CHAPTER 10

Emergence/Re-emergence of Infectious Agents and Epidemic Risks in Central African Forests

Coordinator: Mathieu Bourgarel[1]

Authors: Alexandre Caron,[1] Ferran Jori,[1] Hélène de Nys,[1] Ilka Herbinger,[2] Florian Liégeois,[3] Augustin Mouinga-Ondémé,[4] Sandra Ratiarison[5]

[1]CIRAD, [2]WWF, [3]IRD, [4]CIRMF, [5]FAO

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Introduction

The years 2020–2021 will always be marked by the COVID-19 crisis. This pandemic was triggered by the coronavirus SARS-CoV-2, which broke the species barrier between a (still unknown) wildlife species and humans, somewhere in China in 2019 (Andersen et al. 2020). Above and beyond the number of deaths directly caused by COVID-19, this crisis will have an impact on our societies over the long term. Yet, this pandemic is not the first of its kind in modern times. The 2014–2016 Ebola virus disease epidemic in West Africa (and its resurgence in 2021) has also been a major warning sign of the threat posed by the transfer of a pathogen from wildlife to human populations (Heymann et al. 2015). A long list of emerging animal pathogens has already threatened to reach – or succeeded in reaching – epidemic or pandemic proportions after interspecies transmission (known as "spillover"). These include HIV, SARS-CoV-1, MERS-CoV, Nipah virus and Rift Valley fever.

Today, emerging infectious diseases (EIDs), defined here as "diseases that have recently increased in incidence or geographic range [and] recently moved into new host populations," (Daszak, Cunningham and Hyatt 2000; Tompkins et al. 2015), are one of the main risks to human health and societies. In fact, these EIDs have been increasing in recent decades (Binder et al. 1999; Woolhouse and Gowtage-Sequeria 2005). More than 60 percent of known EIDs are due to an animal pathogen (Morens, Folkers and Fauci 2004; Jones et al. 2008), and it is estimated that 75 percent of these infectious diseases that have emerged in the past three to four decades have been caused by wildlife (Woolhouse 2002; Wolfe, Dunavan and Diamond 2007).

These zoonoses are diseases that are based on transmission from animals to humans and triggered by complex interactions between humans, domestic animals and wildlife (Cleaveland, Laurenson and Taylor 2001; Karesh et al. 2012). In order to design and implement surveillance and control systems for these EIDs, it is essential to understand the mechanisms and factors that lead to this spillover.

Jones et al. (2008) have attempted to identify the factors that cause these diseases. Human density associated with anthropogenic and demographic changes is one of the main drivers of EIDs. The wide range of host wildlife is also an important factor to consider. Their predictive model indicates that low-latitude developing countries are the most exposed to EIDs, from wildlife or transmitted by vectors. In 2017, Allen et al. (2017) refined the Jones et al. (2008) model for wildlife-derived EIDs. This new model suggests that the risk of emergence is higher in tropical forest regions with high mammalian biodiversity and subject to changes in land use due to encroachment by human populations and agricultural activities.

These global studies therefore point to African tropical forests as a hotspot for EID emergence. In this chapter, we will detail the known emergence mechanisms of pathogens that cause EIDs at human/wildlife interfaces in the forest environment. We shall do so through i) a summary of knowledge on biodiversity-health relationships in the context of Central African forests and global drivers of EID emergence; ii) a focus on the human/animal interface as occasions for emergence; iii) a presentation of the recent major viral EIDs in these systems; iv) an analysis of the strengths and weaknesses of EID surveillance systems in Central Africa; and v) a reflection on the risks related to EIDs in the framework of global changes and the COVID-19 pandemic.

10.1 Central African biodiversity and the factors/mechanisms behind the emergence of infectious agents

10.1.1 Biodiversity and emerging diseases

Of all terrestrial ecosystems, tropical forests are home to the greatest number of species. They alone are home to nearly 50 percent of the Earth's biodiversity (Mayer, Tesh and Vasilakis 2017; Wilson 1988). This includes wild animals (over 1,200 species of fish, 400 species of mammals, 1,000 species of birds and a still unknown number of insects) and flora, with about 10,000 vascular plant species (Harrison, Brummett and Stiassny 2016). All these animal and plant species are potential reservoir hosts, intermediate hosts or vectors for a very large number of known or unknown bacteria, parasites and viruses. The number of pathogenic micro-organisms increases the closer the latitude is to the equator (Guernier et al. 2004). This biodiversity therefore makes the forests of Central Africa significant sources of new infectious agents compared to other types of habitat.

Currently, the Congo Basin is still relatively well preserved compared to other African ecosystems, but it is undergoing transformation related to human activities. These activities destroy or transform forest habitats and exert impact on biodiversity (Harrison, Brummett and Stiassny 2016). From a theoretical point of view, the impact of this loss of biodiversity on the risks of emergence and transmission of EIDs can be positive or negative (Keesing et al. 2010). But the relationship between biodiversity loss and EIDs is complex. The loss of species has a direct impact on the structure of the interspecific biotic network and the functioning of ecosystems (Cardinale et al. 2012). This modifies the food webs and, as a result, all the mechanisms of infectious agent spillover (Morris et al. 2016; Rulli et al. 2017).

The dilution effect is often put forward to explain the effect of biodiversity loss on EID increase (Wood et al. 2014). It is based on the fact that host individuals in a community characterized by a high level of biodiversity have a lower risk of being contaminated by a given pathogen, simply

because of the lower probability of encounter between the pathogen and the individual (Wood et al. 2014). However, the dilution effect, which has been observed on small spatial scales for some diseases, is being challenged by studies performed at various scales (Randolph and Dobson 2012; Wood et al. 2014; Halliday and Rohr 2019). Indeed, host species represent the habitats and resources of pathogens: if these latter are host-dependent, then in the event of loss of this main host, these pathogens will disappear at the same time as their host species (Wood et al. 2014). Conversely, in the event of biodiversity loss that spares efficient reservoir or intermediate host species, an amplifying effect may increase the risk of transmission of a pathogen carried by these host or reservoir species (Pongsiri et al. 2009). The consequences a loss of biodiversity may have on the risks of disease transmission will thus differ according to the pathogen, its hosts and the environments in question. Pathogens, like all other animal species, undergo changes (anthropogenic or not) and have different intrinsic adaptive capacities that will make them "losers" or "winners."

Often, habitat modifications lead to selection of so-called generalist species, which are more likely to host pathogens and put more specialized species at a disadvantage. Thus, the densities of large mammals are often impacted first in the event of biodiversity loss, while the density of micromammals, which are privileged carriers of pathogens, tends to increase (Young et al. 2014). Some EIDs may also pose major risks to biodiversity and in particular to the conservation of the Congo Basin's iconic species. For example, an outbreak of Ebola virus disease severely reduced great ape populations in some areas of the Congo Basin during the 2000s, and in several months ruined years of work and massive investments in the protection of chimpanzees (*Pan* spp) and gorillas (*Gorilla* spp) (Walsh 2003; Bermejo et al. 2006).

10.1.2 Emergence factors

Emergence of a zoonotic infectious disease, which usually results in an epidemic in the susceptible host population, is due to a combination of intrinsic and extrinsic factors (Daszak, Cunningham and Hyatt 2000; Morens, Folkers and Fauci 2004; Woolhouse and Gowtage-Sequeria 2005). First of all, some factors are related to the characteristics of the pathogen itself, the reservoir and/or intermediate hosts, and the vectors (if any). Other factors are related to the environment (or climate) more or less favourable to the circulation of the infectious agent. Territorial factors are the product of human activity and the risk behaviours of human populations (Ludwig et al. 2003). Examples are a lack of or poorly performing disease surveillance systems, ineffective programmes for monitoring vectors or other carrier species, and failed water supply systems. Additional factors include human-induced environmental changes, such as deforestation, agricultural practices, loss of biodiversity, logging and mining. Mention should also be made of all human activities that increase contacts between people and wildlife or that facilitate the circulation of infectious agents outside their natural habitats: hunting, consumption and trade of bushmeat, transportation and tourism.

10.1.3 Emergence mechanisms

For emergence of a zoonotic disease, several steps are required: invasion, establishment and persistence of an infectious agent in new host populations (Anderson and May 1986). First, when there is contact between a reservoir animal and a human, the pathogen must be transmitted successfully and be able to multiply and then be transmitted from human to human. Finally, the epidemic must shift from a local to a national or international scale.

