

**Purpose:** Many unknowns remain concerning the role of animal species in the epidemiology of ebolavirus (EBOV) and transmission risk to humans. The 2018 Ebola outbreak led the Food and Agriculture Organization of the United Nations (FAO) to update its qualitative risk assessment on EBOV release from animals or their products and human exposure.

**Methods & Materials:** A literature review identified recent publications (since January 2015, when FAO's last EBOV risk assessment was published). International scientists provided information from ongoing research, both laboratory and field studies. FAO colleagues from affected and at risk countries contributed field knowledge. Utilizing the information collected from various sources, the likelihood for human exposure to EBOV was assessed considering close contact, handling and consumption of (i) wild animal species or (ii) domestic animal species in areas where EBOV is present, as well as (iii) the likelihood of EBOV introduction into non-infected countries through trade, handling or consumption of meat from susceptible wild animals originating from affected areas.

**Results:** The likelihood for human exposure from susceptible wild animals, such as fruit bats, non-human primates and duikers, in areas where EBOV is present was assessed as low. For domestic animals in these areas, such as pigs and dogs, the likelihood was assessed as very low. The likelihood of EBOV introduction into non-infected countries through trade, handling and consumption of wild meat was also assessed as very low. Given limited availability of surveillance or field study data, the level of uncertainty in the assessment remains high.

**Conclusion:** Investigations of historic human outbreaks suggest that EBOV is initially introduced into human populations through contact with infected wild mammals or their meat. However, in line with the assessed low likelihood, this is considered a rare event. The public health impact of spillover, when occurring, is however devastating due to the huge consequences that human outbreaks entail. The risk assessment helped consolidating current knowledge on EBOV in animals and highlighted outstanding knowledge gaps, including EBOV survival in the environment, susceptibility of animal species in field settings, and information on wild meat trade movements.

<https://doi.org/10.1016/j.ijid.2018.11.024>

### 03.004

#### **Ebola West Africa, 2014–16: an analysis of a filovirus outbreak**

A. Duse

NHLS & University of Witwatersrand, School of Pathology, Johannesburg/ZA

**Purpose:** Zoonotic infections are those that can be transmitted between animals and humans. Approximately two-thirds of human infections are zoonoses and caused by microorganisms as diverse as viruses, bacteria, fungi and parasites. Many of the pathogens causing zoonoses are considered to be either emerging or novel agents. Health of humans is inextricably linked to the health of animals and the environment. More broadly, the environment not only encompasses physical, geographical, climatic, ecological, agricultural and veterinary dimensions, but also the social, cultural, political and religious factors that influence those human behaviors that shape it.

Addressing the connections between health and the environment requires an urgent expansion of interdisciplinary collaborations and strong political and global will. Viral hemorrhagic fever agents pose serious challenges to human health due to the fact that: (i) Filovirus outbreaks are largely created by man and driven by human behavior, (ii) there is significant nosocomial

(hospital) amplification of disease, (iii) there is an associated high morbidity and mortality, (iv) case management is difficult and, as yet, there are no *commercially* available vaccines and therapeutic agents, (v) prevention of infections is fraught with difficulties, and (vi) infection prevention and control strategies can be frustratingly unsuccessful.

**Methods & Materials:** Case study approach.

**Results:** The presentation focuses on the complexity of the 2014–16 West African Ebola outbreak in which there has been multi-country involvement (Guinea, Liberia and Sierra Leone) and is deemed to be the largest Ebola outbreak ever described. Challenges and controversies related to VHF outbreak responses, international health regulations, environmental and sociocultural factors, as well as lapses in infection prevention and control interventions are contextualized. Current knowledge gaps, and future research areas, are highlighted.

**Conclusion:** The viral hemorrhagic fevers (VHFs) of Africa, and more specifically, filoviral infections provide the perfect illustration of the interconnected nature of man, microbe and the environment. With the increasing frequency of filovirus outbreak reports and the threat that filoviruses pose to local, national and global health, knowledge gaps need to be urgently addressed with high quality interdisciplinary research. For this, the One Health approach provides the perfect platform.

<https://doi.org/10.1016/j.ijid.2018.11.025>

### 03.005

#### **The detection of diverse coronaviruses, including MERS-related coronaviruses, in South African bat populations and their associated ecology in *Neoromica capensis***

N. Cronjé<sup>1,\*</sup>, N.L. Ithete<sup>1</sup>, M.C. Schoeman<sup>2</sup>, W. Preiser<sup>3</sup>

<sup>1</sup> