4 The Nature of Plagues 2013–14

A Year of Living Dangerously

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The 12 months from June 2013 to May 2014 were, in many ways, typical in the emerging infectious disease events that occurred. There were no huge shocks, no massive outbreaks nor new pandemics, but every month there were important events and together the year's events form a good illustration of what is a 'normal' rhythm of events for emerging infectious diseases. However, after May 2014 the Ebola epidemic in West Africa (described, in its infancy, under 'March' in this chapter) rapidly expanded to become a very large epidemic, illustrating how quickly small outbreaks can become very large problems given circumstances that favour human to human transmission and rapid spread.

Whilst many people think of 'emerging infections' as only the brand new infections like SARS and HIV, the definition of emerging infections is broader and includes five types of infections that are in some sense 'new'. Table 4.1 describes those five types and gives examples of each from the past.

In England, Public Health England (an agency of the Department of Health) routinely gathers up evidence about new infectious disease both nationally and internationally. This 'horizon scanning' activity is an important part of identifying new infectious hazards that may pose a risk to public health. Each month Public Health England, along with other government bodies, publishes a two-page summary of notable events of public health significance.[1] These summaries are widely circulated in government and academia and are publically available. They form both an excellent warning of current events and a record of how events unfold over months and years.

In this article I have picked one event from each of the past twelve months to illustrate the 'normal' rhythm of incidents. Those events have been chosen to illustrate the five types of emerging infectious disease events. They include the three events of 2013–14 that are most likely to

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Table 4.1 *Five types of emerging infectious disease events.*

Type of event	Historical example
A novel infectious pathogen never previously seen or not previously seen in man	HIV (1983) and SARS (2002)
A pathogen spreading into new geographical areas	West Nile Virus spreads to N. America (1999)
The re-emergence of an infectious agent that was previously being brought under control	Tuberculosis (ongoing)
Newly evolved variants of known infections	Influenza and drug-resistant malaria (ongoing)
A pathogen newly associated with a known disease	*Helicobacter pylori* and stomach ulcers (1983)

trigger substantial, global problems in the future: the ongoing MERS-coronavirus outbreak in the Middle East (July 2013), the ongoing zoonotic cases of Avian Influenza in China (February 2014) and the re-emergence of Polio in early 2014 (May 2014). Despite the ongoing fears about a devastating influenza pandemic, the biggest realised threat from emerging infections continues to be the evolution of antimicrobial resistance. This is a slow, chronic problem that is happening everywhere all the time and therefore never triggers a single 'event'. However, during these twelve months WHO published its first global report on surveillance for antimicrobial resistance.[2] The findings from this report are described here under April 2014 in recognition of the importance of antimicrobial resistance as a form of emerging infection.

The article commences with a map showing where the twelve incidents occurred. Each incident is then described in turn before the article ends with a discussion of what we can learn from studying these dozen emerging infectious disease events (see Figure 4.1).

June 2013: a Novel Cyclovirus

The year in question kicked off with the discovery of a new virus: found in the cerebrospinal fluid of twenty-six patients with acute central nervous

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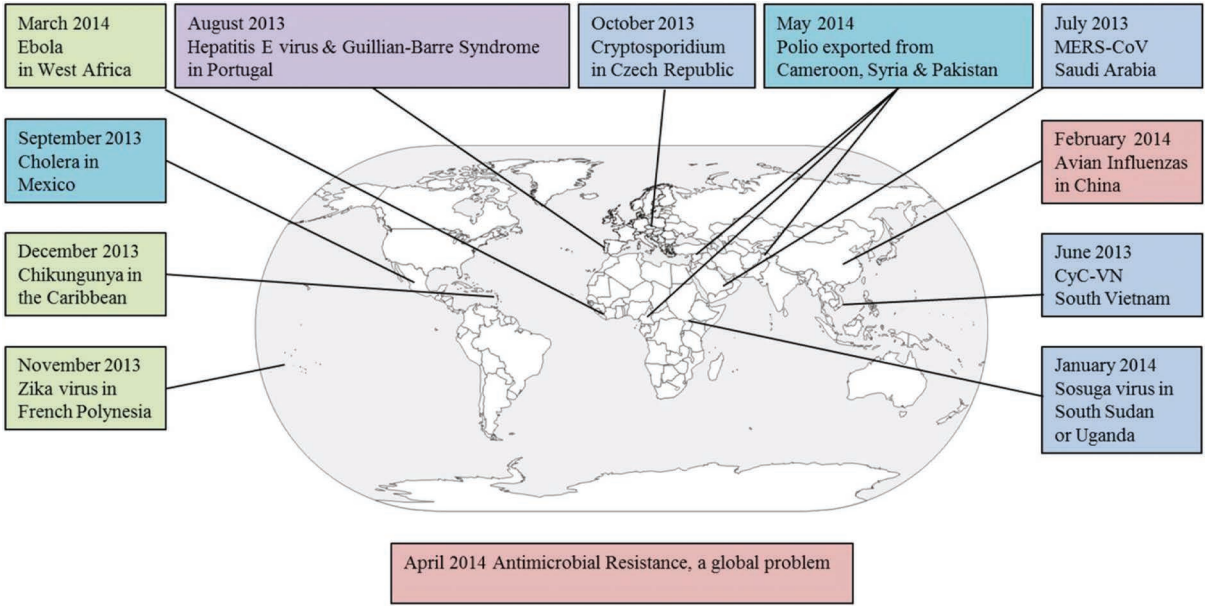

