Food and Agriculture Organization of the United Nations

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ANIMAL HEALTH **RISK ANALYSIS**

ASSESSMENT No. **6**

# ADDRESSING ZAIRE EBOLAVIRUS (EBOV) OUTBREAKS

## *Qualitative entry and exposure assessment update*


### SUMMARY

- This qualitative risk assessment update addresses the likelihood of human exposure to *Zaire ebolavirus* (EBOV) from animals or animal products. The reader should note that the assessment focuses on EBOV suitable areas as defined by Pigott[1] and does not attempt direct comparison of different risk levels between countries or regions. The level of uncertainty in the assessment remains high because of scarce field data on EBOV epidemiology as well as mechanisms of EBOV transmission between animal species and from animals to humans. Some assumptions had to be made, e.g. laboratory findings or modelling results were extrapolated to field settings and general conclusions were drawn from limited field findings. While EBOV spillover from animals to humans is considered a rare event, the public health impact of such spillover, when it occurs, is serious due to the devastating consequences of a large human outbreak.
- The outputs from this update of the previously published rapid qualitative exposure and release assessment[2] (January 2015) are highlighted below.
- The **likelihood** that humans are **exposed** to EBOV in EBOV suitable areas of Africa through close contact[3], handling or consumption of:
  - **fruit bats**, such as *Hypsignathus* spp., *Epomops* spp., *Micropterus* spp., *Rousettus* spp. and *Myonycteris* spp., is considered to be **very low to low**, with increased risk[4] during bat migration periods and when a high proportion of juveniles are present in fruit bat populations, hence increasing contact between susceptible bats and the human population.
  - **other wild mammalian species**, such as non-human primates like gorillas (*Gorilla gorilla*) and chimpanzees (*Pan troglodytes*), non-primate species like black-backed duikers (*Cephalophus dorsalis*) or bush pigs (e.g. *Potamocherus porcus*) is considered to be **very low.**
- Investigations of historic human Ebola outbreaks suggest that EBOV is initially introduced into the human population through contact with wild mammals (e.g. non-human primates, duikers and bats) or their carcasses, consumption of wild animals found dead, or preparation and consumption of hunted wild meat. However, while wildlife hunting and consumption are common practice in affected areas, EBOV spillover to humans is a rare event. After introduction, the most effective route of Ebola spread within human populations is through


[1] Pigott *et al.*, 2016; see also Figure 1 on p.3

[2] See http://www.fao.org/3/a-i4364e.pdf

[3] Close contact is defined as any contact with live animals or their carcasses, blood or bodily fluids or excretions.

[4] Risk may also be increased in Central Africa compared to other regions (e.g. West Africa), as wild meat hunting is reported to be more intensive there, providing increased opportunity for human-wild animal interactions.

human-to-human transmission via contact with bodily fluids of an EBOV-infected person. Despite the assessed very low to low likelihoods, the public health impact of such spillover events, when occurring, is serious due to the devastating consequences of a large human outbreak.

- The **likelihood** that humans are **exposed** to EBOV in EBOV suitable areas of Africa through close contact with domestic mammals, such as:
  - **dogs** is considered to be **very low to low**, with low occurrence in areas where a human Ebola outbreak is ongoing. In such a context, hunting or stray dogs can pose a risk by physically moving the remains of infected animals or people closer to human populations, with the potential to indirectly expose humans to EBOV.
  - **domestic pigs** is considered to be **very low**.
- The role of domestic mammalian species in Ebola epidemiology is still unclear. Even though dogs seem refractory to EBOV disease, their scavenging behaviour with potentially infected carcasses could play a role in spreading the virus within affected areas. In laboratory settings, Landrace pigs (*Sus scrofa*) are shown to be susceptible to EBOV infection and able to transmit the virus to naïve pigs and macaques (*Macaca fascularis*) via direct and indirect contact, respectively. However, data from field studies are scarce and their potential role in Ebola spillover or spread could not be confirmed to date. Instead, the majority of index cases from previous Ebola outbreaks could be linked to close contact with wildlife, handling or butchering carcasses, and preparation or consumption of wild meat, especially raw monkey or bat meat. Recent field data on serologically positive pigs in Ebola-affected areas highlight the need to conduct further epidemiological research to assess their potential role as biological carriers and/or amplifiers in the epidemiology of EBOV.
- The **likelihood** of EBOV **spreading** from EBOV suitable areas of Africa **to an unaffected area** through trade, handling or consumption of meat or other products from susceptible wild animals is still considered to be **very low**.
- Hunting wildlife for consumption is a common activity in sub-Saharan Africa but the extent of trade between countries is unknown in terms of volumes, movements or their direction. Even if, as a rare event, a wild animal infected with EBOV is hunted and its meat sold, the latter is usually shipped, sold and consumed well-cooked, dried or smoked. These processes are expected to reduce the load of viable virus in meat or animal products, thus further decreasing the risk of Ebola spread to non-affected geographical areas.