A number of natural barriers must be overcome in order for spillover to occur. These barriers are variable in time and space. The probability of transmission of an infectious agent from its reservoir to a human being actually depends on a variety of factors:

1. The distribution and density of the reservoir species: greater presence of the reservoir species in the habitat used by humans increases the probability of encounter and contact between the two.
2. Pathogen dynamics in the reservoir host: greater prevalence in the reservoir species makes human-animal contact more of a risk.
3. Human exposure to the pathogen: if the animal is infected, the intensity of the infection will determine transmission probability. The main transmission routes of the infectious agent as well as the behaviours of the human and/or the vector (if involved in the transmission mechanism) are decisive: transmission may come from the skinning of hunted animals or from repeated stings of a vector insect. The more the human or vector is in contact with the body fluids or organs in which the infectious agents are concentrated, the greater the risk of transmission.
4. Internal factors of the person in contact will determine their susceptibility to infection. These include genetic, physiological and immunological characteristics (Plowright et al. 2017). If these characteristics enable multiplication of the infectious agent in the contact case, the latter can then become the index case of the epidemic and contaminate other people, as was the case of the Ebola virus disease (EVD) epidemic in Luebo, the Democratic Republic of the Congo (DRC), in 2007 (Leroy et al. 2009b).

All these various steps are barriers that must be overcome for transmission of the infectious agent from a reservoir host to a recipient host (Plowright et al. 2017). For disease emergence to occur, all these barriers must be breached one after the other, at the right time and place. This "alignment of breaches" in the barriers is ultimately very rare for viruses such as filoviruses (Ebola and Marburg) and coronaviruses (SARS-COV, SARS-CoV-2 and MERS-CoV), but more or less permanent for other zoonotic diseases such as trypanosomiasis, for which incidence is high in Africa due to almost permanent exposure to infected animals and vectors (tsetse flies) and low-level resistance in humans (Simarro et al. 2012). This chain of low-probability events suggests that observed emergences represent only a small portion of spillover events, most of which do not result in the infectious agent staying in the human population (Wolfe et al. 2005a).

10.2 Health risks at the human/animal interface in Central Africa

More than half of the new infectious diseases that appeared between 1996 and 2009 occurred in Africa (Wood et al. 2012). Spillover of these EIDs in large human populations is facilitated by anthropic activities and the processes of globalization, urbanization, movement of goods and people, and climate change. Various factors further this spillover: land use and transformation, fragmentation of natural habitats and the ensuing loss of biodiversity, hunting, and agricultural and customary practices (Wood et al. 2012; Lloyd-Smith et al. 2009; Morse et al. 2012).

10.2.1 Climate change, deforestation and forest fragmentation

Climate change is going to exert wide-ranging impact on ecosystems and their inhabitants (both human and non-human), including on pathogens (Chidumayo et al. 2011). However, the

consequences of climate change on the dynamics of spillover are difficult to predict. It can alter the dynamics of diseases caused by pathogens that spend part of their life cycle outside their hosts and that are thus exposed to the effects of environmental variations. This concerns pathogens transmitted by vectors (insects and ticks), by water and by food (Baylis 2017). Climatic conditions also alter the population dynamics of hosts and vectors, and thus indirectly those of pathogens (McMichael and Lindgren 2011). In Africa, several examples of emergence or re-emergence associated with climate change have been described: Rift Valley fever (Linthicum et al. 1999; Rweyemamu et al. 2000), malaria (Nchinda 1998; Gunda et al. 2017) and chikungunya (Paupy et al. 2012; El-Sayed and Kamel 2020).

Deforestation in Central Africa is the result of human activities. In order of severity, these are 1) land clearing for subsistence agriculture, firewood and charcoal extraction; 2) logging; and 3) mining (Bogaert et al. 2008; Abernethy, Maisels, and White 2016). Each of these activities can lead to a health risk (Epstein 2001). Deforestation and forest fragmentation influence the behaviour and abundance of wildlife, including both small and large mammals (Jones et al. 2013). They are modifications that alter biological interactions between living organisms and that may promote the alignment of events required for infectious emergence in humans (Guégan et al. 2020). For example, deforestation affects habitat use by frugivorous bats (Zhang et al. 2005), and there is a link between destruction of natural bat habitats and transmission of their viruses to other animals and humans (Jones et al. 2013). Several studies suggest that the likelihood of an outbreak of EVD in a given site is linked to recent deforestation events there (Olivero et al. 2017; Rulli et al. 2017).

Furthermore, meta-analysis based on PREDICT data[1] shows that rodent species known to be disease reservoirs were significantly more abundant in modified habitats, while non-reservoir species were more abundant in unmodified habitats (Mendoza et al. 2020). The same is true with bacteria. When forest fragmentation disrupts the ecology of non-human primates (NHPs), it influences bidirectional spillover of bacteria within those fragments (Goldberg et al. 2008). These findings confirm that deforestation and habitat fragmentation generally have an impact on biodiversity that may involve a higher risk of transmission of zoonotic pathogens.

10.2.2 Subsistence and commercial hunting

In rural Central Africa, bushmeat is an important source of protein and income for local people. Bushmeat consumption was estimated at between 1 and 5 million tonnes in the Congo Basin in the 2000s (Wilkie and Carpenter 1999; Fa, Currie and Meeuwig 2003; Fa, Ryan and Bell 2005) with an estimated hunting pressure of between 23 and 897 kg/km^2/year (Van Vliet and Nasi 2008). In Central Africa, bushmeat is often more accessible and affordable than farmed meat. Bushmeat is also an integral part of the culture of the rural and urban populations of the Congo Basin, and demand for it increases along with household purchasing power (Wilkie et al. 2005; Fa et al. 2009). To meet this growing demand for bushmeat, hunters hunt and harvest throughout the year to feed their families and their village (subsistence hunting) and to feed urban centre markets (commercial hunting) (van Vliet and Mbazza 2011). Growing demand from cities is leading to higher selling prices. Consequently, hunters prefer the bushmeat value chain to target urban markets or other countries rather than rural areas.

1 https://www.ecohealthalliance.org/program/predict

Over the past two decades, this commercial hunting, even though informal, has developed at national, regional and international levels to such an extent that it furthers the circulation and emergence of known or unknown zoonotic diseases in the Congo Basin and the rest of the world. For example, the scales and flesh of pangolins (*Smutsia gigantea*, *Phataginus* spp), which are hunted in Central Africa, can be found in Asia, where they are used for traditional medicine and meat consumption (Zhang et al. 2020; Ingram et al. 2018). Further, to increase hunting success and meet demand, hunters are using new technologies such as hunting rifles, flashlights and even GPS, thereby increasing the number of catches and the pressure on a greater number of animal species (Bowler et al. 2020).

Hunting and more specifically the capture, handling, preparation and transport of carcasses generate direct contact with potentially infected wild animals (Wolfe et al. 2005b; Mitman 2014; Magouras et al. 2020). But as these activities target rodents, bats and gorillas alike, their level of risk depends on the wildlife species hunted and handled. Bats, for example, are suspected to be reservoirs of filovirus (Marburg and Ebola) and coronavirus. Great apes (chimpanzees and gorillas), on the other hand, are phylogenetically closer to humans (Wolfe et al. 2005a) and may be carriers of a large number of zoonotic pathogens. Risk increases when the hunter kills a sick animal or picks up a fresh carcass of an animal that died in the forest (Pourrut et al. 2005; Guégan et al. 2020).

The risk of transmission of consumption-linked diseases is likely to be lower, as cooking can destroy pathogens. On the other hand, little is known about the effects of bushmeat preservation methods on pathogen survival. Salting, drying or smoking the meat is likely to be damaging to some of these infectious agents, but their effect remains little known. Some studies suggest that these methods are not 100 percent safe, as several species of viruses have been detected by biomolecular analysis in thoroughly smoked bushmeat cuts (Smith et al. 2012).

10.2.3 Logging and mining

Central Africa's rich and considerable natural resources (chiefly mining and forestry resources) are heavily exploited. The mining sector in Africa has invested heavily and intensified exploitation. In some Central African countries, such as Cameroon, gold mining is dominated by artisanal mining (Aoudou Doua, Narke and Layen Ndiong 2018). More and more people have been engaging in this smuggling activity over the past few decades, leading to massive influxes of migrants. This increase in population is generally accompanied by a pioneer front of farming and mining, leading to serious environmental consequences. "Gold fever" has developed to the extent that small isolated camps of artisanal workers have turned into small but well-structured villages (Aoudou Doua, Narke and Layen Ndiong 2018). These mining and forestry activities in the Congo Basin lead to the opening up of trails and human settlements in previously untouched forests, thereby facilitating access to new hunting areas (Wolfe et al. 2005b; Chomel, Belotto, and Meslin 2007). The result is that new interfaces between humans and wildlife are created. Most of the health risks associated with mining and forestry are due to the creation of these new interfaces and to the hunting that always accompanies them – not only to feed the workers, but also to develop the bushmeat trade. However, some disease re-emergence has been linked directly to mining, as seen by the Marburg haemorrhagic fever epidemic in a gold-mining village in the DRC in 1998, where 52 percent of cases were miners working in an underground mine. The epidemic ended when the mine was flooded (Bausch et al. 2006).

