The reason why the 2013–14 Ebola outbreak was widespread remains debatable. There is currently no treatment for the Ebola virus. More recently, the WHO announced “an extremely promising development” in the search for an effective vaccine for Ebola disease.

21.2.2 West Nile Virus

The WNV\(^5\) epidemic in North America is a good example of the spread of a mosquito-borne zoonotic virus due to climate change. WNV is a member of the family Flaviviridae and is transmitted via mosquito (Fig. 21.6). Thus, it is also known as an arbovirus.\(^6\) It was first identified in the West Nile subregion in the East African nation of Uganda in 1937.

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\(^5\) West Nile Virus (WNV) A mosquito-borne zoonotic arbovirus belonging to the genus *Flavivirus* in the family Flaviviridae.

\(^6\) Arbovirus Arbovirus is a descriptive term applied to hundreds of predominantly RNA viruses that are transmitted by arthropods, notably mosquitoes and ticks. The word *arbovirus* is an acronym (Arthropod-Borne virus).
FIGURE 21.4  Ebola virus transmission to humans. The Ebola virus is transmitted by bodily fluids (blood, secretions, etc.) of infected animals such as chimpanzees, gorillas, and fruit bats can be also transmitted from human to human.

FIGURE 21.5  Ebola outbreaks in Africa. (A) Ebola outbreak casualty. The damage by the past Ebola outbreak was limited to less than 500 casualties per outbreak. By contrast, the 2013–14 Western Africa Ebola outbreak caused 27,872 cases and 11,295 deaths, as of July 2015. The magnitude of casualty was at an unprecedented level. The mortality rate was about 40%. (B) Regions affected by the Ebola outbreak. Since the first Ebola outbreak occurred in 1976 in Zaire, Ebola virus outbreaks were confined to Central Africa including Uganda, Zaire, and Congo. By contrast, the 2013–14 Ebola outbreak differs with respect to the region affected. The outbreak occurred in Western Africa including Guinea, Liberia, and Sierra Leone.
Approximately 80% of WNV infections in humans are subclinical, meaning that no symptoms are associated with the infection. For the rest, symptoms include fever, headache, fatigue, and rash. Less than 1% of the cases are severe and result in neurological disease.

The WNV has typically been confined to temperate and tropical regions. Prior to the mid-1990s, WNV disease occurred only sporadically and was considered a minor risk for humans. The WNV has now spread globally. The first case in the Northern Hemisphere was identified in New York City in 1999. Over the next 5 years the virus spread across the continental United States and north into Canada (Fig. 21.7). The arrival of an outsider in New York City in 1999 drew the media’s attention. Heavy media coverage on the epidemic caused panic among residents. The WNV is now considered to be an endemic pathogen in the United States. In 2012 the United States experienced one of the worst epidemics, in which WNV killed 286 people.

The WNV epidemic in the United States warned of the risk of mosquito-borne zoonotic virus. It is believed that global warming is attributed to the spread of tropical mosquito-borne zoonotic viruses to the Northern Hemisphere (Table 21.2).

21.2.3 Sin Nombre Virus

A mystery respiratory illness causing deaths among young Navajo was first reported in 1993 in the “Four Corners” region of the western United States (Fig. 21.8). Clinical resemblance to hantavirus infection, which occurred during the Korean war (1950–53), led investigators to look for the culprit in rodents. Until then no known cases of hantavirus infection had ever been reported in the United States. The culprit was a deer mouse discovered near the home of one of the initial patients. Not surprisingly, newly discovered Sin Nombre virus (SNV) is related to the hantavirus. Hantavirus was discovered by Ho-Wang Lee in Korea in 1776 as the etiological agent responsible for the Korean hemorrhagic fever outbreak which occurred among American and Korean soldiers during the Korean War. Patients with hantavirus pulmonary syndrome (HPS) had mild flu-like symptoms such as malaise, headache, cough, fever, with a sudden onset of pulmonary edema, and finally death. In this epidemic, 24 cases were reported with a 50% mortality rate. SNV belongs to the Hantavirus genus of family Bunyaviridae (see Table 16.4). SNV infection occurs wherever its reservoir rodent carrier (the deer mouse) is found. This includes the entire populated area of North America except for the far southeastern region. SNV can be contracted through the inhalation of virus-contaminated deer mouse excretion.