## BACKGROUND

On 8 May 2018, the Ministry of Health of the Democratic Republic of the Congo declared an outbreak of Ebola virus disease (EVD) in the Bikoro Health Zone, Equateur Province. This is the ninth outbreak the country has experienced since the emergence of the disease in 1976 in its northern part. The current Ebola outbreak, caused by *Zaire ebolavirus* (EBOV), occurred one year after the last outbreak in Likati, Bas-Uélé Province, from May to July 2017. On 13 June 2018 WHO (WHO, 2018) reported confirmed Ebola infections in 53 persons, leading to the death of 29. The origins of the outbreak are still under investigation and the index case or its potential infection source are not yet identified.

Fruit bats, especially those from the *Pteropodidae* family, are considered a natural reservoir of EBOV. Aspects of their ecology, behaviour and distribution as well as evidence from serological and polymerase chain reaction (PCR) field and laboratory studies strongly suggest fruit bats can maintain the virus and play a key role in spillovers to other wildlife or human populations. EBOV is initially introduced into human populations through contact with infected wild animals or their meat. Although this is a rare occurrence, once introduced the highly contagious and infectious virus can spread quickly between humans, depending on the level and type of contact, with devastating consequences, causing high morbidity and mortality.

Prompted by the ongoing outbreak of EVD in the Democratic Republic of the Congo, the Food and Agriculture Organization of the United Nations (FAO) in June 2018 updated its qualitative risk assessment addressing EBOV, originally issued in January 2015.

The likelihood of human exposure to EBOV through close contact with wild animal species, hunting, handling and consumption of meat from different wild animal species as well as the likelihood of introduction and onward transmission of EBOV in unaffected areas through the trade and consumption of wild animal meat or other products are assessed in this update. The potential role domestic animals may play in human exposure to EBOV is also investigated.

This qualitative risk assessment is based upon information available up to 5 July 2018 and will be revised as circumstances change. The reader should note that the level of uncertainty in the risk assessment remains high because of the limited field data on EBOV epidemiology and transmission between animal species and from animals to humans.

## ASSESSMENT

### Risk questions assessed

- What is the likelihood that humans are exposed to EBOV in EBOV suitable areas of Africa according to Pigott *et al.*, 2016 (see also Figure 1 below), through close contact, handling or consumption of susceptible wild mammalian species?
- What is the likelihood that humans are exposed to EBOV in EBOV suitable areas of Africa through close contact with domestic mammals?
- What is the likelihood of EBOV spreading from EBOV suitable areas of Africa to an unaffected area through trade, handling or consumption of meat or other products from susceptible wild animals?

### Methodology for qualitative risk assessment and uncertainties

The risk assessment defined the likelihood of entry and exposure from highest to lowest levels as follows: high (highly likely to occur); moderate (potentially occurring); low (unlikely to occur); very low (very unlikely to occur); and negligible (extremely unlikely to occur). The evidence used to answer each risk question of the assessment can be found in the January 2015 assessment (see footnote 2) and in the Considerations section below. Given the limited availability of surveillance data and field studies on EBOV in different animal species at the time of the assessment, the reader should note that **the uncertainty in the risk assessment of the different levels of likelihood remains high**.

### CONSULTED EXPERTS

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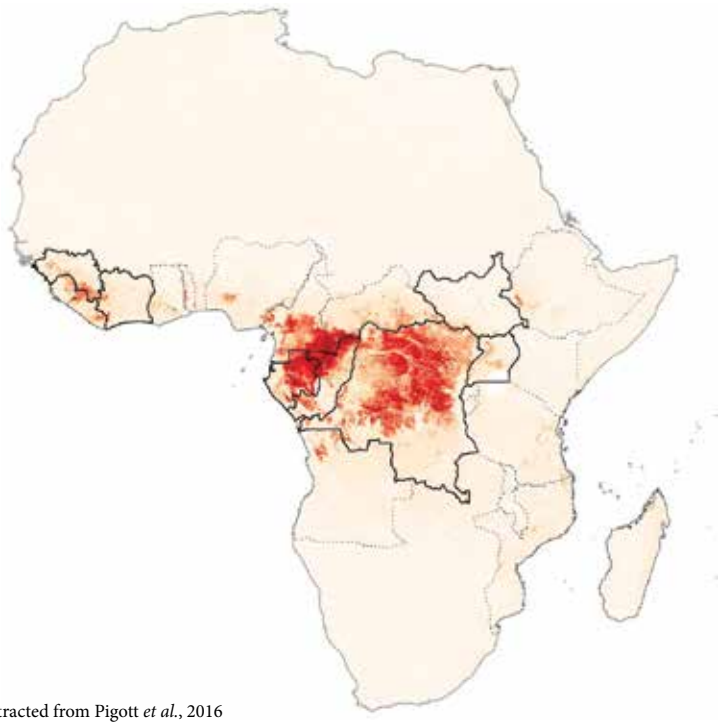
**FIGURE 1:** *Predicted areas of environmental suitability*




Areas closer to dark red (1) are most environmentally similar to locations reporting Ebola virus occurrences; areas in light yellow (0) are least similar. Countries with outlined borders are those which are predicted to contain at-risk areas for zoonotic transmission based on a thresholding approach.

