

Defining an emerging disease

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Summary

Defining an emerging disease is not straightforward, as there are several different types of disease emergence. For example, there can be a 'real' emergence of a brand new disease, such as the emergence of bovine spongiform encephalopathy in the 1980s, or a geographic emergence in an area not previously affected, such as the emergence of bluetongue in northern Europe in 2006. In addition, disease can emerge in species formerly not considered affected, e.g. the emergence of bovine tuberculosis in wildlife species since 2000 in France. There can also be an unexpected increase of disease incidence in a known area and a known species, or there may simply be an increase in our knowledge or awareness of a particular disease. What all these emerging diseases have in common is that human activity frequently has a role to play in their emergence. For example, bovine spongiform encephalopathy very probably emerged as a result of changes in the manufacturing of meat-and-bone meal, bluetongue was able to spread to cooler climes as a result of uncontrolled trade in animals, and a relaxation of screening and surveillance for bovine tuberculosis enabled the disease to re-emerge in areas that had been able to drastically reduce the number of cases. Globalisation and population growth will continue to affect the epidemiology of diseases in years to come and ecosystems will continue to evolve. Furthermore, new technologies such as metagenomics and high-throughput sequencing are identifying new microorganisms all the time. Change is the one constant, and diseases will continue to emerge, and we must consider the causes and different types of emergence as we deal with these diseases in the future.

Keywords

Biodiversity – Bluetongue – Bovine spongiform encephalopathy – Bovine tuberculosis – Emerging disease – Globalisation – Lyssavirus – Re-emerging disease – Zoonosis.

Introduction

The term 'emerging disease' is included in the glossary of the *Terrestrial Animal Health Code* of the World Organisation for Animal Health (OIE) (1) (hereafter referred to as the *Terrestrial Code*). The definition appearing in the 2014 edition is as follows: 'a new occurrence in an animal of a disease, infection or infestation, causing a significant impact on animal or public health resulting from: a) a change of a known pathogenic agent or its spread to a new geographic area or species; or b) a previously unrecognised pathogenic agent or disease diagnosed for the first time.' Ten years ago, Toma and Thiry (2) proposed the following definition: 'a disease whose actual incidence increases significantly in a given population, in a given area over a given period,

compared with the customary epidemiological status of that disease.' The same authors added: 'This definition applies equally to diseases of humans, animals and plants. Although most emerging diseases are infectious, they may also be toxic, metabolic or another variety'. Use of this definition also makes it possible to exclude biases linked with an apparent increase in incidence (as a result of improved diagnostic methods, for instance). However, this paper considers only infectious and parasitic emerging diseases and focuses on the OIE's definition.

Therefore, this brief article does not set out to revolutionise the concept or its associated concepts, but instead it simply puts forward a few ideas to illustrate and expand the definition. There are two concepts that should be considered more closely in connection with emerging

disease: evolution and biodiversity. It would appear that, in medicine, the notions of origin and emergence (not to be confused) continue to intrigue and surprise (3). The fact that those in the medical field are surprised that some of these emerging diseases are zoonoses or diseases of animal origin – which are not quite the same thing either (4) – is a sign that medicine has probably not yet taken enough account of evolution and biodiversity (5, 6).

Biodiversity, for its part, is far from a mere collection of ecosystems, species or genetically distinct populations within species (7). First and foremost, biodiversity is the set of functional relationships linking these entities within ecosystems. Such relationships may be grouped into the ‘predator–prey’ or ‘host–pathogen’ categories. Both these groups of relationships are known to be powerful drivers of evolution. At the same time, taxonomists have realised that, throughout the living world, the number of species yet to be described probably surpasses the number of known species. New microorganisms are being discovered every day, thanks mainly to molecular biology tools, such as high-throughput sequencing.

Emerging diseases

The literature on emerging diseases, including (but not limited to) emerging infectious diseases of humans or animals, is already extensive (2, 8). Not surprisingly, the types of emergence described are those found in the glossary definitions in the *Terrestrial Code*. It may be a case of real disease emergence, an emergence of knowledge, a geographic emergence (a disease already recognised in some places that invades a new area of the world), emergence in a species formerly not considered responsive or susceptible (susceptible with or without clinical signs), or else an unexpected increase of disease incidence in a known area and a known species. In all these cases, predicting disease emergence remains tricky (9) and this is probably the biggest concern of the Government departments directly concerned: public health, animal health and plant health. It is therefore possible to speak of genuine emergence or of apparent emergence. The latter can be categorised even further using yet more conceptual frameworks and types of classification, e.g. ‘emergence’ as a result of improved diagnostic methods or of increased media coverage.

The general phenomenon of evolution, as it was first described by Darwin and as it has been developed by biologists since, conflicts with the ideas of balance and stability, which are sometimes thought to be the norm. The time parameter is often poorly understood. Every individual ages, the human population has been increasing for thousands of years, the climate changes, and ecosystems evolve all the time. All these parameters are important in epidemiology. New

microorganisms frequently meet potential new hosts, and some of these contacts have consequences. Added to this is the fact that the time required for new generations of viruses, bacteria and vertebrates to develop is not the same. This means that it is difficult to determine if a microorganism has already evolved when discovered for the first time and it is only when the new strain begins to have consequences that its emergence becomes apparent.