FIGURE 4.1 Twelve emerging infectious disease events around the world: June 2013–May 2014. The colour coding follows the same scheme as Table 4.1. In blue are the novel infections, in green infections spreading to new geographical areas, turquoise denotes a re-emergence event, pink a newly evolved variant of a known infection and violet a new association between a known infection and a known disease.

system infections from Southern and Central Vietnam.[3] This new virus belongs to a family of viruses (the Cycloviruses) that infect many species: genomes have been detected in samples from humans, a range of other vertebrates and in insects.[4]

The new findings from Vietnam were interesting because they raised the possibility that this new virus was a zoonotic cause of acute central nervous system infections. Acute infections of the central nervous system are a substantial cause of morbidity and mortality but in the majority of cases it is not possible to identify the causative agent. Finding novel pathogens that cause such diseases is therefore important. The novel cyclovirus (named CyC-VN) was present in the cerebrospinal fluid of 4 per cent of patients with acute central nervous system infections whilst absent in the cerebrospinal fluid of control patients with non-infectious neurological disorders. It was also present in the faeces of healthy children, pigs and poultry from the same regions of Vietnam. However, no definitive causal link was claimed and the European Centre for Disease Prevention and Control warned that 'increased sensitivity may on occasion lead to spurious associations'[4] and that further studies were warranted to assess the risk posed by the newly identified virus (see Table 4.2). A follow-up study published six months later found only limited geographic distribution,[5] illustrating very clearly that sometimes what appears to be an exciting new finding is only of local significance.

It is not yet clear if CyC-VNvirus is causing disease in South and Central Vietnam, or is just associated with it. What is clear is that modern genomic techniques now allow the identification of infectious agents without the need to grow them in laboratory culture. These metagenomic techniques[6] have opened a window on a whole new world of microbiology that was previously unknown. This new-found ability to identify novel infectious agents will undoubtedly find important new pathogens, but will also create false leads. Separating the signal from the noise will be a major task.

July 2013: Middle East Respiratory Syndrome Coronavirus (MERS-Cov)

Middle East respiratory syndrome (MERS) is a new disease caused by a newly discovered virus called MERS coronavirus (MERS-CoV). It was

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Table 4.2. *The prevalence of the newly discovered virus, a cyclovirus, designated CyCV-VN, in samples from a range of patients, healthy controls, animals and geographic locations.* [3,5]

Prevalence	%	Sample type	Patients	Location
10/273	3.7%	Cerebrospinal fluid	Adults and children with acute central nervous system infection of unknown cause	South and Central Vietnam
16/369	4.3%	Cerebrospinal fluid	Adults and children with acute central nervous system infection with other pathogens	
0/122	0%	Cerebrospinal fluid	Patients with non-infectious neurological disorders	
8/188	4.2%	Faeces	Healthy Children	
38/65	58%	Faeces	Pigs and Poultry	
0/615	0%	Cerebrospinal fluid	Acute central nervous system infections	North Vietnam, Cambodia, Nepal, Netherlands

first described in September 2012 and by the end of July 2013 there had been ninety-four laboratory-confirmed cases, of whom forty-six had died. Common symptoms are fever, cough, shortness of breath and muscle pain and many patients also have digestive tract problems. The great majority of cases are reported in Middle Eastern countries. It is thought that dromedary camels are the source of human infections, but human-to-human transmission is possible and is a particular problem in health care settings.