Cameroon, Gabon, the Congo and mainland Equatorial Guinea are now predicted to be more environmentally suitable than in the previous analysis (Pigott *et al.* 2014). The regions of Central Africa, particularly Gabon and the Congo remain most environmentally suitable for zoonotic EVD transmission. Mean enhanced vegetation index (EVI) is the highest relative predictor covariate for zoonotic EVD transmission while Group 1 bat distributions, i.e. those found to have been Ebolavirus ribonucleic acid (RNA) positive is the second. Mean night-time land surface temperature (LST), elevation and mean daytime LST complete the top five predictors.

*Source:* extracted from Pigott *et al.*, 2016

## CONSIDERATIONS

What is the likelihood that humans are exposed to EBOV in EBOV suitable areas of Africa through close contact, handling, or consumption of susceptible wild mammalian species?

- Evidence presented in the January 2015 assessment (see footnote 2).
- Recently published studies carried out in Cameroon, Guinea and Zambia found seropositivity against EBOV in bats, either frugivorous (e.g. *Eidolon helvum*, *Myonycteris angolensis)* or insectivorous (*Mops* sp.), suggesting circulation of EBOV in these populations (Ogawa *et al.*, 2015; De Nys *et al.*, 2017). These studies support the results of serological screenings conducted in the past in multiple bat species including *Epomops franqueti, Hypsignathus monstrosus, Epomophorus gambianus, Myonycteris torquata, Micropteropus pusillus, Mops condylurus* and *Rousettus aegyptiacus* (Olival and Hayman, 2014).
- Susceptibility of bats to EBOV infection and replication are shown to be species-dependent and certain bat species seem more likely candidates to act as a natural reservoir for EBOV, especially where both anti-EBOV IgG and RNA were detected. These species include *Hypsignathus monstrosus*, *Epomops franqueti*, and *Myonycteris torquata* (Leroy *et al.*, 2005). Egyptian rousettes (*Rousettus aegyptiacus*) are shown to be refractory to experimental EBOV infection, with very low levels of EBOV RNA found in tissues and no evidence of viremia or viral shedding (Jones *et al.*, 2015; Paweska *et al.*, 2016), although seropositivity was observed repeatedly in wild populations (Hayman *et al.*, 2012; Pourrut *et al.*, 2007; Pourrut *et al.*, 2009; Leroy *et al.*, 2005).
- A stochastic compartmental model for filovirus persistence, including EBOV, in bat populations suggests that biannual birth pulses in fruit bat species and longer incubation periods (>21 days) facilitate persistent circulation and maintenance of EBOV in bat colonies of similar size to those found in the field. The potential for EBOV persistence would increase with highly gregarious bat species and bat populations from different species that geographically overlap and are able to transmit the virus to each other (Hayman, 2015). Seasonal birthing may increase infection prevalence in African bat populations during certain times of the year, varying with different bat species, as a result of a higher proportion of juvenile and thus immunologically naïve bats susceptible to EBOV infection. For instance, biannual birthing of *H. monstrosus* is thought to occur during August-September and October-December (Wolton *et al.*, 1982) whereas birthing of *M. torquata* takes place in August-September and February-March (Nowak, 1999). Annual birthing of *E. helvum* was observed in February-March (Mutere, 1967), while *E. franqueti* seems to not have a fixed breeding or birthing season (Jones, 1972; Kingdon, 1974). These four fruit bat species are distributed in areas of Equatorial Africa (IUCN, 2018) where Ebola outbreaks were reported in humans and animals.
- Bat birthing periods may also coincide with migration patterns, increasing the potential for EBOV circulation in bat populations through greater mixing and contact, one of the scenarios described by Plowright *et al.* (2016). Subsequently, these settings may play a role in the spillover to humans, especially as interactions between potentially infected bats and humans are reported to increase during migration with the presence of more bats, including juveniles, which are available for hunters and invade human habitats in search of fruits as food. Indeed, field investigations in the 2007 outbreak areas of the Democratic Republic of the Congo showed that migrating bats, including *H. monstrosus* and *E.franqueti*, were observed roosting and nesting in a massive palm oil plantation several weeks prior to Ebola spillover into humans (Leroy *et al.*, 2009).
- The two year old human index case in the West Africa epidemic that originated in Guinea in December 2013 may have been infected by playing in a hollow tree housing a colony of insectivorous free-tailed bats (*Mops condylurus*), supporting the assumption of Ebola spillover through contact with bats or their bodily fluids (Marí Saéz *et al.*, 2015). Besides, the date of the index case occurrence coincided closely with one of the two annual birthing seasons of *H. monstrosus* and *R. aegyptiacus* in West Africa (Hassanin *et al.*, 2016). In 2007, the human index case of the Ebola outbreak in the Democratic Republic of the Congo had also been in contact with bats in a context of massive fruit bat migration before the onset of the disease, even though investigations did not confirm the epidemiological link between the bats and the human infection (Leroy *et al.*, 2009; Muyembe-Tamfum *et al.*, 2012).
- EBOV infections have been recorded in the carcasses of many mammal species, especially non-human primates such as gorillas (*Gorilla gorilla*) and chimpanzees (*Pan troglodytes*) and also in one dead duiker (*Cephalophus dorsalis*) (Olson *et al.*, 2012; Leroy *et al.*, 2004). Non-human primates were severely affected during past Ebola outbreaks, with significant mortalities observed in different species, and are considered dead-end hosts (Bermejo *et al.*, 2006; Leroy *et al.*, 2004). Handling carcasses and consumption of recently deceased wild animal species, in particular non-human primates and duikers, is very common practice in Equatorial Africa and poses a risk of EBOV spillover from wildlife into the human population.
- Although no formal evidence is available to date, wild mammal mortalities including bush pigs (*Potamocherus*