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7. Zoonotic viruses A virus transmitted between species (sometimes by a vector) from animals to humans.
8. Sin Nombre virus (in Spanish, “the nameless virus”) (SNV) Its original name was “Four Corners virus.” The name was changed after local residents raised objections.
The fatality rate of SNV-induced HPS in the United States was reported to be about 66.7%. However, since that time the fatality rate has steadily declined as more mild cases have come to be recognized.

21.2.4 Nipah Virus

The Nipah virus was first identified in April 1999 on a pig farm in peninsular Malaysia when it caused an outbreak of neurological and respiratory disease. The outbreak resulted in 257 human cases, 105 human deaths, and the culling of 1 million pigs (Fig. 21.9). Symptoms of infection from the Malaysian outbreak were primarily encephalitic in humans and respiratory in pigs. Respiratory illness in humans has been seen in later outbreaks, increasing the likelihood of human-to-human transmission and indicating the existence of more dangerous strains of the virus. Based on seroprevalence data and the data from viral isolations, the primary reservoir for Nipah virus was identified as Pteropid fruit bats. The transmission of Nipah virus from bats to pigs is thought to be due to an increasing overlap between bat habitats and piggeries in peninsular Malaysia.

A related Hendra virus was discovered in September 1994 when it caused the deaths of 13 horses and a trainer at a training complex in Hendra, a suburb of Brisbane in Queensland Australia. Nipah virus, along with Hendra virus, belongs to the genus Henipavirus belonging in the family Paramyxoviridae (see Table 16.1).

21.2.5 SARS-Coronavirus (SARS)

SARS is a viral respiratory disease of zoonotic origin caused by the SARS-CoV. Between November 2002 and July 2003, an outbreak of SARS in southern China led to 8273 cases and 775 deaths in multiple countries. The majority of cases were in Hong Kong (9.6% fatality rate) according to the WHO. Within weeks, SARS spread from Hong Kong to

9. The name “Nipah” refers to the place, Kampung Baru Sungai Nipah in Negeri Sembilan State, Malaysia, the source of the human case from which Nipah virus was first isolated.
| Family       | Zoonotic Virus                        | Outbreak (Reported Year) | Frequency | Source of Human Infection | Reservoir Host | Disease                                | Human Cases (Fatality), Region |
|--------------|--------------------------------------|--------------------------|-----------|---------------------------|----------------|----------------------------------------|-------------------------------|
| Influenza virus | Avian Influenza H5N1                | Vietnam (2003−)          | Rare      | Chicken                   | Wild birds     | Respiratory disease                    | ~566 (~60%) in SE Asia        |
| Influenza virus | Avian Influenza H7N9                | China (2013)             | Rare      | Chicken                   | Wild birds     | Respiratory disease                    | ~127 (~20%) in China          |
| Filovirus    | Ebola virus                         | Africa (1976−)           | Rare      | Primates                  | Bat            | Hemorrhagic fever                      | >800 (~90%) in Africa         |
| Flavivirus   | Dengue virus                         | Asia, Africa, S. America (1953−) | Endemic | Mosquito                  | Monkeys        | Hemorrhagic fever                      | 50−100 million/yr (1−5%) in Southeast Asia |
|              | Japanese encephalitis virus (JEV)   | Asia (1935−)             | Endemic  | Mosquito                  | Birds, bats    | Encephalitis                           | 30,000–50,000/yr in Asia (0.3–60%); ~10,000 death/yr |
|              | West Nile virus                      | Uganda (1937−)           | Endemic  | Mosquito                  | Birds          | Encephalitis                           | >10,000 (~0.7%) in the United States, since 1999 |
| Bunyavirus   | Hantaan virus                        | Korea (1951−)            | Common    | Mouse                     | Wild mouse     | Hemorrhagic fever                      | ~200,000/yr, (~15%) in Asia   |
|              | Sin Nombre virus                    | United States (1993)     | Rare      | Mouse                     | Wild mouse     | Hantavirus pulmonary syndrome (HPS)    | ~12 (~60%) in the four corners region of the United States |
| Coronaviruses | SARS-CoV*                           | China (2002)             | Very rare | Bats                      | Bats           | Severe acute respiratory syndrome (SARS) | 8273 (775 death) (9.6%) in China, Hong Kong, etc. |
|              | MERS-CoV*                           | Saudi Arabia (2012−)     | Very rare | Bats                      | Camel          | SARS-like                              | 1084 cases and 439 death (40%) in Middle East and others |
| Paramyxovirus | Hendra virus                        | Australia (1994−)        | Very rare | Horses                    | Bats           | Hemorrhage in lung                     | ~76 horse died (~60%), since 1994 |
|              | Nipah virus                         | Malaysia (1999−)         | Rare      | Pigs                      | Bats           | Encephalitis                           | ~257 (~40%) in 1999          |
| Rhabdovirus  | Rabies virus                        | Europe (18th)            | Endemic  | Animals (dog)             | Wild animals (bats, racoon, etc.) | Paralysis and hydrophobia           | ~55,000 (>90%) death/yr, worldwide (Asia and Africa) |
infect individuals in 37 countries in early 2003 (Fig. 21.10). It was eradicated by January of the following year. Phylogenetic analysis of these viruses indicated a high probability SARS-CoV originated in bats and spread to humans either directly or indirectly through animals held in Chinese markets.