During July 2013, the growing number of cases and high case fatality rate caused the World Health Organisation (WHO) to convene an

Emergency Committee to advise whether MERS-CoV constituted a 'Public Health Emergency of International Concern'. The term 'Public Health Emergency of International Concern (PHEIC)' is defined in the International Health Regulations (2005) as:

> an extraordinary event which is determined. . .: (i) to constitute a public health risk to other States through the international spread of disease; and (ii) to potentially require a coordinated international response

The advice of the Emergency Committee was that the conditions for a PHEIC had not been met, but that the situation clearly warranted better surveillance, infection control, risk communication and research.[7]

In the ensuing ten months the number of cases increased dramatically. By the end of May 2014 there had been more than 665 laboratory-confirmed cases, including 205 deaths. Of these, about one-half were primary cases, and the other half were secondary cases (i.e. having had known contact with a confirmed case before they fell ill). Sources of infection thus fall into three groups: zoonotic, human-to-human in a health care setting and human-to-human in households. At the time of writing the dramatic increase in the number of cases is attributed to three possibilities: increasing zoonotic transmission, sub-optimal infection control in hospitals and better case detection.[8]

During May 2014 WHO's Emergency Committee was convened again. It noted its concern about the growing number of cases and indicated that 'the seriousness of the situation had increased in terms of public health impact'. However at that moment there was no evidence of sustained chains of human-to-human transmission and for this reason the committee determined that the conditions for a PHEIC had not been met.[9]

MERS-CoV carries its genetic information as RNA. RNA viruses have particularly high mutation rates and there is therefore concern that MERS-CoV may adapt to its new human hosts and become better able to transmit from one human to another.[10,11] At the moment it is estimated that although human-to-human transmission is possible, each case, on average, causes less than one secondary case. Under these circumstances sustained chains of transmission are not possible. The ongoing concern is that through viral adaptation this could change and that large epidemics or even a pandemic might ensue.

August 2013: Hepatitis E Virus as the Cause of Guillain-Barré Syndrome

August's story is a case report of an individual who developed Guillain-Barré syndrome triggered by infection with Hepatitis E virus.[12]

Guillain-Barré syndrome is an autoimmune disease of the peripheral nervous system. In about 60 per cent of cases Guillain-Barré syndrome occurs after a bout of infection with one of a number of bacteria or viruses. Hepatitis E virus is a cause of viral hepatitis. It is rare in wealthy countries and is thought to be most commonly acquired through consumption of undercooked meat products.

This case report highlights a relationship between a known virus and a known disease. This association had been described before,[13,14] so this report adds weight to an emerging view that this Hepatitis virus can trigger Guillain-Barré syndrome. Thus this is the type of emerging infection in which an old disease is newly associated with a known infectious agent.

September 2013: Cholera Re-Emerges in Mexico

In September 2013, after more than a decade of virtual absence, Cholera re-emerged in Mexico. By the time the outbreaks ended in mid-November there had been 180 confirmed cases and one death. This was the first time there had been sustained transmission of Cholera in Mexico since it had been brought under control in 2001 (Figure 4.2).

The strain of Cholera that caused the 2013 outbreak in Mexico was different from that which had circulated during the endemic period from 1991–2001, but similar to strains circulating in Haiti, Dominican Republic and Cuba at the same time.[16] All the evidence pointed towards multiple introductions to Mexico from neighbouring states which had been experiencing sustained Cholera epidemics since Cholera re-emerged in Haiti in 2010.[17]

October 2013: Hedgehog Associated Cryptosporidium, First Human Case

A spectacular example of the power of modern molecular diagnostics gave rise to the story from October. An immunocompetent man with

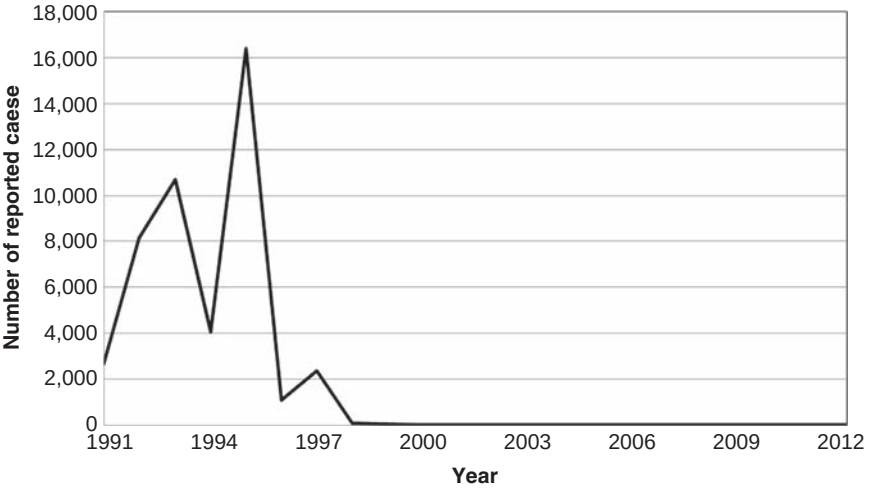

FIGURE 4.2 Cholera in Mexico 1991–2012[15]

gastroenteritis was found to be infected with a genotype of *Cryptosporidium* first described in hedgehogs.[18] The patient did not report recent hedgehog contact, and as the brief report so aptly put it 'further research is required to determine the transmission route'.