10.2.4 Agricultural practices

Subsistence agriculture is one of the main causes of forest degradation in the Congo Basin (Tyukavina et al. 2018). Small-scale land clearing leads to significant fragmentation of forest cover and enlarges the areas of interface between humans and wildlife. There is an increase in direct and indirect contact with wildlife which are a potential source of pathogens. In addition, newly formed forest edges are subject to changes in biodiversity as well as to changes in the abundance and communities of wild species (Pfeifer et al. 2017). All these factors can impact the risk of zoonotic transmission of infectious agents circulating in the forest.

The crop and secondary forest areas associated with agriculture are attractive food resources for wildlife. This is the case for the frugivorous bat *Hypsignathus monstrosus*, which prefers to use these areas near forest villages for food and is suspected of playing a role in the natural cycle of the Ebola virus (E. Schloesing, forthcoming). When wildlife uses these habitats which are in close proximity to humans, it promotes direct and indirect contact between wildlife, livestock and humans, thereby increasing the risk of spillover. Bacterial exchanges between NHPs, domestic animals and humans have been confirmed in fragmented forest areas and are linked, among other things, to the plundering of crops by these primates (Goldberg et al. 2008).

Forest communities raise livestock (goats or pigs) or poultry that move freely. These domestic animals share the same habitats and resources as wildlife, including fruit trees favoured by many wildlife species (including bats and NHPs). For example, domestic pigs can roam distances of several kilometres in forests, making for significant risk of direct contact with wildlife due to their scavenging behaviour (Atherstone et al. 2017). Livestock rearing in forest areas therefore increases occasions for pathogen transmission from wildlife to domestic animals, which can in turn act as an intermediate or amplifying host before transmission to humans.

Finally, a little documented but common agricultural practice in Africa (M. Bourgarel, pers. obs.) is the collection of bat guano from the caves to fertilize fields, which can promote the emergence of infectious diseases. A study conducted in Zimbabwe shows, for example, the presence of coronavirus and paramyxovirus in guano used for this purpose, thereby highlighting the risks associated with this practice (Bourgarel et al. 2018).

10.2.5 Beliefs and customs

The beliefs and customs of people living in the Congo Basin play a major role in the perception of diseases, the risks associated with their activities such as hunting and their interactions with wildlife, and the management of epidemics. In fact, some ethnic groups do not have a biomedical conception of the causes of diseases. There is even a saying in the DRC that "Congolese don't die from germs"[2] (Sabuni 2007). Witchcraft was often cited as the cause of illness among ethnic groups such as the Bira and Nande in the DRC and Gabon during the 2001–2002 EVD outbreaks (M. Bourgarel, pers. obs.).

Customs and beliefs also lead people living in forests to engage in risky behaviours involving wildlife in addition to those involving hunting and handling bushmeat. Several ethnic groups interact with dead animals when hunting or shortly after childbirths, thereby increasing risk of disease

2 "Congolais hakufi na microbe".

transmission. For example, they may put a newborn in the rib cage of a freshly killed gorilla so that the child takes in the animal's strength, or they may practise rites that put them in close contact with dead wildlife to increase their success in hunting (F. Liégeois and M. Bourgarel, pers. obs.).

Finally, beliefs and customs can in fact have an impact on the management and control of an epidemic by health services and governments. Looking again at the example of EVD epidemics, the local population living in epidemic zones can often be seen to refuse to believe in the epidemic, claiming that it is government propaganda and used to obtain foreign funds, control the population or procure human organs (Agusto, Teboh-Ewungkem and Gumel 2015). Added to this is the fact that some infected people refuse to be quarantined and go into hiding in the forest. There is also the fear of not being able to give loved ones an appropriate traditional burial, as the bodies are not returned to the family but cremated by health services. These traditional beliefs and customs incite some families to hide their sick relatives in order to escape the health system, thereby slowing down control of the epidemic significantly (Agusto, Teboh-Ewungkem and Gumel 2015).

This problem of lack of confidence among forest populations in health systems stems in part from a lack of communication and awareness-raising by health system actors. During the 2001 and 2002 EVD outbreaks, these services focused on case management, without really communicating to local populations about the fate of quarantined and deceased patients. This led the public to believe that sick patients placed in quarantine disappeared or were murdered for their organs (M. Bourgarel, pers. obs.). It is therefore crucial to i) take these beliefs and customs into account and to respect them as much as possible, ii) properly communicate to the various people involved in the management of epidemics, and iii) limit the tensions or even social violence which can emerge from these crises (Sabuni 2007).

10.2.6 Other human activities

Every year, millions of live animals are sold around the world, for use as pets. More often than not, these animals are illegally captured to meet the demand for exotic animals. This global black market is estimated at several billion dollars per year (Rosen and Smith 2010). In Central Africa, trade in live animals predominantly concerns certain species such as the grey parrot (*Psittacus erithacus*), the royal python (*Python regius*) and several species of NHPs (Stiles et al. 2013; Martin, Senni and D'Cruze 2018; Devaux et al. 2019a; Norconk et al. 2020).

Beyond the conservation problem it poses, this trade is highly effective in exposing host populations to new pathogens (Karesh et al. 2005; Can, D'Cruze and Macdonald 2019) and is recognized as a potential source of future pandemics. The first outbreak of monkeypox outside Africa occurred in the United States in 2003, following the importation of rodents from West Africa which infected other local mammals and subsequently a total of 47 people (Mackay and Arden 2015). The risk for a country to experience the emergence of a new disease depends on many complex socioeconomic, ecological and biological factors that have already been detailed. The volume of live animals imported into the country is one such factor. Good understanding of this often informal trade is thus crucial to optimize the limited efforts and resources allocated to the prevention of zoonotic disease epidemics (Karesh et al. 2005; Can, D'Cruze and Macdonald 2019).

In the international tourism market, demand for animal tourism has increased sharply over the last decade (Fennell et al. 2012). This type of tourism is a significant source of income for the countries visited and contributes to the conservation of species and habitats. It can also generate educational and socioeconomic benefits for local people (Macfie and Williamson 2010). Today's tourists seek

out close encounters and personal experiences with wildlife and are particularly attracted to endangered species in remote and fragile habitats (Macfie and Williamson 2010). However, this activity modifies the behaviour of certain species which, attracted by the frequent supply of food from tourists, lose their fear of humans. This close and regular contact between people and wild animals increases the probability of pathogen transmission between them.

This risk is especially significant between humans and NHPs, which – because of their strong capacity for interaction and their phylogenetic proximity – share a large number of infectious agents (Davies and Pedersen 2008). In several national parks of Central Africa, groups of great apes have become habituated (i.e., made to accept human observation), to improve the quality of tourism products. These parks include Lopé in Gabon, Odzala and Nouabalé-Ndoki in the Republic of Congo, Dzanga-Sangha Special Reserve in the Central African Republic, and Virunga and Kahuzi-Biega in the DRC. There are also many great ape sanctuaries which offer tourists close contact with habituated great apes. Forest tourist camps similarly promote closer contact with wildlife, which are attracted to food and garbage. This proximity facilitates the transmission of infectious and parasitic agents between the two groups (Odeniran, Ademola and Jegede 2018; Devaux et al. 2019b), including rabies, herpesvirus type B, Marburg, Ebola, monkeypox and other pathogens. This tourism of mingling with NHPs can also have an impact on the conservation of these species via transmission of human diseases to the latter (Devaux et al. 2019b). Cases of transmission of respiratory pathogens sometimes leading to death in great apes have been recorded in Africa (Köndgen et al. 2008; Dunay et al. 2018; Grützmacher et al. 2018; Mazet et al. 2020). Beyond indirect contacts, there are also serious risks that tourists may be bitten by wild animals that have lost their fear of humans and come looking for food in the camps (Devaux et al. 2019b). To limit these risks of transmission related to ecotourism, several measures have been proposed by primatologists, such as limiting the frequency and duration of visits, reducing the number of visitors, prohibiting sick tourists from access, banning the consumption of food on-site, determining a minimum observation distance or physically separating animals from visitors, and mask wearing (Macfie and Williamson 2010; Gilardi et al. 2015).