*porcus*), rodents (e.g. *Atherurus africanus*) or members of the *Cephalophus* genus (small antelopes), have been attributed to Ebola outbreaks (Olivero *et al.*, 2016; Spickler, 2014; Lahm *et al.*, 2007).

- EBOV RNA extracts were found in organs of apparently healthy small wild mammals (rodents and shrews) captured in peripheral forest areas of the Central African Republic, but neither live virus nor virus antigen was detected in organ samples (Morvan *et al.*, 1999). These findings suggest the susceptibility of certain wild rodents to EBOV infection but their potential epidemiological role in terms of virus amplification and transmission to other susceptible animals or humans is unknown.
- Modes of EBOV transmission between forest-dwelling animal species are poorly documented but one study reported predation of bats by monkeys (Tapanes *et al.*, 2016) and this behaviour could play a role in Ebola spillover into non-human primate populations. Chimpanzees are also known to hunt bush pigs which may provide an opportunity for EBOV transmission between infected pigs and chimpanzees (Atherstone *et al.*, 2015). The mechanisms of EBOV infection of wild animals through consumption of fruits or crops contaminated by bat fluids or faeces are unknown but remain a potential pathway. Although their diet is predominantly herbivorous, duikers have been observed eating or licking the flesh of decomposing carcasses, which may directly expose them to EBOV (Rouquet *et al.*, 2005). Once spillover occurred into a susceptible wild animal species, transmission of EBOV within the population is likely, depending on the ecology, with higher potential for onwards transmission if the species is gregarious.
- Even though certain wild animal species may be unable to maintain EBOV circulation due to their high susceptibility (e.g. non-human primates, duikers and potentially bush pigs), interspecies transmission of EBOV could occur when infected species cluster with other susceptible hosts around feeding spots particularly if resources are scarce, hence promoting spread of the virus (Delgado and Simón, 2018).
- In laboratory settings, EBOV has been shown to change infectivity and lethality in mice after multiple passages in guinea pigs and non-human primates. These findings suggest that human infection with EBOV may depend on the donor species (e.g. bats or non-human primates) and perhaps the prior species-transmission chain which may affect the virulence of EBOV (Gale *et al.*, 2016).
- A study in south-western Uganda showed that 5.3 percent of 331 febrile patients screened for filovirus infection were positive in EBOV serology but negative in PCR. The most significant risk factor associated with seropositivity to EBOV was identified to be close contact with duikers (i.e. touching), reported to occur frequently in the region


*Duikers, which are susceptible to EBOV infection, are hunted for their meat in Equatorial Africa.*

(Evans *et al.*, 2018). Such results indicate that human EBOV infection may occur regularly without necessarily leading to severe clinical signs or death. This suggests that EBOV infection in humans may be generally underestimated, this is likely due to isolated cases in remote areas rarely being reported to medical authorities.

- Wild meat hunting is a common activity in many parts of equatorial Africa, especially Central Africa, constituting an important source of protein for local communities. Wild animals like fruit bats, rodents, ungulates (including duikers and bush pigs), and non-human primates are hunted regularly, providing opportunity for EBOV spillover into humans (Mickleburgh *et al.,* 2009; Kamins *et al.,* 2011; Van Vliet *et al.,* 2012; Evans *et al.,* 2018). Field information from Central Africa indicates that bats are often consumed entirely, viscera included. Hunters may also feed bat viscera to their dogs.