November 2013: Zika Virus Outbreak in French Polynesia

Zika virus is a mosquito-borne virus. It was first discovered in Uganda in 1947 and outside Africa and Asia is designated an emerging infectious disease. In November 2013 an outbreak was described in three archipelagos of French Polynesia. The symptoms of Zika virus infections are generally mild and it is considered to be a self-limiting febrile illness which lasts for about a week. The largest, previous, well-described outbreak was in Yap (Federated States of Micronesia) in 2007 and consisted of thirty-one cases.[19] In November 2013 the French Polynesian outbreak stood at 400 clinically suspected cases. However, by early February 2014, 8262 suspected cases had been reported through a syndromic surveillance network.[20] About half the samples sent for laboratory confirmation were confirmed to be Zika virus infections by genomic analysis. Furthermore, more than 28,000 individuals (more than 10 per

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cent of the population of French Polynesia) had sought medical care with Zika-like symptoms. With this huge burden of infection, uncommon complications became a problem, even though this is normally a mild, self-limiting disease. For example, during the outbreak there were thirty-eight cases of Guillain-Barré syndrome subsequent to Zika virus infection. This is four to ten-fold more than the usual annual number of cases of Guillain-Barré syndrome in French Polynesia and the complex clinical needs of these patients put a severe stress on intensive care resources in this very remote setting (ECDC 2014a).[8]

As an emerging infection spreads into a population without prior immunity very large outbreaks like this are possible if transmission is suitably efficient. Even though the great majority of Zika infections are mild and self-limiting, if enough people are infected, even rare complications start to impose a serious public health problem.

December 2013: Chikungunya Virus in the Americas

Chikungunya virus is another mosquito-borne infection. It has never before been known to be transmitted in the Americas. The symptoms are more serious than those of Zika virus infection, consisting of fever and joint pain which can last for weeks or months.[21] It is endemic in parts of Africa, SE Asia and India. There was a large outbreak in 2005–6 that started on Reunion[22] and smaller outbreaks in Italy and France in 2007 and 2010, respectively.[23,24]

In early December 2013, two cases of Chikungunya were reported on the French part of the island of St Martin.[25] The epidemic then took hold with cases doubling approximately every two weeks, so that six months later, by mid- June 2014, there had been over 160,000 suspected cases and 14 deaths with cases in 19 different Caribbean countries (see PAHO 2014[26] for updated figures). Infection spreads well in Caribbean islands because the population has never been exposed before, so there is virtually no acquired immunity and the mosquitos that can spread Chikungunya are present. These two risk factors are equally present in large parts of South and Central America, the South-Eastern parts of the USA and Southern Europe. The presence of very large Chikungunya outbreaks in the Caribbean increases the risk of very large outbreaks elsewhere in the Americas, particularly in poorer countries in Central and South America where control of the transmitting insect is more difficult.

January 2014: Sosuga Virus, a Novel Virus in a Wildlife Biologist

January 2014 saw the discovery of Sosuga virus, a novel virus isolated from a hospitalised wildlife biologist.[27] In 2012 a wildlife biologist fell seriously ill shortly after returning to the USA from a six-week field expedition to South Sudan and Uganda (hence the name of the new virus, Sosuga). Five days after returning to the USA she was admitted to hospital with a fever. Because of her work she had been in contact with a large range of bats and rodents and this raised the possibility that her illness was one of the very serious viral haemorrhagic fevers (Marburg, Ebola, Lassa, Lujo, etc.) so blood samples were sent away to be tested. Tests for a range of human pathogens that would cause a similar illness proved negative.

A pathogen discovery protocol was then put in place to see if her disease was caused by a new infection. Techniques of non-specific deep-sequencing and computer-based sequence analysis like those used to discover the novel cyclovirus described above revealed that she was indeed infected with a novel paramyxovirus. This virus had never been seen before and was most closely related to viruses previously isolated from fruit bats in China and Ghana (Figure 4.3). It proved possible to isolate the virus by infecting mice then propagating viruses present in mouse brains.