10.3 Emerging/re-emerging diseases in Central Africa: background, epidemiology and health response

10.3.1 Central African haemorrhagic fevers

Haemorrhagic fevers (HFs) are diseases caused by viruses from various families, which affect several organs at the same time. These diseases can be accompanied by bleeding, called haemorrhagic symptoms (CDC 2013). While some HFs are relatively mild diseases, most known HFs (e.g., Lassa HF, Crimean-Congo HF, Rift Valley fever, and the Ebola and Marburg viruses) are extremely serious and deadly. These HFs are present on all continents and are generally zoonotic diseases (CDC 2013). Dengue is the most common HF in the world (100 million cases and 60,000 deaths/year). It is followed by yellow fever, which is transmitted by arthropods and affects about 200,000 people each year. In Central Africa, yellow fever and Ebola and Marburg (filovirus) virus diseases are the most common HFs (Zapata, Cox and Salvato 2014). Ebola and Marburg are the HFs with the highest mortality rate (50 to 88%) along with the Crimean-Congo fever of Africa, which has been detected in West Africa and also circulates in Central Africa.

The yellow fever virus belongs to the family Flaviridae. It was isolated in Africa in 1927 (Fleury 2009) and is endemic in 34 African countries and throughout the Congo Basin (Barrett and Monath 2003). It is an arbovirus (virus transmitted by hematophagous arthropod vectors), whose vector in Africa is a mosquito of the genus *Aedes*. This virus is maintained in the forest through a mosquito-monkey-mosquito cycle in which humans are generally not included. Yellow fever is a very old zoonotic disease whose first major epidemics affected tropical America in the 17th century. Today, Africa is the continent most affected by it (95 percent of the world's cases). The frequency of epidemics and isolated cases has increased in recent years, chiefly in Sudan, Angola, Uganda and the DRC (Institut Pasteur 2021), in places where immunization coverage is insufficient. It is currently possible to prevent yellow fever thanks to a vaccine that is very (99%) effective, safe, inexpensive, and that protects against the disease for life. There is no specific antiviral treatment for this disease, but the treatment of symptoms significantly improves survival rates (WHO 2021). The fight against yellow fever requires vector control in order to reduce the risks of transmission. This involves the elimination of potential larval deposits (stagnant water). The vectors targeted are *Aedes aegypti* as well as other *Aedes* species. While mosquito control campaigns are possible and effective in urban areas, they are much more difficult to implement in forest areas. In these latter, it is necessary to use personal protection strategies (e.g., clothing covering arms and legs, and repellents), which remain the most effective means of prevention (WHO 2021).

Several other arbovirus diseases responsible for major human epidemics have emerged from viruses circulating in forest areas before spreading to different parts of the world (Monath 2001; Mayer, Tesh and Vasilakis 2017). It has been observed that some of these viruses, such as dengue, khikungunya and Zika viruses, undergo sylvatic cycles in Central African forests, where transmission between NHPs occurs via mosquitoes (Valentine, Murdock and Kelly 2019). Depending on the virus, these sylvatic cycles play a more or less significant role in triggering human epidemics in Africa, and so-called urban cycles should be taken into account in surveillance and control strategies for these arbovirus diseases (Valentine, Murdock and Kelly 2019; Vasilakis et al. 2007). In addition, the invasion of Central African regions by invasive vector species such as *Aedes albopictus*, which arrived in Africa in the 1990s (Cornel and Hunt 1991) leads to new risks of emergence of arbovirus diseases there, and in the Congo Basin in particular. *A. albopictus* is a mosquito capable of transmitting several arbovirus diseases. It has already been responsible for outbreaks of dengue, chikungunya and Zika in Africa in anthropized rural and urban environments. This vector could spread to forest habitats and also increase the health risks associated with zoonotic arbovirus diseases and new cases of emergence (Ngoagouni et al. 2015).

The Ebola virus was discovered in 1976 during two successive epidemics in South Sudan and in the DRC (formerly Zaire), near a small river named "Ebola." This virus belongs to the family Filoviridae, which includes five genera (Kuhn et al. 2010; Negredo et al. 2011), three of which are present in mammals: the genera Ebola virus (EBOV), Marburg virus and Cuevavirus. The genus *Ebola* comprises six distinct species (Goldstein et al. 2018): *Sudan ebolavirus* (SUDV), *Zaire ebolavirus* (ZEBOV), *Tai Forest ebolavirus* (TAFV), *Bundibugyo ebolavirus* (BDBV), *Reston ebolavirus* (RESTV) and *Bombali ebolavirus* (BOMBV). There is only one species each of the *Marburg* genus and the *Cuevavirus* genus: *Marburg marburgvirus* (MARV) and the Lloviu virus (LLOV) respectively.

Since the discovery of Ebola viruses, 35 epidemics or cases of infections have been reported to date, including 27 epidemics and 5,980 cases recorded in Central Africa (CDC 2021): 12 in the DRC, 3 in the Republic of Congo, 3 in Gabon, 6 in Uganda and 3 in South Sudan (Pigott et al. 2014). The epidemics in the DRC are mainly due to the ZEBOV virus, except for one BDBV case in 2012. For all but two of these epidemics, the origins are unknown: that of 2007, when contact with a frugivorous bat was

described (Leroy et al. 2009), and that of 2014, in which the index case had cut up a tree monkey found dead in the forest (Maganga et al. 2014). In the Republic of Congo, the three epidemics were due to ZEBOV. Contacts with great apes are thought to be the cause. The three epidemics in Gabon were also due to ZEBOV, the origin of which is believed to be contacts with frugivorous bats and/or great apes. In Southern Sudan, only the species SUDV was detected during the three epidemics. While the origin is unknown for the 1976 epidemic, bats and a baboon *(Papio anubis*) are suspected to be the cause of the 1979 and 2004 epidemics respectively (WHO 2005). In Uganda, only the 2019 epidemic due to the ZEBOV virus has a known origin (a case imported from the DRC). The other 5 epidemics due to the SUDV virus (4) and the BDBV virus (1) are of unknown origin.

Although EBOV viruses have not yet been isolated from frugivorous bats, these latter are suspected to be reservoir hosts and to play a role in the ecology of Ebola viruses (Caron et al. 2018). Numerous epidemiological, serological and virological investigations link these animals to Ebola viruses (Leroy et al. 2005; Hayman et al. 2011; De Nys et al. 2018). In addition, filoviruses do not appear to be pathogenic to bats (Paweska et al. 2012). Research projects continue to track Ebola viruses in Central Africa using "One Health" approaches in order to better understand the ecology of viruses and to better target species, habitats and periods during which to take samples from bats and thereby increase the chances of finding the active virus (e.g., the EBO-SURSY project[3]).

EBOV is transmitted by direct contact with body fluids (blood, secretions, biofluids) from infected animals found in the forest (Dowell et al. 1999). Human-to-human transmission occurs as a result of direct or indirect contact with body fluids from a person who has the disease or has died from it. Health workers in the early stages of the epidemic (when health precautions are not yet in place) are particularly vulnerable. Funeral rites during which the immediate family is in direct contact with the dead body play a significant role in the transmission and spread of the disease. The incubation period is 2 to 21 days. EVD patients remain contagious for as long as the virus is present in the blood, but it has recently been shown that genetic material (RNA) from the virus can remain in the semen of surviving males for up to 18 months after recovery (Deen et al. 2017; Mackay and Arden 2015; Sow et al. 2016). Currently, there is still no specific cure for EVD other than symptomatic treatments. However, several treatments (blood products, immune therapies and drug treatments) are under evaluation (Agnandji, Fernandes and Bache 2017) and were tested in a randomized controlled trial setting (WHO 2019) during the most recent epidemics of 2018–2019 in the DRC. An experimental vaccine (rVSV-ZEBOV) developed in 2015 was also used during the epidemics of 2018–2019 in the DRC and 2021 in Guinea. Initial data show that this vaccine is safe and seems to be highly effective (WHO 2019).

The latest EVD outbreaks in the DRC in 2018–2020 and in Guinea in 2021 each suggest that the source of these respective outbreaks is individuals who had been infected during previous outbreaks (more than five years previously in the case of Guinea). If confirmed, these data could force a review of the epidemiology of the disease by taking into account the "human reservoir" of the virus or the possibility of seeing resurgences appear after large-scale epidemics, as happened with the epidemics in Guinea (2014–2016) and the DRC (2018–2020). In addition to the risk of resurgence, which increases with the number of survivors, there is the problem of the stigmatization of these EVD survivors (Keita et al. 2021).

The Marburg virus (MARV) was first identified in 1967 during three simultaneous outbreaks in Germany (Marburg and Frankfurt) and Serbia (Belgrade) (Kissling, Murphy, and Henderson 1970).