Therefore the likelihood that humans are exposed to EBOV in EBOV suitable areas of Africa through close contact, handling or consumption of:

- **fruit bats**, especially of the genera *Hypsignathus*, *Epomops*, *Mops*, *Micropterus*, *Rousettus* and *Myonycteris*, is considered to be **very low to low.** This takes into account evidence to date that spillover to humans through close contact with EBOV-infected fruit bats is a rare event. Fruit bats are thought to be natural carriers of the virus and can develop infection without showing clinical signs. Fruit bats may also shed the virus via their faeces, even though evidence of such shedding is poor (Swanepoel *et al.*, 1996) and little is known about shedding duration or the potential for intermittent shedding. In addition, the available data regarding the persistence of the virus in bat populations are poor and the transmission dynamics between bats remain unclear. The proportion of infected bats is suspected to be very low throughout the year and EBOV spillover to humans occurs rarely and only in specific settings. Recent modelling efforts suggest that EBOV prevalence may increase in certain fruit bat populations (e.g. *H. monstrosus*, *M. torquata*, *E. helvum*) during specific months of the year related to birth pulses and occurring once or twice a year depending on the species.

Consequently, factors that may increase human exposure risk to EBOV include an increased proportion of juveniles (i.e. immunologically naïve animals) in bat populations and increased contact between humans and bats, through bat hunting, as a result of encroachment or during bat migrations where thousands of bats fly over villages and feed on fruit tree or crop plantations.

Likelihood of EBOV spillover from bats may increase in future as a consequence of continued forest conversion, especially in Central Africa. This, in combination with frequent hunting for wild meat, unhygienic food preparation or poor general hygiene practices may increase human exposure risk.

- **Other wild mammalian species**, such as non-human primates like gorillas (*G. gorilla*) and chimpanzees (*Pan troglodytes*) or non-primate species, like black-backed duikers (*C. dorsalis*), is considered to be **very low.** Even

if forest-dwelling animals are in contact with fruit bats and may be infected, particularly when the virus actively circulates among bat populations during fruit bat seasonal birthing and migrations, EBOV prevalence in wild animal species is considered to be very low. Non-human primates, duikers and potentially bush pigs appear to be dead-end hosts and develop severe clinical signs that often result in death, preventing the persistance of EBOV in such populations. Nevertheless, wild mammals are regularly hunted for their meat throughout the year which may expose humans to potentially infected animals and contaminated carcasses. The major known route of Ebola spillover into humans to date is close contact with infected wild animals through handling, preparation or consumption of infected wild meat. Exposure could be mitigated by raising awareness on good hunting, food preparation and hygiene practices and monitoring/reporting of wildlife mortalities in susceptible species. The likelihood that humans are exposed to EBOV is thus considered to be **high** when sick or dead EBOV-infected wild animals are handled or consumed.

There are still many unknowns concerning the potential role in Ebola spillover to other wild animal species, such as rodents, that show susceptibility in laboratory settings and are often hunted for their meat. Furthermore, no information is available about the capacity of infected wild mammals to transmit EBOV to humans. It may be supposed that non-human primates, those most closely related to humans, may be effectively transmitting EBOV to humans with an analogy of human-to-human transmission.

The reader should note that **uncertainty in the assessment of the different levels of likelihood remains high**, since there is a need for better understanding of the epidemiology of EBOV in the different animal species.

Even though contact with infected wild animals seems to be the mechanism for initial Ebola spillover into humans, further spread and development of a human epidemic are then due to human-to-human transmission of this highly infectious virus, through contact with bodily fluids of an EBOV-infected person.

### What is the likelihood for humans to be exposed to EBOV in EBOV suitable areas of Africa through close contact with domestic mammals?

- Evidence presented in the January 2015 assessment (see footnote 2).
- In 2016, large-scale serological screening conducted in Sierra Leone detected three out of 400 domestic pig samples to be positive to EBOV nucleoprotein (NP) antigen in areas that were affected by the recent West Africa Ebola epidemic and where interactions between wildlife and livestock are known to occur (Fischer *et al.*, 2018). Field studies in pigs in Uganda, sampled during 2015-2016, are underway (Fischer *et al.*, 2018).
- In Uganda, domestic pigs usually roam freely beyond the smallholder farms (Ouma *et al.*, 2014) leading to interactions with wildlife species such as non-human primates, bats and wild pigs. Domestic pigs compete for food in specific spots, especially around fruit trees, with some aggressive interactions between them and primates reported by local communities (Atherstone *et al.*, 2015). Such interactions are a risk factor for transmission of zoonotic pathogens between domestic pigs and wildlife species and potentially onwards to humans, given that domestic Landrace pigs (*Sus scrofa*) are susceptible to EBOV infection and experimental EBOV transmission occurred directly between pigs and indirectly from pigs to macaques (*Macaca fascularis*) (Kobinger *et al.*, 2011; Weingartl *et al.*, 2012).
- After the onset of the Ebola outbreak in Bas-Uélé Province, the Democratic Republic of the Congo in March 2017, active surveillance conducted in May 2017 identified pig deaths dating back to April in eight villages in the outbreak area. This could suggest a likely Ebola spillover into domestic pig populations (Research Triangle Institute, 2017). However, no evidence was available to confirm the link between EBOV and the pig deaths as other diseases circulating in the region could have led to pig mortality, e.g. African swine fever.
- EBOV transmission from pigs to humans still needs to be proven in field settings, but experimental studies in animal models suggest that it cannot be excluded, given the effective transmission from pigs to non-human primates in laboratory settings and the close genetic relationship between humans and non-human primates. Even though Ebola epidemiology in humans is not consistent with widespread food-borne transmission from pork and pork products, a previous risk assessment indicated that human Ebola outbreaks caused by *Sudan ebolavirus* in Uganda were associated with high density of pigs and times when large numbers of pigs were slaughtered and eaten (Atherstone *et al.*, 2014).
- *In vitro* experiments on primary canine and feline fibroblasts indicated that both types of cells were susceptible to EBOV Glycoprotein mediated infection. However, the infectivity of the canine and feline cells was significantly reduced compared to the infectivity of non-human primate cells (Han *et al.*, 2016).
- The active role of domestic dogs in the epidemiology of Ebola remains unclear and despite a seroprevalence of 31.8 percent observed in dogs in highly affected areas during the 2001-2002 Ebola outbreaks in Gabon (Allela *et al.*, 2005), clinical signs, viremia, replication and shedding in dogs are still unknown. Test results from this study should