This story exemplifies several important points in emerging infections. First, the huge power of modern genetic sequencing technologies to detect novel human pathogens. Second, the importance of 'sentinel populations' – people who have extraordinary levels of exposure to potential human pathogens – as a source of early warnings about transmission from animals to humans of infections that we have not yet discovered. Third, that the species barrier is not the defining threshold for emerging infections. Single cases that cause no secondary infections are medically important, but pose no threat to public health. The defining threshold is the ability of an emerging infection to cause sustained human-to-human transmission.

February 2014: Human Infections with Avian Influenza Viruses in China

In February, the European Centres for Disease Control (ECDC) published a risk assessment concerning human infection with bird-derived influenza

FIGURE 4.3 Many emerging infections are transmitted to people from wild animals. Examples of this process described here include: (a) *Cryptosporidium* from hedgehogs (*Erinaceus europaeus*). © Michael Gäbler/Wikimedia Commons/CC-BY-SA-3.0 (b) MERS CoV from Dromedary Camels (*Camelus dromedaries*) © Peretz Partensky/Wikimedia Commons (c) Susoga virus perhaps from fruit bats (*Eidolon helvum*) reservoir of the most closely related virus of African origin. © Fritz Geller-Gromm/Wikimedia Commons.

viruses in China.[28] Ever since 1997, when six people died of H5N1 avian influenza in Hong Kong, there has been rumbling concern about the potential for a bird-derived influenza to cause a pandemic. This concern focused upon H5N1 influenza for many years. From 2003 until May 2014, 665 cases of H5N1 from 16 countries around the world were confirmed, 392 of whom died. In China, over the same period, there were 46 cases of H5N1 influenza, 30 of whom died.

In the spring of 2013, China reported cases and deaths caused by a different influenza, designated H7N9. By February 2014 there had been 354 H7N9 influenza cases in China, including 113 deaths. This is 100-fold more H7N9 cases than H5N1 cases in China over an equivalent time period.

For the two years that H7N9 has been observed there seems to be a strong seasonality, with all but a handful of cases occurring during the winter. All known cases have been acquired in China and the great majority of infected people have had some contact with poultry or live-bird markets.

Increased surveillance for avian influenza in China led to the detection of cases with two further types of influenza: three cases infected with H10N8 influenza and one with H6N1. Neither of these types of influenza had ever been seen to infect humans before.

H5N1 and H7N9 influenza share the following characteristics. In humans the great majority of cases are acquired from poultry. There is evidence for occasional human-to-human transmission, but not for sustained chains of transmission. Both infections have a high case fatality rate in humans: 59 per cent for H5N1 and 32 per cent for H7N9.

However, there are also differences. H7N9 infections are currently confined to China, (with just one exported case) whilst human H5N1 infections have occurred in sixteen different countries. H7N9 cases show a strong pattern of seasonality, whilst H5N1 infections in China do not. The two infections seem to have different age distribution (mean age at infection fifty-five years for H7N9 and twenty-eight years for H5N1), and there are more H7N9 infections in men, with no such bias for H5N1. However, the major difference is the much greater number of H7N9 cases: since 2003 there have been 46 cases of H5N1 in China and since 2013 there have been 354 cases of H7N9.

Why is there suddenly so much avian influenza in China? The small numbers of rare infections (H10N8 and H6N1) can most likely be attributed to heightened surveillance. The large number of H7N9 cases is much more worrying. H7N9 infection does not cause severe disease in poultry (unlike H5N1). This has the unfortunate effect that the first sign of infection of a poultry flock can be cases of severe disease in humans. One explanation for the growing number of human cases in China is, therefore, that there is a hidden zoonotic epidemic with sporadic transmissions to humans. Under this scenario the greatest threat from H7N9 is further spread amongst poultry – possibly to other countries.

There is also the lingering concern that H7N9 influenza might, through mutation, acquire the ability to cause long chains of human-to-human transmission.[10,11,29] To our knowledge no H7-type influenza virus has ever circulated widely in humans, so the pool of susceptibles would be very large. A large susceptible pool, a virus with efficient human-to-human transmission and a high case fatality rate would be a recipe for disaster (Figure 4.3).

March 2014: Ebola Virus Disease in West Africa

On the 23 March the Ministry of Health in Guinea (West Africa) notified WHO of a 'rapidly evolving outbreak of Ebola virus disease (EVD)'. At that time forty-nine cases including twenty-nine deaths had been reported. That was already more cases than the median-sized outbreak (forty-four) in the twenty-four outbreaks since the first description of EVD in 1976 (Figure 4.4).