3 https://rr-africa.woah.org/en/projects/ebo-sursy-en/

Since 1976, 12 sporadic epidemics have occurred in various sub-Saharan African countries, including several in the Congo Basin (Towner et al. 2006; Bausch et al. 2006; Adjemian et al. 2011). These were in the DRC (between 1998 and 2000), Angola (between 2004 and 2005) and Uganda (three, in 2007, 2012 and 2014). Unlike Ebola, the MARV reservoir host has been identified (the Egyptian roussette bat – *Rousettus aegyptiacus*); this occurred in 2009, 40 years after the first epidemic (Towner et al. 2009; Amman et al. 2020). However, the role of other wildlife species in the circulation and emergence of MARV cannot be ruled out (Bourgarel and Liégeois 2019). Infection of an individual is usually due to a prolonged stay in mines or caves that are home to bat colonies. The incubation period is 2 to 21 days. As with EVD, human-to-human transmission occurs through direct contact with biofluids from contaminated and infectious humans or animals. The mechanisms of transmission and spread of the disease are the same as for EVD, and sexual transmission of MARV has been documented up to seven weeks after recovery (WHO 2018).

10.3.2 Human immunodeficiency virus (HIV): an example of successful emergence

Central Africa has always been associated with the emergence of human retroviruses, such as human immunodeficiency virus type 1 (HIV-1) and human T-cell lymphoma (HTLV). All are the result of spillover of NHP retrovirus to humans. Since the first clinical description of acquired immunodeficiency syndrome (AIDS) in 1981, more than 32 million [24.8 – 42.2][4] people have died of this infection. Human immunodeficiency viruses (HIV) have infected more than 75 million people and continue to infect 1.7 million [1.2 – 2.2][4] people annually. The number of AIDS deaths worldwide for the year 2020 is estimated at 680,000 [480,000 – 1,000,000][4] people, 63 percent of which occurred in sub-Saharan Africa. In 2020, the number of people living with HIV was estimated at 37.7 million [30.2 – 45.1][4] (UNAIDS 2020).

Two types of HIV can be distinguished depending on their genomic organization and phylogenetic relationships: human immunodeficiency virus type 1 (HIV-1), which is the main cause of the AIDS pandemic, and type 2 (HIV-2) (Barré-Sinoussi et al. 1983; Clavel et al. 1986; Chakrabarti et al. 1987).

Molecular study of the various HIV isolates has revealed that they are variants derived from the same virus related to ungulate lentiviruses, the archetype of which is the sheep virus Maedi-Visna (Gonda et al. 1985). Around the same time, viruses with similar characteristics were isolated from several simian species (Chakrabarti et al. 1987). Simian immunodeficiency viruses (SIV) infect a wide variety of NHPs in sub-Saharan Africa (Peeters et al. 2002). Two of these viruses, chimpanzee (*Pan troglodytes troglodytes*) SIVcpzPtt and sooty mangabey (*Cercocebus atys*) SIVsmm, have been transmitted to humans on multiple occasions and generated the human immunodeficiency virus type 1 M and N and type 2 (HIV-2) groups respectively (Boué et al. 2015; Peeters, Jung and Ayouba 2013). The exact conditions and circumstances of these spillovers remain unknown. Human exposure to NHP blood during hunting and skinning activities is the most plausible source of infection (Peeters, Jung and Ayouba 2013). The initial epicentres of HIV-1 and HIV-2 infection are in Central and West Africa respectively, reflecting the natural habitat of the chimpanzee (*Pan troglodytes troglodytes*), the gorilla (*Gorilla gorilla*) and the sooty mangabey (*Cercocebus atys*) (Peeters, Jung and Ayouba 2013; Santiago et al. 2005). The initial genetic diversity of HIV is associated with multiple introductions of simian viruses into humans, and the different groups of HIV-1 (M, N, O and P) and HIV-2 (A-I) are the result of independent spillover events (D'arc et al. 2015; Boué et al. 2015; Visseaux et al. 2019).

4 Confidence interval.

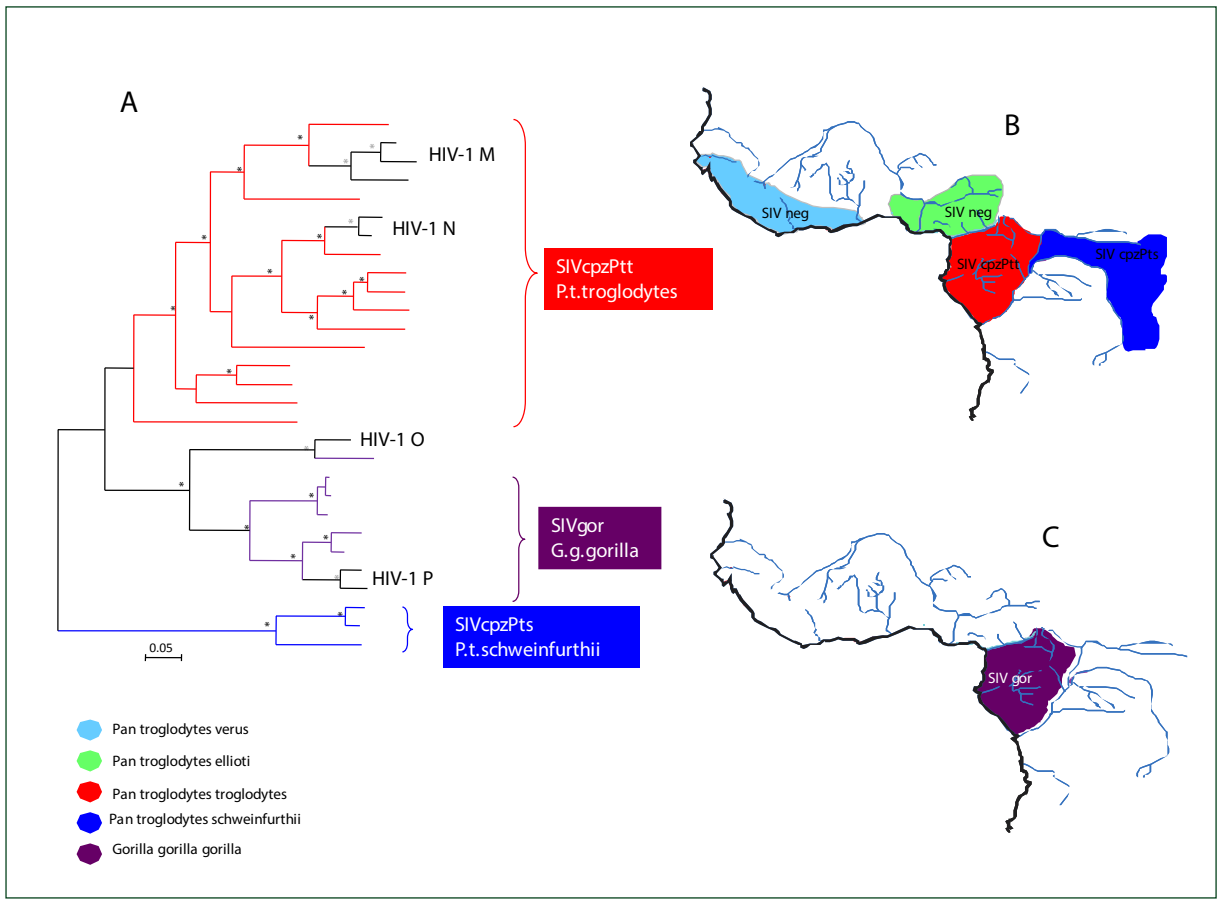

Figure 10.1: Phylogenetic relationship between simian immunodeficiency virus strains in great apes (chimpanzees and gorillas) and the different groups of human immunodeficiency virus type 1 (A. Ayouba)

The close phylogenetic relationship between the SIVcpzPtt strains from West and Central Africa and the HIV-1 strains from the three M and N groups, as well as the great diversity of the M group strains in West Equatorial Africa and their overlap with the habitat of the *Pan troglodytes troglodytes* supported the hypothesis that the HIV-1 M and N group strains originated in the Congo Basin. This hypothesis was confirmed by an analysis of several hundred samples of chimpanzee faeces collected from different locations in Cameroon. It was shown that these wild animals had indeed been infected with SIVcpzPtt with observed prevalence of 30–50 percent (Van Heuverswyn et al. 2007; Keele et al. 2006). Genetic analysis made it possible to characterize the ancestors of the HIV-1 group M and N strains, thereby confirming the origin of these HIVs (Fig. 1). In addition, separate SIVcpzPtt strains in Cameroon and Gabon have been isolated. This suggests that the strains can spill over and give rise to the emergence of a new HIV in human populations (Boué et al. 2015; Van Heuverswyn et al. 2007).