be interpreted with caution as test specificity is not well established. However, dogs and even cats could potentially carry the virus and act as fomites while feeding on infected carcasses and moving the remains closer to human populations.

- Domestic ferrets are shown to be susceptible to Ebola when challenged with a wild, non-adapted EBOV strain, resulting in the death of all infected individuals. Replication with high viral titres was observed in certain organs such as liver and spleen, but attempts to isolate the virus were unsuccessful (Cross *et al.*, 2016). Such findings emphasize the likely potential that is as yet unknown of small domestic or wild mammals becoming infected, replicating and spreading the virus in areas affected by Ebola.

Therefore the likelihood that humans are **exposed** to EBOV in EBOV suitable areas of Africa through close contact with:

- **dogs** is considered to be **very low to low**. Indeed, the only additional piece of information available since the last assessment in 2015 are results from the *in vitro* experiment on canine cells, showing low susceptibility of these cells to EBOV infection. Evidence available so far indicates that dogs can develop asymptomatic infection and immune response, but transmission to humans has not been demonstrated. However, the likelihood of dogs spreading the virus mechanically after feeding on infected corpses or on bodily fluids in highly infected areas is still considered to be **low**. In areas where deceased Ebola victims are appropriately buried to prevent access by carnivores, this likelihood will decrease to very low.
- **domestic pigs** is considered to be **very low**. The susceptibility of pigs to EBOV infection was proven in laboratory settings and is supported by findings from field serological studies, indicating exposure of pigs to EBOV-like viruses and subsequent infection. Observed pig die-offs that coincided geographically and concurrently with the Ebola outbreak in the Democratic Republic of the Congo in 2017, frequent pig interactions with wildlife around feeding spots like fruit trees and the ability of pigs to transmit the virus experimentally to macaques, support the assumption that pigs are biological carriers. Pigs may also act as potential amplifying hosts by replicating and shedding EBOV, up to 14 days after infection in the oronasal mucosa, according to Kobinger *et al.*, 2011), which could be further transmitted to humans through regular and close contact. However, such a link has yet to be demonstrated in field settings.
- Instead, the majority of index cases from previous Ebola outbreaks could be linked to wildlife, through handling, preparation or consumption of wild meat, especially raw monkey or bat meat, while the main exposure of humans to the virus during an epidemic remains close contact with bodily fluids from EBOV-infected humans.

A continuous rapid increase in human population density, associated with growing numbers of domestic pigs in many African countries (e.g. Uganda and the Democratic Republic of the Congo) and increased interaction with wild animal species, will provide favourable conditions for Ebola spillover into humans.

### What is the likelihood of EBOV spreading from EBOV suitable areas of Africa to an unaffected area through trade, handling or consumption of meat or other products from susceptible wild animals?