EVD is a severe viral infection with an unusually high case fatality rate. The twenty-nine deaths from forty-nine cases by March 2014 yield a case

fatality rate of 60 per cent and this is not abnormal; of the ~2400 cases that occurred between 1976 and 2012 (see Figure 4.4) nearly 1600 died.

EVD is not endemic in humans. Outbreaks arise when people become infected after contact with the wild animals that are the natural reservoir. Illness is characteristic of a viral haemorrhagic fever: fever, fatigue and signs of both internal and external bleeding. Transmission from human to human happens through close contact with infected patients or their bodily secretions. There are serious problems with transmission of EVD in hospitals or during funeral ceremonies which include close contact between mourners and the body of the deceased. At the beginning of this outbreak in 2014 there was no vaccine and no specific anti-viral treatment.

The EVD outbreak in West Africa continued to evolve through the spring of 2014 and spread to Sierra Leone and Liberia. In late May 2014 there was a marked rise in the number of cases. By late June 2015 there had been over 27,000 cases and over 11,000 deaths,[31] making this the largest ever outbreak of EVD. The fear, dimensions and global concerns that this epidemic raised and how it changed medical processes are discussed in Chapter 1.

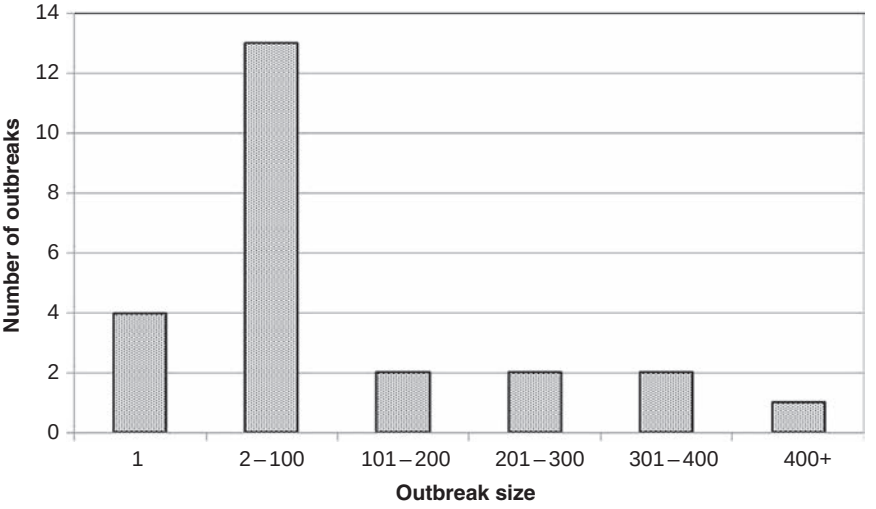

FIGURE 4.4 Outbreak size distribution for twenty-four outbreaks of Ebola virus disease between first description in 1976 and 2012.[30]

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April 2014: Antimicrobial Resistance

April's story tells not of a single disease outbreak but of the slowly unfolding global disaster of the evolution of antimicrobial resistance. The extent of the spread of drug-resistant pathogens is dramatically highlighted by WHO's first global report on surveillance for antimicrobial resistance. The report[2] (WHO 2014a), published in April 2014, focuses upon seven common bacterial infections, and finds evidence of widespread antibacterial resistance for all of them.

For example, *Staphylococcus aureus* is a bacterium that can cause a wide range of skin, bloodstream and bone infections. When resistance to penicillin evolved in the 1940s new drugs were developed that overcame this resistance. *Staphylococcus aureus* strains resistant to these new drugs (called methicillin-resistant *Staphylococcus aureus* or MRSA) first emerged in the 1960s and have now spread around the world. The newly published survey found that in five of six WHO regions at least one country reported national data in which more than half of *Staphylococcus aureus* isolates are methicillin resistant. Patients with such infections are more difficult and more expensive to treat. This pattern of widespread resistance is the norm for bacteria that are commonly acquired in a hospital setting. It does not mean that half of all *Staphylococcus aureus* is methicillin resistant, but it does mean that in most of the world there is at least one country where a national survey reported such high levels of resistance.

A global survey of this nature must, perforce, cope with varying levels of data quality. For example, South East Asia is the only WHO region with no country reporting >50 per cent MRSA in national data, but only three countries from that region provided national data. There are other sources of variability, like the size of the sample and the kind of patient from whom isolates were collected. Indeed, the second key finding of the whole study is that there are significant gaps in the data.