These studies also revealed lentiviral infections in gorillas from the western plains (*Gorilla gorilla gorilla*) in southern Cameroon. These viruses, called SIVgor, are related to HIV-1 of groups O and P. They are the source of these two HIV strains (D'arc et al. 2015) (figure 10.1).

10.3.3 Foamy viruses (spumaretroviruses)

Foamy viruses, also known as spumaretroviruses, are transmitted to humans from NHPs. They are present in several species of NHPs in Central Africa and have been isolated from hunters from Gabon

and Cameroon. Simian spumaretroviruses were first described in 1954 in the United States from a cell culture of the kidney of a macaque monkey (*Macaca mulatta*) (Enders and Peebles 1954).

The simian prototype is the "Simian Foamy Virus" (SFV). The prevalence of SFV in naturally infected NHPs is generally high but may vary among animal species (Meiering and Linial 2001; Bastone, Truyen and Löchelt 2003; Mouinga-Ondémé et al. 2010). In captive and semi-free-ranging populations of NHPs, seroprevalence can vary between 75 and 100 percent in adults but is generally lower in younger individuals (Mouinga-Ondémé et al. 2010; Calattini et al. 2006).

Unlike other SIV infections, which are geographically limited, those of SFVs are widespread among NHPs. Most New- and Old-World simian species and great apes are SFV carriers (Meiering and Linial 2001; Hussain et al. 2003; Betsem et al. 2011). Africa is the continent with the most NHP species, and in 2004 Calattini et al. (2004) were the first to describe SFV infection in gorilla, mandrill and drill in the Congo Basin. Subsequently, it was shown that all species of chimpanzees are infected by SFVs (Liu et al. 2008). These viruses can be transmitted within the same species, but also from one NHP species to another, as has been shown between colobus monkeys and chimpanzees in the Tai National Park of Côte d'Ivoire (Leendertz et al. 2008; Morozov et al. 2009).

Transmission of NHP foamy viruses to humans may occur during hunting, mostly through bites or contact with biological fluids from the animal at the time of skinning or preparation. Human infection with SFVs was first described in 1971 (Achong, Mansell and Epstein 1971; Achong and Epstein 1978). It was also shown that this strain is a variant of simian origin acquired during zoonosis (Herchenröder et al. 1994). Other spillovers of SFVs to humans have been documented, mainly in individuals exposed to close contact with NHPs (e.g., animal technicians and veterinarians) and forest hunters (Mouinga-Ondémé et al. 2012; Gessain and Calattini 2008). At present, there is no human prototype of foamy virus, the only strains isolated from humans being those transmitted by NHPs.

As is the case with NHPs, human infection is persistent and asymptomatic and not currently associated with any pathology. In addition, no human transmission of this retrovirus has ever been reported (Gessain and Calattini 2008; Khan 2009).

10.3.4 Other zoonotic diseases

In addition to viruses responsible for haemorrhagic fevers and retroviruses of zoonotic origin such as HIV, which are known to the general public due to their significant and/or global impact on human health, other pathogens continue to emerge or re-emerge. One example is the simian orthopoxvirus, also known as the monkeypox virus (MPV). It is of the same genus as the human smallpox virus and was first discovered in humans in 1970 in the Republic of Congo (Marennikova et al. 1972). Monkeypox is a re-emerging disease in West and Central Africa, where human cases have been increasingly reported for more than 20 years (Petersen et al. 2019). These cases are the result of repeated zoonotic introductions and human-to-human transmission. NHPs can also be infected from it (Radonić et al. 2014). The ecology of this virus is still not clearly understood, but multiple species of wild animals seem to be involved in its zoonotic maintenance and transmission, including rodents (certain squirrel species) that could act as reservoirs (Khodakevich, Ježek and Kinzanzka 1986; Doty et al. 2017). The resurgence of human cases could be linked to the end of vaccination against human smallpox in the early 1980s, as this vaccine probably provides cross-protection against MPV (Petersen et al. 2019). However, changes in habitat, increases in small

mammal populations, and practices leading directly or indirectly to increased rodent-human contact may also play a role in the increasing number of cases.

The Central African forests are home to many other infectious agents for which spillover from animals has not yet been reported or whose pathogenicity remains unknown, but which are genetically close to pathogens that have already emerged from wildlife in other parts of the world. Examples include certain viruses that circulate in different species of bats. After the first emergence of EVD, bats in Central Africa have been particularly studied in comparison with other orders of forest-dwelling animals. The many virological sampling and testing campaigns to which they have been subjected have led to identification of other infectious agents. Some species of African bats, for example, are carriers of paramyxoviruses, some of which are similar to the highly pathogenic zoonotic viruses Hendra and Nipah (genus *Henipavirus*) which circulate in bats in Australia and Asia (Weiss et al. 2012; Drexler et al. 2012; Drexler et al. 2009; Field et al. 2001). This is the case of the African bat, *Eidolon helvum*, a frugivorous migratory species whose habitat spreads over three-quarters of sub-Saharan Africa and which is hunted in many regions for its meat (Weiss et al. 2012; Drexler et al. 2009). Henipavirus-positive serologies have been found in *E. helvum*, domesticated pigs (Hayman et al. 2011), as well as in human populations. Observed prevalence was higher in individuals who handled bat meat (Pernet et al. 2014). However, it remains to be determined whether these equatorial African henipaviruses are capable of emerging and causing pathologies in humans and domestic animals (Weiss et al. 2012).

Another example of a pathogen to monitor at the human/wildlife interfaces of Central African forests is coronaviruses. The seven human coronaviruses described to date seem to have originated from coronaviruses in small mammals. Emergence appears to occur via an intermediate host (Cui, Li and Shi 2019). This is the case, for example, of Middle East respiratory syndrome coronavirus (MERS-CoV) and severe acute respiratory syndrome (SARS-CoV1), whose ancestors are bat coronaviruses and which are transmitted to humans by camels and civets respectively (Li et al. 2005; Ithete et al. 2013; Sabir et al. 2016). The same is true for SARS-CoV2, the 2019 coronavirus (COVID-19), which also seems to have originated in bats but whose intermediate host, if any, remains unknown (Zhou et al. 2020). Bats on the African continent are host to a great diversity of coronaviruses, some of which are part of the same phylogenetic group as SARS or MERS viruses (Bourgarel et al. 2018; Markotter et al. 2019; Letko et al. 2020; Lacroix et al. 2020). The risks of interspecies and zoonotic transmission of coronavirus circulating in forest areas are still largely unknown, but they must be taken into account in surveillance of emergence.

10.4 Surveillance and control of infectious and zoonotic diseases in Central Africa

Central Africa is considered a particularly high-risk area for the emergence of zoonotic diseases, due to the convergence of several risk factors. These latter include the transformation of forest ecosystems (Wolfe et al. 2005b); conditions of poverty (Molyneux et al. 2011); and frequent and close contact with wildlife, which occurs through hunting, handling and consumption of bushmeat (Magouras et al. 2020). The setting up of surveillance systems can help to better understand, monitor and control the dynamics of some pathogens at the human/animal interface.

10.4.1 Definition and theoretical objectives of surveillance

A surveillance system is a process whereby information on the presence of a disease or a health event within a target population is systematically and regularly collected for the purpose of managing that disease or a health event. As zoonoses are diseases shared between animals (in this case wildlife) and humans, information can be collected from animals (surveillance performed by veterinary services) and from the exposed human population (surveillance often performed by public health services). Animal health surveillance approaches and systems vary and are fundamentally dependent on the objectives to be achieved and the means available. If the objective is early detection of an emerging zoonosis such as EVD in terrestrial vertebrates in remote rainforest environments, the most suitable option is to set up event-based surveillance. It is from this angle that extraordinary efforts have been made in the Republic of Congo to detect abnormal mortalities among gorillas and chimpanzees and to collect samples to identify the infectious agent causing these outbreaks (Leroy, Rouquet et al. 2004; Leroy, Telfer et al. 2004b).

Today, permanent surveillance of groups of habituated great apes and of animals found dead in the forest, as well as systematic collection of vectors (e.g., meat flies), are carried out at various sites in Central Africa (Dzanga Sangha in the Central African Republic, Nouabale Ndoki in the Republic of the Congo, Campo Ma'an in Cameroon, and Malebo in the DRC). This type of systematic and event-based monitoring relies on a large-scale awareness-raising effort targeting local populations and the staff of NGOs and national parks. This will enable them to detect mortalities and sound the alarm so that scientific teams can be sent to the field to collect samples from the carcasses of great apes or other mammals (Antonation et al. 2016; Grützmacher et al. 2016; Grützmacher et al. 2018; Kuisma et al. 2019). On the other hand, if the objective is to detect zoonotic agents that circulate unnoticed in wildlife or simply to try to characterize the zoonotic pathogens circulating more frequently in the bushmeat value chain, it is necessary to adopt a type of surveillance that targets not a specific pathogen, but rather a species or taxonomic group (e.g., NHPs, bats and rodents) susceptible of hosting zoonotic pathogens (Levinson et al. 2013).