- Evidence presented in the January 2015 assessment (see footnote 2).
- EBOV can spread widely in susceptible hosts through viremia, reaching and infecting different organs (e.g. liver, spleen) and tissues (e.g. skin, muscles, bones). EBOV has also been found in the muscles of non-human primate carcasses sampled in the forest between Gabon and the Congo (Rouquet *et al.*, 2005). The collection, consumption or sale of animal carcasses is very common in the forests of the Congo Basin and certain species consumed regularly are known or presumed to be susceptible to EBOV infection, like non-human primates, duikers, bush pigs or rodents (Monroe *et al.*, 2015). In historic Ebola outbreaks, the majority of index cases were linked to the handling, preparation or consumption of wild meat (especially raw monkey and bat meat), comprising a very important source of protein for communities. Carcasses appear to be infectious only up to three or four days after death, mainly due to decomposition, fly eggs quickly covering carcasses and maggots consuming the flesh (Rouquet *et al.*, 2005).
- When present in Vero E6 cells, EBOV can be inactivated by thorough heating, e.g. at 100°C for ten minutes or at 120°C for five minutes (Haddock *et al.*, 2016). The core temperature of meat or animal products should thus reach, at a minimum, these temperatures for the length of time indicated to ensure inactivation of the virus. However, no clear information is available regarding EBOV survival in meat or animal products, in particular using other processing methods like drying and smoking. EBOV can survive on contaminated surfaces at low temperatures (4°C), when internalised in meat products and when not directly exposed to sunlight (i.e. ultraviolet radiation) (EFSA, 2014). EBOV has also been shown to tolerate multiple freezing-thawing and to remain stable during long-term storage at negative temperatures (Chepurnov *et al.*, 1995).
- A study in Kisangani market, in the east of the Democratic Republic of the Congo showed that most wild meat, comprising rodents, large ungulates and to a lesser extent, primates, is sold smoked and constitutes one of the cheapest sources of protein year-round (Van Vliet *et al.*, 2012). Fruit bats are also commonly sold at Kisangani market and locals


*Domestic pigs are often free-ranging in Equatorial Africa and interact frequently with wild forest animals.*

greatly appreciate bat meat for consumption, as pointed out by local news in the Democratic Republic of the Congo (Radio Okapi, 2018). The wild meat sold at Kisangani market may be transported hundreds of kilometres from cities like Ituri, Ubundu, and Lubutu (Van Vliet *et al.*, 2017).

- Although poorly documented, informal cross-border movements for wild meat trading purposes occur in the forested areas of the Congo Basin which may expose neighbouring countries of the Democratic Republic of the Congo to meat or animal products contaminated with EBOV. To date, authorities in the Democratic Republic of the Congo have not implemented wild meat restrictions anywhere and no information is available concerning restrictions on wildlife hunting related to the ongoing Ebola outbreak.
- The introduction of wild animal meat from Africa to Europe and the United States of America is significant and despite strict regulations and controls at the different ports of entry, airports and harbours, wild meat from West and Central Africa is often brought informally to unaffected countries (Bair-Brake *et al.*, 2014; Falk *et al.*, 2013; Chaber *et al.*, 2016). When transported to other African countries or elsewhere, wild meat is either raw or processed in various forms: dried, smoked, or cooked. However, studies have shown that wild meat products, even when processed, can harbour unsafe levels of bacteria and zoonotic bacterial or viral pathogens (Chaber and Cunningham, 2016; Smith *et al.*, 2012), and may be contaminated by EBOV if originating from affected areas. Nevertheless, to date, no EBOV human infection has been reported outside Africa from handling, preparation or consumption of illegally imported wild meat.
- Although certain African countries like Gabon, the Democratic Republic of the Congo, or the Congo, experienced several Ebola human outbreaks caused by EBOV during the last decades, these outbreaks were localized and did not spread to other countries as compared to the West Africa epidemic of 2013-2016 which started in Guinea and subsequently spread to Liberia and Sierra Leone. Ebola-infected travellers were even detected in Mali, Senegal, Nigeria, Spain, the United States of America, Italy and United Kingdom. Pigott modelled the risk of EBOV spillover and spread in Africa and showed that, even if certain areas rank at high risk for localized outbreaks (e.g. the Congo), Ebola outbreaks in forested areas are comparatively less likely to spread nationally or regionally due to their remote locations (Pigott *et al.*, 2017).

Therefore:

- The likelihood of EBOV spreading from EBOV suitable areas of Africa to an unaffected area through trade, handling or consumption of meat or other products from susceptible wild animals is considered **very low** for unaffected areas of affected countries or countries neighbouring affected areas, but decreasing with the processing method applied, especially cooking and potentially smoking and drying, to become negligible for thoroughly cooked meat.

## CONSEQUENCES ASSESSMENT

As mentioned previously, Ebola spillover from wildlife to human populations is considered a rare event. Despite the assessed very low likelihood of this happening, the public health impact of such spillover, when it occurs, is rather serious due to the potential for further human-to-human transmission related to risky practices observed during funerals, burials or provision of health care in affected areas and the virulence of the *Zaire ebolavirus* (EBOV) associated with a high case fatality rate.

EVD outbreaks can place undue strain on health and medical services, economies, livelihoods and food systems across the most affected countries. The tragic loss of life is one of many negative impacts. During the epidemic in West Africa from 2014-2016, attempts to control the epidemic, fears of infection and overall panic caused many people to abandon their everyday life, including farming, taking care of livestock and marketing of products, such as milk or eggs. This can translate into loss of income and a fall in food production and sales, resulting in a decrease in food availability and access. Depending on the scale and duration of the outbreak, prolonged disruption to the harvest and subsequent planting can drive hundreds of thousands of vulnerable people deeper into poverty and hunger as food sources dwindle.