However, the first key finding is that there are already very high rates of drug resistance in common bacterial infections across the globe. This leads to the following gloomy prognostication in the report's foreword:

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A post-antibiotic era – in which common infections and minor injuries can kill – far from being an apocalyptic fantasy is a very real possibility for the 21st century.

May 2014: Polio, a Public Health Emergency of International Concern

The most dramatic emerging infectious disease event of the twelve months described here was the May 2014 declaration of a 'Public Health Emergency of International Concern' (PHEIC) over the international spread of Polio. This is only the second time a PHEIC has been issued since they were introduced under the International Health Regulation in 2005. The first PHEIC was issued during the early circulation of H1N1 influenza in what eventually became the 2009 pandemic.

The 'emergency' label was activated because during the first four months of 2014 Polio had spread out of three different countries: from Pakistan to Afghanistan, from Syria to Iraq and from Cameroon to Equatorial Guinea. January to April would normally be the low transmission season, so there was particular concern that the onset of the high transmission season in May and June might lead to further international spread.

Data at 18 June 2014 showed ongoing problems in Pakistan, with 82 cases in the year-to-date (of a global case-count of 103) of which 7 cases had been reported in the preceding week. The other two exporting countries had, at 18 June, had no new cases since January.[32]

There is a horrible irony in the fact that the one infectious disease event that was deemed an 'international emergency' of these twelve months was caused by a once-common childhood infection against which there is a cheap, safe and (largely) effective vaccine. The re-emergence of polio is a lesson to us all that keeping such infections under control requires constant vigilance.

Discussion

Across the twelve months recorded here emerging infectious disease events of all types occurred. Four infections new to man were described: the novel virus attacking the central nervous system of patients in Vietnam; the hedgehog-associated *cryptosporidium* from an individual in the Czech Republic; Sosuga the new virus from a wildlife biologist and

MERS-CoV from the ongoing outbreak in the middle East. There were three examples of infections detected in new geographic regions: EVD in West Africa; Chikungunya in the Caribbean and Zika virus in French Polynesia. Two infectious diseases re-emerged: Cholera in Mexico and Polio in multiple countries with unusual examples of cross-border infection. There were two examples of emerging new variants of known infectious agents: H7N9 influenza in China and the global spread of antimicrobial pathogens of many sorts. Finally, there was just one case of a new association between a known pathogen and a known disease: the link between Hepatitis E virus infection and Guillain-Barré syndrome.

If, instead of picking one event from each month, one were to review all events of the past twelve months the impression would be one of constant activity. New infections are discovered, old infections spread to new places and diseases that were once controlled re-emerge as control efforts fail. But are there more emerging infectious diseases than there were in the past? In terms of cases of infection with agents that would be classed as 'emerging' there probably are more than there were in the past. There are three drivers for this. First, there are more people, more of whom live in densely populated cities. Second, those people mix more freely, allowing infections that would once have been confined to small villages to spread widely. Third, our collective ability to detect and characterise infectious agents has taken a step change upwards in recent years. The metagenomic techniques that allow the identification of pathogens that cannot be cultured allows the identification of infectious agents that would simply have been invisible in years gone by.

Although there are more emerging infectious disease events, it is not obvious that there are more infections. For deaths from infection the trend is clearly in the opposite directions. Figure 4.5 records adult male mortality by cause in Great Britain through the twentieth century. Deaths from infections (in orange) pick up at the beginning of the First World War in 1914, peak with the Spanish Influenza pandemic of 1918 (with an even larger peak among deaths from respiratory causes in red), pick up again at the start of the Second World War in 1939, then melt away with the introduction of antibiotics in the mid-1940s.

Around the world similar patterns are coming into play.[33] In 1990, communicable diseases accounted for 25 per cent of global deaths; by 2010 this had fallen to 19 per cent. However, this global figure under-

emphasises the continuing importance of infections as a cause of death for many poorer parts of the world; in low-income countries, communicable diseases are still responsible for one-third of all deaths.

For three of the events of the past twelve months the ready availability of a pool of susceptible individuals played a large role in generating an outbreak. Both Zika virus and Chikungunya are insect-transmitted diseases that have recently moved into new geographic areas. Because they have not circulated in these locations the population is not immune. Since the transmitting insect is present this has, in both cases, lead to explosive outbreaks. Polio outbreaks too are caused by the presence of too many susceptible individuals. However, in the case of polio it is failure to vaccinate young children that has caused the pool of susceptible individuals to grow large enough to trigger outbreaks.

Thus the distribution of people around the world and their immune status with respect to different infections is crucial information for understanding where risks for the spread of new infections will lie.