### 21.2.6 MERS-Coronavirus

Another novel human coronavirus, MERS-CoV was isolated from a patient with acute pneumonia in 2012 in Saudi Arabia. As of March 2015, MERS-CoV infection has led to 1084 cases and 439 deaths reported in multiple countries.
The fatality of MERS-CoV is considerably higher than SARS-CoV, approaching 30%. MERS-CoV may be originating from bats due to its high sequence homology to the bat virus. It is speculated the virus spreads from bats to human via dromedary camel (Fig. 21.11). Almost all cases have been linked to Saudi Arabia. Although human-to-human transmission seems to be inefficient, it has been shown to spread between people who are in close contact. As of June 2015, MERS-CoV cases have been reported in 23 countries including Saudi Arabia, Malaysia, Jordan, Qatar, Egypt, the United States, South Korea, and China. Most importantly, MERS-CoV transmission is not yet under control. A recent MERS-CoV outbreak in South Korea started in May 2015 from a single patient who visited Arab countries. It has been the largest outbreak outside of the Middle Eastern region leading to 182 reported cases including 33 deaths (case-fatality rate 16%) as of June 2, 2015.

21.2.7 Why Do New Viruses Emerge?

Why are new human pathogenic viruses continually emerging? In most cases, outbreaks have been known to occur in tropical regions in which there were no human inhabitants. An increase in contact with wild animals, due to the expansion of the human habitat, is believed to be the main cause for the emergence of new viruses. Changes in the environment such as rainforest developments have led to an increase in contact between wild animals and humans. As a result, viruses which only existed in rainforests are able to be transmitted to a new human host. Climate changes such as global warming are another cause for the emergence of new viruses. This is demonstrated by the WNV outbreaks in the Northern Hemisphere. Many of these newly emerging viruses are zoonotic viruses. In particular, bats serve as reservoirs to many newly emerging viruses. Bats are natural reservoirs for the Ebola virus, SARS-CoV, and the Nipah virus. What makes bats so special? Bats are unique because they are mammals that can fly. As mammals, they are a closer relation to humans than to birds. In addition, it is speculated that the immunity of bats is conspicuously tolerable to viruses. Many types of viruses found in bats (ie, virome\textsuperscript{10}) are currently being analyzed with the implementation of next generation sequencing technology. The bat virome is expected to provide insight on newly emerging viruses that have yet been discovered.

21.3 REEMERGING VIRUSES

Besides newly emerging viruses, the variants of existing viruses also cause serious epidemics. These viruses have infected humans in the past. However, they continue to appear in drug-resistant forms or reappear after apparent control
or elimination. These variant viruses are termed “reemerging viruses.” Influenza virus represents the best example. Three distinct kinds of influenza virus variants are responsible for flu epidemics: the seasonal flu, the pandemic flu, and the avian flu. Since the mechanisms underlying seasonal and pandemic flu emergence have been described in chapter “Influenza Viruses,” these two kinds of variants will be described briefly. On the other hand, the avian influenza virus will be described with an emphasis on the mechanism of zoonotic infection.