As humans are merely one of the species involved in biodiversity, they contribute to these truly universal phenomena along with the other species. Change is therefore the only constant. Emerging diseases are just one of the consequences.

A few examples

Examples of emerging diseases in the field of animal health, each of which is presented below, include: bovine spongiform encephalopathy (BSE); bat lyssavirus infection; bluetongue of sheep in Europe; bluetongue of cattle and, lastly, the resurgence of bovine tuberculosis in some areas of France since the early 2000s.

Bovine spongiform encephalopathy

Bovine spongiform encephalopathy was diagnosed in cattle in the United Kingdom in the 1980s. It does not appear to have been identified either there or elsewhere before that time. It seems, therefore, that this was a case of a real emergence of a new prion disease. It is most often linked with changes in the technological processes used for manufacturing meat-and-bone meal, in particular the rendering method. It was not long before the issue of possible transmission of the BSE agent to other species was raised, even though scrapie – the existing model of a transmissible spongiform encephalopathy – had always been specific to one species (sheep) (10). Unfortunately, in the early 1990s it became apparent that the human species was indeed susceptible. In the veterinary field, cats have also proven susceptible but not so dogs, underlining how hard it is to make predictions.

An analysis of the prion strains isolated over the past 30 years has made it possible to look again at the phenomenon, with interesting results (11). Although the BSE epidemic is associated with a particular prion strain, a few sporadic cases involving a variety of other strains do seem to occur in cattle. These are described as ‘atypical’ and they went undetected prior to the epidemic. One of them would appear to have taken advantage of changes in meat-and-bone meal manufacturing in 1980 to become ‘typical’ and cause BSE.

Lyssavirus

Also in the 1980s but in a very different field, two new strains of *Lyssavirus* (family *Rhabdoviridae*) emerged in Europe. They were European bat lyssaviruses 1 and 2. At that time they were the fifth and sixth known viral 'species' of the genus, respectively. Since then, virologists have been making new discoveries all the time. The diversity of bat lyssaviruses continues to be revealed slowly but surely. The figure today stands at 15 identified 'species' (12). Clearly, this is attributable to a better understanding of the bat virome, combined, of course, with the development of ever more efficient methods of identification. Metagenomics and high-throughput sequencing are just two of the methods that have improved our understanding of bat lyssaviruses. These technologies have also increased our knowledge of other epidemiological patterns and other types of emergence. In the case of lyssaviruses, unlike that of BSE, the new knowledge that has been acquired does not seem to suggest that the level of risk to public or animal health is any higher than before.

Bluetongue

Bluetongue virus (BTV) is a classic arbovirus of ruminants in the tropics and Mediterranean region. There are 26 recognised serotypes associated with this *Orbivirus* (family *Reoviridae*), which is specific to ruminants and transmitted by dipteran insects of the family *Ceratopogonidae*, mainly of the genus *Culicoides*. In the 1990s, the European Union's Veterinary Services became aware that the virus was circulating among sheep in the Mediterranean basin. This virus circulation stemmed from trade in infected animals as a result of insufficient health checks, coupled with a probable northward extension of the area in which competent vector species can be found. The arrival of bluetongue virus serotype 8 (BTV-8) in the region of Maastricht in the Netherlands in 2006 was a nasty surprise. Yet again, it was probably the result of poorly tracked trade flows, combined with the fact that temperate-climate *Culicoides* species proved to be just as competent at transmitting the virus as the more southerly species absent from these latitudes. The disease swept through much of Europe in less than four years but, following a mass vaccination campaign, it has been eradicated from virtually all European countries (13).

At the same time, it was discovered that the – admittedly fairly unknown – BTV-8 serotype was perfectly capable of causing illness in both sheep and cattle. Up to that point, although cattle had been deemed susceptible, they had not shown any clinical signs. This was therefore a case of geographic emergence, coupled with emergence in a new species, with a significant economic impact.

Bovine tuberculosis

The last example is a classic disease of livestock: bovine tuberculosis caused by *Mycobacterium bovis*. Starting in the 1950s, France and other European countries organised the fight against this disease and gradually built a global control programme. In 2001, France obtained official disease-free status from the European Union with regard to bovine tuberculosis (this status does not mean that the disease has been eradicated but that annual herd prevalence is less than 0.1%). A relaxation of screening and surveillance seems to have occurred at around the same time, or slightly beforehand. This led to a real increase in the number of cases in some areas of France, unnoticed at first, which, unfortunately, was accompanied by transmission of the bacterium – once again locally – to a few wild species, including the red deer (*Cervus elaphus*), wild boar (*Sus scrofa*) and badger (*Meles meles*). This changed the epidemiological context of the disease and made prevention and control more complex. This is a case of re-emergence in cattle, from which the disease had not yet completely disappeared, and of emergence in wildlife, where the bacterium was hitherto unknown in that country (14, 15).

Conclusion

These examples of emerging animal diseases illustrate the concepts mentioned in the introduction and the different ways in which an infectious disease can emerge or re-emerge. It also appears that one of the major factors responsible for constantly evolving epidemiological patterns is the human species and its activities. It is inevitable that population growth, the evolution of society, increasing human population density, globalisation in all its forms, the need for new land, the use of already occupied land, and the impacts on ecosystems in general will have health consequences.

Any decisions for dealing with these emerging diseases should take into account the major causes (rather than just the consequences) and also the types of re-emergence in question. There can be no single response.

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