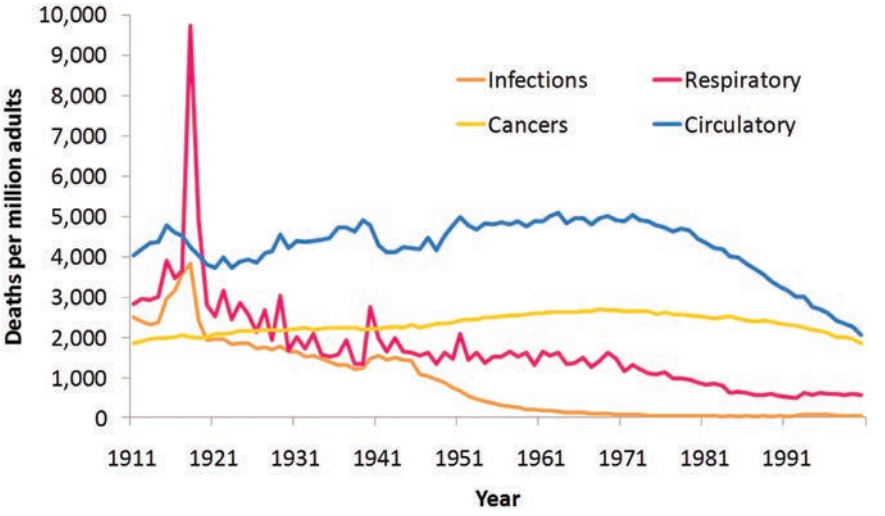

FIGURE 4.5 Adult male mortality by cause, Great Britain 1911–2000. Figures are deaths per million adults aged 15–74. From orange – infectious disease, red – respiratory disease, yellow – cancers, blue – circulatory disease.
(Data Source: Office for National Statistics)

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Figure 4.6 sketches population data per square kilometre around the world. As many people live inside the circle centred upon South East Asia as live outside it. Some authors have identified this part of the world as a 'hot spot' for generating emerging infections.[34] But since so many humans live there, it is, perhaps, not surprising that many infections of humans should arise there.

The big fear for emerging infectious diseases is of a global pandemic caused by a novel infectious agent that transmits well, spreads fast, has a high case fatality rate and for which there is neither vaccine nor cure. It is for fear of such an event that the progress of H7N9 influenza and MERS-CoV in the Middle East are so carefully monitored, watching in case either infection were to gain the ability to transmit well from human to human. However, some argue[36] that the evolution of antibiotic resistance is the more dangerous threat, and a relatively indefensible one that is already amongst us.

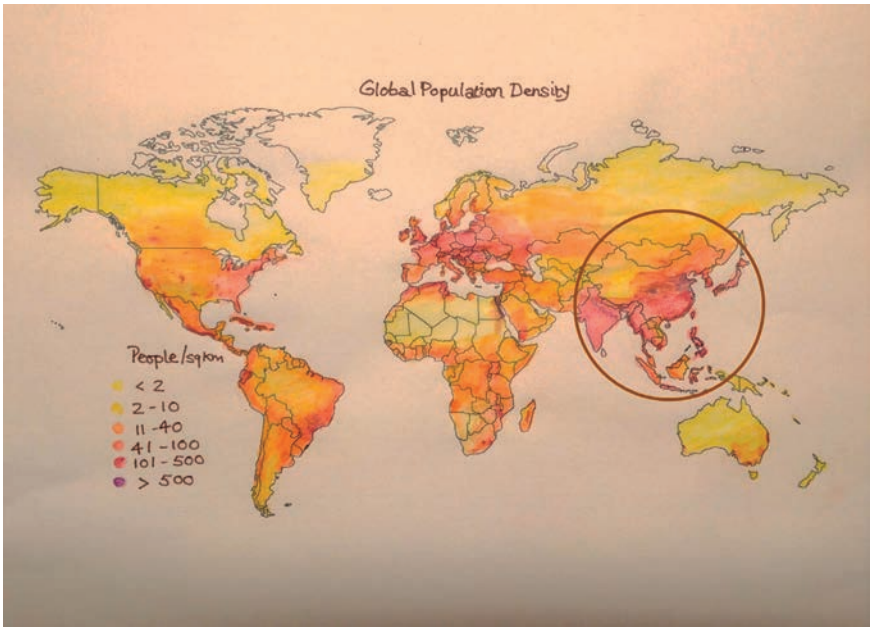

FIGURE 4.6 Global population density. As many people live inside the brown circle as live outside it. (redrawn from Center for International Earth Science Information Network maps, available online[35]).

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Further Reading

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