Seasonal Flu: The seasonal flu, as its name implies, is a flu epidemic that occurs yearly. Why are influenza viruses able to infect people who have previously been infected in the past? Multiple reinfection capabilities represent a salient feature of influenza virus infection. The reason for this is because variants with distinct antigenicity emerge each year. This is known as “antigenic drift” (see Fig. 15.15). The antibodies circulating in the person previously infected are unable to neutralize a new seasonal strain.

Pandemic Flu: The pandemic flu which occurred in the 20th century has already been described (see Box 15.2). Here, specific features of the 2009 H1N1 influenza pandemic are described. The epidemic started in Mexico in April of 2009. It rapidly spread globally, resulting in up to 300 million infections and over 16,000 deaths. During the pandemic, many international meetings were canceled because many people were afraid to travel abroad without proper protection. The culprit was quickly identified to be a swine influenza virus which first infected a boy living near a pig farm in Mexico. The lack of an appropriate flu vaccine during the pandemic frightened the public. An antiviral drug, Tamiflu was the only protective means until a vaccine became available (see Box 15.1). The 2009 H1N1 pandemic was notable. First, it was the first swine influenza virus that caused a pandemic. Second, it was not the typical double reassortment. It was an unprecedented triple reassortment (Fig. 21.12).
H5N1 Avian Flu: It was established that avian flu virus does not normally infect humans. However, transmission of the avian virus to humans has occurred, although rarely, in the past decade. Thus, the avian influenza virus has become a global concern as a potential pandemic threat. Since the first H5N1 outbreak occurred in 1987, the highly pathogenic influenza subtype has killed millions of poultry in many countries throughout Asia, Europe, and Africa (Fig. 21.13). Because a significant species barrier exists between birds and humans, the virus does not easily cross species. Since 2003 human cases of H5N1 have been reported in 15 countries: 359 people have died from H5N1 in 12 countries (including China, Cambodia, and Vietnam) as of August 10, 2012. The mortality rate for humans with H5N1 is 60%. One of the growing concerns is that it could be mutated further and spread via human-to-human infection.

Why is avian H5N1 often fatal? The short answer is it has to do with different sites of infection of the seasonal H1N1 virus versus the avian H5N1 virus (Fig. 21.14). HA of human influenza virus prefers to bind the sialic acid linked to glycans via $\alpha$-2,6 linkage typically found in glycans distributed in the upper respiratory tract. In contrast, HA of the avian virus prefers to bind the sialic acid linked to glycans via $\alpha$-2,3 linkage typically found in glycans distributed in the lower respiratory tract (see Fig. 15.5). The lack of $\alpha$-2,3 linked glycans in the upper respiratory tract serves as a barrier to prevent avian flu virus transmission to humans.

H7N9 Avian Flu: Influenza virus subtype H7N9 is a novel avian influenza virus first reported to have infected humans in 2013 in China. Most of the reported cases of human infection have resulted in severe respiratory illness. As of the end of June 2013, 133 cases had been reported and 43 deaths (32% mortality). The number of cases detected after April 2013 fell abruptly. The decrease in the number of new human H7N9 cases may have resulted from the containment measures taken by Chinese authorities (closing live bird markets), a change in seasons, or possibly a combination of both factors.

21.4 NEW EPIDEMIC OF EXISTING VIRUSES

Besides new emerging viruses, new epidemics caused by existing viruses represent serious public health concerns. The measles virus is a good example of this in the Western Hemisphere.
FIGURE 21.14 Infection pathology of human influenza virus versus avian influenza virus. Seasonal H1N1 influenza virus infects the upper respiratory tract and is easily spread but, rarely fatal. In contrast, avian H5N1 influenza virus infects the lower respiratory tract, spreads slowly, and is often fatal. The affected area is colored in red.

FIGURE 21.13 Geographical distribution of H5N1 avian influenza virus. Regions affected by H5N1 influenza virus in poultry and wild birds from 2003 to 2007 are indicated. About 360 human casualties occurred in Southeast Asian countries including China, Cambodia, and Vietnam.
Measles Virus: Measles is caused by measles virus, which belongs to the family Paramyxoviridae (see chapter: Other Negative-Strand RNA Viruses). Live vaccines, first developed in 1961, effectively prevent youngsters from infection. Measles outbreaks continue to occur in the 21st century. Although an effective measles vaccine is available, a controversy regarding the popular MMR vaccine\textsuperscript{11} formulation in the late 1990s led to a reduction of vaccinations in some countries. This disrupted efforts toward the eradication of measles. After the MMR vaccine controversy began, MMR vaccination compliance dropped sharply in the United Kingdom from 92\% in 1996 to 84\% in 2002 (Fig. 21.15). After the vaccination rates dropped the incidence of two out of the three diseases increased greatly in the United Kingdom. In 2008, for the first time in 14 years, measles was declared endemic in the United Kingdom. The disease was sustained within the population. This was caused by the preceding decade’s low MMR vaccination rates which created a population of susceptible children able to spread the disease.