10.4.2 The state of surveillance systems in Central Africa

Zoonose surveillance is heavily focused on the viral emergencies that have struck Central Africa in recent decades (EVD, yellow fever, monkeypox). However, many other pathogens circulate without being tracked (and are thus not detected), even though their impact on public health and their socioeconomic effects on the human populations exposed to them are far from negligible (Asante, Noreddin and El Zowalaty 2019). The problem here is the differential risk between the need for surveillance of diseases that affect local populations and the need to monitor and control pandemic-risk diseases that can affect everyone. The means for each are not the same and are often biased in favour of pandemic-risk diseases.

As zoonoses are diseases shared by humans and animals, they can be monitored in human and animal populations. Ideally, in the context of an integrated health approach (the "One Health" approach), the two should be coordinated. In Central African countries, there is a significant gap between the human health system and the animal health system in terms of their level of organization and the resources allocated to them. Human health facilities monitor a list of five or six priority

Table 10.1: List of zoonotic diseases monitored in various Central African countries by public health facilities

Diseases	Gabon	Republic of Congo	Democratic Republic of Congo (DRC)	Central African Republic	Cameroon
Ebola	+	+	+	+	+
Avian influenza	+		+	+	+
Monkeypox		+	+	+	
Bovine tuberculosis	+	+			+
Rabies	+	+	+	+	+
Trypanosomiasis		+			
Rift Valley fever		+		+	
Salmonellosis			+		
Anthrax					+
Yellow fever	+	+	+		
References	WHO, 2019a	WHO, 2019b	WHO, 2018	WHO, 2019c	WHO, 2017

zoonotic diseases based on human transmission mapping and risk assessment (see Table 10.1). On the other hand, veterinary services (often under the Ministry of Agriculture) generally have very limited resources in comparison to carry out surveillance on the same zoonoses in animals, and such surveillance remains passive and very modest because of the weak capacities of diagnostic laboratories.

Diseases among wildlife are even more rarely monitored on a systematic basis, with the exception of responses to specific epidemic crises such as Ebola or monkeypox when they have threatened great ape populations or caused significant outbreaks among humans. However, in recent years, Central African countries have developed "One Health" strategies to facilitate coordination between the human health, animal health (both domestic and wild), and conservation sectors. These recent strategies are not always operational, or they may lack the human and financial resources to be effective. WHO has conducted health systems assessment missions and identified the priority need to strengthen surveillance and One Health strategies (WHO 2017, 2018a, 2019, 2018b).

10.4.3 Recommendations to improve the surveillance of zoonoses in wildlife in Central Africa

To optimize the detection of zoonotic agents and in particular viruses, it is advised to sample the freshest possible animal carcasses, as a virus has limited survival outside a living host and degrades rapidly (Greatorex et al. 2016). It is therefore necessary to optimize the chances of detecting pathogens by organizing sample collections with the help of hunters or stakeholders in the field who have access to fresh game carcasses, upstream of the value chain.

Box 10.1: Linking the key One Health pillar of biodiversity/ environment to the sustainable development agenda

The possible wild animal origin of the Sars-COV-2 virus has rekindled concerns about the risks of transmission and spread of emerging zoonotic diseases at the various interfaces between humans, domestic and wild animals, and the environment, and in particular throughout the wildlife value chains. Recent reviews of the literature on the subject (Stephen et al. 2021; Kock and Caceres-Escobar 2022) show not only that there is a lack of convincing data to characterize these risks, but also that there is very little information available on what actions to take to prevent, detect and respond to these risks as well as the effectiveness of those actions. Nevertheless, in the light of current knowledge, all reflections on prioritizing future risk management actions at these different interfaces acknowledge two aspects: 1) the importance of factors and stakeholders related to biodiversity and the environment in the implementation of both preventive and reactive solutions, and 2) the need for integrated multisectoral approaches aligned with the sustainable development agenda to address these risks and respond equitably to local and global health issues and challenges (De Garine-Wichatitsky et al. 2021). This is a necessity for human and animal health as well as for the health of complex socio-ecosystems in which conservation issues are greatly at stake (Lindsey et al. 2020).

Since December 2021, this has been reflected in an updated definition of "One Health" proposed by the One Health High-Level Panel (OHHLEP). This definition now speaks of *"an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and inter-dependent. The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for clean water, energy and air, safe and nutritious food, taking action on climate change, and contributing to sustainable development."*

Given the information gaps and uncertainties, making the One Health approach effectively operational must rely on productive intersectoral institutional coordination capable of making the complex trade-offs between the different sectoral and geopolitical interests, all the while taking into account the available scientific knowledge and the sociocultural and economic contexts of the countries. A recent review of efforts to implement the One Health approach initiated in 2012 by the countries of the subregion shows that progress varies between countries but is still insufficient overall.

Beyond the need for ownership of the approach, it is essential to strengthen the capacities and resources to meet the priority needs, particularly in coordinating and promoting involvement by the biodiversity/environment sector (de Garine-Wichatitsky et al. 2020). Various initiatives are currently supporting Central African governments in this area, including the REDISSE 4 and EBO-SURSY projects, the SWM and ECTAD programmes, PREZODE,[b] and others.

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[a] Conclusions of the ECCAS-FAO subregional meeting held from 14 to 15 December 2021 in Douala to review the implementation of the recommendations of the 2012 and 2017 workshops on the "One Health" approach for the Central African subregion.

[b] REDISSE 4: Regional Disease Surveillance Systems Enhancement Project in Central Africa; EBO-SURSY: viral haemorrhagic fever capacity building and surveillance; SWM: Sustainable Wildlife Management Programme; ECTAD: Emergency Centre for Transboundary Animal Disease; PREZODE: PREventing ZOonotic Disease Emergence

Ecotourism or research projects in protected areas could contribute significantly to zoonotic disease surveillance through direct observation of wildlife (habituated apes), systematic and event-based sample collection (carcass surveillance or vector capture) and on-site facilities (mobile and/or fixed laboratories, logistics, etc.).

Sample collection can be optimized by using new technologies for collection and storage. There are many logistical and technical constraints to setting up wildlife surveillance systems under natural conditions or at remote sites, including being able to detect diseased animals or fresh carcasses and conserving samples until they reach the laboratory. However, some of these material and logistical constraints have changed considerably thanks to the emergence of new technologies. For example, the collection of samples using filter papers or the availability of buffer solutions that preserve genetic material (RNAlater[5]) greatly simplify the work of collecting field samples.

The development of diagnostic systems based on molecular detection, such as next-generation genetic sequencing techniques (Gardy and Loman 2018), enables the simultaneous detection of multiple pathogens in a single biological sample. This solves, for example, the problems of validating immunological tests, which are often cumbersome for detecting antigens or antibodies in wild species.

The "One Health" approach should be promoted for the control of zoonotic diseases. Information from the detection of circulating pathogens in hunted species would help to identify the risks to which human populations interacting with these hosts are exposed. Systematic monitoring of these same pathogens within these human populations (hunters, breeders, butchers, taxidermists, restaurateurs, consumers, etc., depending on the pathogen) could then be set up by the public health facilities or local health posts.

For logging companies which already have management plans in place, promoting "HEALTH SMART" indicators in their certification systems would help to mitigate the environmental and social impact of their activity, as well as reduce any impact on the health of people exposed to zoonotic risks as a result of their forestry activity. To do so, it is necessary to identify single health indicators that can be measured over time.

Conclusions

Emerging infectious diseases are spreading more and more rapidly not only in Central Africa, but in Africa as a whole and the entire world, as a result of increasingly expanding and rapid national, regional and international trade and travel. The COVID-19 pandemic is a perfect example of these global interconnections and the associated risks of the global spread of EIDs.