*Bat juveniles may play a key role in the circulation and persistence of EBOV in bat populations.*

Results from EBOV risk models suggest that, even if certain areas are at high risk of localized outbreaks (e.g. the Congo), Ebola outbreaks in forested areas are less likely to spread nationally or regionally due to their remote locations (Pigott *et al.*, 2017).

It is important to consider that the likelihood of EBOV spillover may increase in future as a result of continued forest conversion and human encroachment, combined with intensive wild meat hunting, especially in Central Africa.

## KNOWLEDGE GAPS

Since *Zaire ebolavirus* (EBOV) was first detected in 1976 in the north of the Democratic Republic of the Congo, there have been many studies to try and shed light on susceptible animal hosts, transmission mechanisms between animals and from animals to humans, as well as the persistence of the virus in wildlife and potential risk factors for spillover into human populations. As is the case with other zoonotic diseases where wildlife play a predominant role in pathogen persistence and transmission, collecting significant and reliable field data is challenging. A number of assumptions were used in the current assessment that warrant further investigation in order to decrease uncertainty and improve precision in likelihood levels. Here we list important knowledge gaps as evidenced by the assessment.

- Additional information on EBOV characteristics: infectious dose, species range, survival in the environment, survival after different processing methods, etc.;
- Studies of fruit and insectivorous bat species: incubation period, shedding and transmission to other bats/species, infectivity in adults and juveniles, bat species distribution, birthing periods, migrations and seasonality;
- Quantification of the spatiotemporal interface between bats and people;
- In Ebola risk models for human spillover, differentiate types of forest, including crop forests and consider forage availability for EBOV-susceptible wild species, e.g. non-human primates, duikers and bats;
- Laboratory studies on susceptibility, shedding and transmission in species where anti-EBOV antibodies or EBOV RNA have been detected in e.g. rodents and domestic dogs;
- Additional serological and virological field investigations into pig and dog populations in recently affected and high–risk areas;
- Additional/updated data on wild meat trade movements and commerce, formal and informal, in West and Central African countries, especially from areas suitable for Ebola and further information on volumes of wild meat or wild animal products from susceptible species that are exported from Africa;


*Bushmeat sold at the weekly market of Yangambi in Orientale Province, Democratic Republic of the Congo.*

- Socio-economic studies in affected areas where EBOV is believed to be circulating to determine what percentage of the population in a given area participates in hunting or butchering activities or in the preparation and consumption of wild meat, in order to apply best approaches for risk communication.

For additional data gaps see FAO's technical meeting report Understanding Ebola Virus at the Animal-Human Interface, available at http://www.fao.org/3/a-i5670e.pdf.

## MITIGATION MEASURES AVAILABLE

For a list of mitigation measures, please refer to the January 2015 assessment (see footnote 2).

For additional information and recommendations on proper food preparation practices, please refer to the FAO Frequently Asked Questions on Ebola virus disease last updated in May 2018, available at http://www.fao.org/3/BU672EN/bu672en.pdf.

Additional information on Ebola virus disease, and advice and recommendations can be found on the following websites:

- FAO EMPRES Ebola website, http://www.fao.org/ag/againfo/programmes/en/empres/ebola/index.html
- World Health Organisation (WHO), http://www.who.int/ebola/en/
- World Organisation for Animal Health (OIE), http://www.oie.int/en/animal-health-in-the-world/animal-diseases/ebola-virus-disease/
- Centers for Disease Control and Prevention (CDC), https://www.cdc.gov/vhf/ebola/about.html

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## NOTES


## RISK ANALYSIS IN ANIMAL HEALTH

Risk analysis is a procedure, which we all do intuitively in our everyday life as we also do in our professional work to assess the risk of any hazard or threat. In animal health, risk analysis has been most widely used as a decision tool to help select the most appropriate health interventions to support disease control strategies, guide disease surveillance and support disease control or eradication strategies.

It should be remembered that risk is not equal to zero and never stays static. Risk changes as drivers or factors of disease emergence, spread or persistence change such as intensification of livestock production, climate change, civil unrest and changes in international trading patterns. Risk analysis should therefore not be seen as a "one off" but as good practice for animal health systems as part of their regular activities. Therefore, risk analysis process should be repeated and updated regularly.

Risk analysis comprises the following components:

**Hazard identification:** the main threats are identified and described.

**Risk assessment:** risks of an event occurring and developing in particular ways are first identified and described. The likelihood of those risks occurring is then estimated. The potential consequences or impact of the risks if they occur are also evaluated and are used to complete the assessment of the risk.

**Risk management:** involves identifying and implementing measures to reduce identified risks and their consequences. Risk can never be completely eliminated but can be effectively mitigated. The aim is to adopt procedures that will reduce the level of risk to what is deemed to be an acceptable level.

**Risk communication:** an integrated process that involves and informs all stakeholders within the risk analysis process and allows for interactive exchange of information and opinions concerning risk. It assists in the development of transparent and credible decision-making processes and can instil confidence in risk management decisions.



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