21.5 PERSPECTIVES

The emergence of new infectious diseases has been recognized in human history well before the discovery of causative infectious agents. Despite extraordinary advances in the development of countermeasures (diagnostics, therapeutics, and vaccines), the ease of world travel and an increase in global interdependence has added layers of complexity to containing these infectious diseases which could affect not only the health but the economic stability of societies. Surveillance such as quarantine at the airport and seaport locations has become critically important. In particular, during an epidemic, special attention should be paid to contain airborne viruses such as the influenza virus and SARS-CoV. These viruses can spread rapidly to other continents via air travel. Countermeasures to control these emerging viruses should be made available in preparation for future pandemics. Recent Zika virus\textsuperscript{12} outbreak started in May 2015 in Brazil reminded us the importance of mosquito-borne flaviviruses (see Box 12.1).

21.6 SUMMARY

- **Newly emerging viruses:** Increased contact with animals, primarily due to the expansion of the human habitat, is the cause for the emergence of new viruses. Newly emerging viruses include HIV, Ebola virus, SARS-CoV, and MERS-CoV.
- **Reemerging viruses:** Besides newly emerging viruses, the variants of existing viruses also cause serious epidemics. Influenza virus represents the best example.
- **New epidemics of old viruses:** New epidemics caused by old viruses represent serious public health concerns. The measles outbreak in the Western Hemisphere is a good example of this.

\textsuperscript{11} MMR vaccine MMR vaccine is an immunization against measles, mumps, and rubella. It is a mixture of live attenuated viruses of the three diseases, administered via injection.

\textsuperscript{12} Zika virus A mosquito-borne flavivirus that was first discovered in 1947 in Zika forest in Uganda.
STUDY QUESTIONS

21.1 Describe three newly emerging viruses since the start of the 21st century and state their cause of emergence.

21.2 List an example of the viral outbreaks that occurred with the following epidemiologic change during the 20th century and state the reason for the change (1) epidemic to pandemic, (2) epidemic to endemic and (3) endemic to sporadic.

SUGGESTED READING

Chan, J.F., To, K.K., Tse, H., Jin, D.Y., Yuen, K.Y., 2013. Interspecies transmission and emergence of novel viruses: lessons from bats and birds. Trends Microbiol. 21 (10), 544–555.

Feldmann, H., 2014. Ebola—a growing threat? N. Engl. J. Med. 371, 1375–1378.

Knipe, D.M., Whelan, S.P., 2015. Rethinking the response to emerging microbes: vaccines and therapeutics in the Ebola Era—a conference at harvard medical school. J. Virol. 89, 7446–7448.

Mokili, J.L., Rohwer, F., Dutilh, B.E., 2012. Metagenomics and future perspectives in virus discovery. Curr. Opin. Virol. 2 (1), 63–77.

Wang, T.T., Palese, P., 2009. Unraveling the mystery of swine influenza virus. Cell. 137 (6), 983–985.

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- Xu, R., Ekiert, D.C., Krause, J.C., Hai, R., Crowe Jr., J.E., Wilson, I.A. 2010. Structural basis of preexisting immunity to the 2009 H1N1 pandemic influenza virus. Science 328 (5976), 357–360.

Highlight: The 2009 H1N1 swine flu is the first influenza pandemic in decades. Interestingly, the 2009 pandemic largely spared the elderly. This structure paper reported the hemagglutinin antigenic structure of the 2009 H1N1 flu virus is extremely similar to that of the 1918 H1N1 Spanish flu virus. This revealed conservation of the epitope in both pandemic viruses which are separated by 91 years. Antigenic similarities between two pandemic viruses provide an explanation of the age-related immunity against the 2009 H1N1 flu virus.