Landscape changes affecting Central African forests can have impact on several mechanisms which may or may not favour the emergence and re-emergence of pathogens. Tropical forests are home to a wide diversity of as yet unknown viruses and bacteria that represent a source of emerging pathogens. The transformation of landscapes takes place through human infrastructure development following a temporal sequence: 1) roads, enabling access to areas previously inaccessible to vehicles; 2) settlements or small villages, where wildlife resources can be extracted for local or more distant markets (e.g., urban centres); 3) sedentarization of human populations,

5 RNAlater Stabilization Solution is an aqueous and nontoxic RNA tissue stabilization and storage reagent which rapidly permeates tissues to stabilize and protect cellular RNA.

which may then be accompanied by peasant or small-scale cultivation of certain areas in the forests that still dominate the landscape; 4) possible development of small urban centres, which gradually transform the surrounding landscape, with a gradual predominance of fields and more commercial crops (e.g., oil palm); and, finally, 5) areas where forest which had been predominant a few years or decades previously resembling agricultural land, with a few patches of protected or unprotected forest left.

These gradual landscape changes will have three main consequences:

1. There will be an increase in the quantity and quality of human-wildlife contacts, as well as in hunting, agricultural practices and commercial exploitation of resources.
2. There will be a transformation in the ecology of animal hosts of pathogens, thereby altering the ecology of diseases: some host species will have the behavioural and genetic plasticity to adapt better than others to anthropized landscapes (e.g., the *E. helvum* bat seems to thrive in urban centres that can provide food resources throughout the year, without the need for migration).
3. These modifications/adaptations of species to their environment will directly or indirectly (e.g., via interspecies competition) contribute to the modification of wildlife communities. These changes will impact the dynamics of the sylvatic cycles of multihost pathogens and the risks of transmission between wildlife and humans. Thus, a rainforest bat community in a given area will no longer be the same when the landscape is transformed and will promote or not promote some pathogens at the expense of others.

The situation of Central African forests is therefore very dynamic, with changing landscapes, a growth in human/wildlife contacts, and wildlife communities that are adapting to these changes. The rate of transformation of these forests will have an impact on the risks of emergence. The study of emergence mechanisms and the assessment of these risks are therefore difficult: the observation of the presence of a pathogen in a host, of animal behaviour or of transmission dynamics may only be a transitory state in these ecological systems undergoing transformation. Efforts to establish surveillance systems and health policies are often under-resourced and therefore complicated, yet they are essential in these forest ecosystems which still host a wide diversity of agents that are potentially dangerous to human and animal health. These surveillance systems should make it possible to contain the epidemic as quickly as possible in order to protect local populations, limit the costs of the measures taken and avoid pandemics. In the DRC, the budget required to fight the 2018–2020 epidemic increased from USD 26 million to USD 57 million when the disease spread to an urban centre on a major transport route in the region (WHO 2018b).

Given the importance of wildlife as a source of protein and income in Central Africa, a considerable part of zoonotic risk management in this region involves setting up surveillance systems within the bushmeat value chain, based on countries' One Health strategies. Such surveillance systems could easily be set up upstream of a chain, with the collaboration of hunters and the distribution of suitable collection equipment. This approach, combined with high-performance diagnostic systems, would make it possible to establish an initial health assessment of the main pathogens susceptible of circulating within the most common species among the number of animals bagged. On the basis of this initial assessment, it would then be possible to set up more targeted screening programmes for the detection or monitoring of certain pathogens or species, depending on the risk identified. Information from the detection of circulating pathogens in the hunted animal species would help to identify the main risks to which human populations interacting with these hosts can be exposed. This approach works relatively well in some countries that have skilled human resources and that can effectively utilize well-equipped and efficient research laboratories after EVD epidemics.

Emerging infectious disease outbreaks are occurring with increasing frequency and growing socioeconomic consequences which are difficult for African governments to cope with. The example of COVID-19 illustrates this. Many African governments have established measures to prevent the spread of the pandemic. However, the simultaneous occurrence of disruptions to domestic supply and production combined with weak external demand, sharp declines in commodity prices, and the disruption of key service sectors such as tourism jeopardize jobs and livelihoods for local people (ATIBT 2020a). The pandemic has also highlighted the weaknesses of economies and health systems that cannot cope with such situations and are dependent on donations from rich countries for health equipment and vaccinations.

The COVID-19 pandemic has had an impact on working conditions in the forest sector and disrupted the organization and smooth running of its activities. This has had considerable repercussions on the social, economic and environmental balance, thereby affecting jobs, source of income, raw material resources, etc. (ATIBT 2020b), thereby endangering production and trade of essential forest products as well as seriously jeopardizing the livelihoods of local people.

The intensification of the emergence of infectious pathogens has many underlying reasons, all of which are related to the increasing anthropogenic impact on nature in a context of growing social and environmental injustices and inequalities.

Tackling EIDs in the forests of Central Africa requires both symptomatic treatments (e.g., surveillance and control of emerging pathogens and diseases) and substantive treatments that will limit human impact on forests and biodiversity loss. Both approaches are necessary and essential, and the COVID-19 crisis has been a painful reminder of the need for in-depth changes in the way we manage the planet as a whole.

Table 10.2: History of human Ebola Virus Disease (EVD) outbreaks

Country	Dates	Emergence locations	Virus	Probable source of infection	No. of human cases identified	Mortality rates
First epidemics						
DRC	1976	Yambuku	ZEBOV	Unknown	318	88%
South Sudan	1976	Nzara	SUDV	Unknown	284	53%
		Maridi				
Epidemics in sub-Saharan Africa						
DRC	1977	Tandala	ZEBOV	Unknown	1	100%
	1995	Kikwit	ZEBOV	Unknown	315	81%
	2007	Kasai Province	ZEBOV	Bats	264	71%
DRC	2008–2009	Kasai Province	ZEBOV	Unknown	32	47%
	2012	Isiro	BDBV	Unknown	36*	36.1%
	2014*	Several villages in the vicinity of the town of Boende	ZEBOV	Monkeys	66	74%

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Country	Dates	Emergence locations	Virus	Probable source of infection	No. of human cases identified	Mortality rates
	2017	Likati	EBOV**		8	50%
	2018	Bikoro, Équateur Province	ZEBOV	Unknown	54	61%
	2018–2020	Province du Nord Kivu	ZEBOV	Inconnue	3470	66 %
	2020	Bikoro, Équateur Province	ZEBOV	Spillover from an unknown wild animal and human-survivor transmission (2018 outbreak in Équateur Province)	3,470	66%
	2021	Biena Health Zone, North Kivu Province	ZEBOV	Human/survivor transmission	In progress	In progress
Rep. of Congo	2001–2002	Mbomo District	ZEBOV	Great apes?	57	75%
		Kelle District				
	2002–2003	Mbomo District	ZEBOV	Great apes?	143	89%
		Kelle District				
	2003	Village of Mbomo	ZEBOV	Great apes?	35	83%
		Village of Mbandza				
Gabon	1994	Mekouka	ZEBOV	Bats?	52	60%
	1996-1997	Booué	ZEBOV	Great apes	60	74%
	2001-2002	Mékambo	ZEBOV	Great apes	65	82%
Uganda	2000-2001	Gulu	SUDV		425	53%
	2007-2008	Bundibugyo	BDBV		149	29%
	2011	Nakisimata	SUDV		1	100%
	2012	Kibaale district	SUDV		11*	36.4%
	2012-2013	Luwero district	SUDV		6*	50%
South Sudan	1979	Nzara	SUDV	Bats?	34	65%
	2004	Yambio	SUDV	Baboon	17	41%
		Maridi				

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Country	Dates	Emergence locations	Virus	Probable source of infection	No. of human cases identified	Mortality rates
Côte d'Ivoire	1994	Tai Forest	TAFV	Great apes	1	0%
Guinea	2021	N'Zérékoré Prefecture	ZEBOV	Human/survivor transmission	In progress	In progress
Multicountry	2014-2016		ZEBOV	Bats?		
Sierra Leone		Entire country			14,124	28%
Liberia		Entire country			10,678	45%
Guinea		Entire country			3,814	66%
Nigeria		Lagos			20	40%
		Port Harcourt				
Senegal		Dakar			1	0%
Mali		Bamako			8	75%
		Kayes				
Imported cases						
South Africa						
from Gabon	1996	Johannesburg**	ZEBOV		2	50%
Spain						
from Sierra Leone	2014	Madrid	ZEBOV		2	50%
Italy						
from Sierra Leone	2014	Sassari	ZEBOV		1	0%
United Kingdom		Laboratory	SUDV		1	0%
from Sierra Leone	2014	Glasgow	ZEBOV		1	0%
United States						
from Liberia	2014	Dallas***	ZEBOV		3	33%
from Gabon	2014	New York	ZEBOV		1	0%

According to CDC: https://www.cdc.gov/vhf/ebola/history/chronology.html#anchor_1526565058132
* Laboratory-confirmed cases
**One human-to-human transmission from the index case
*** Two human-to-human transmissions from the index case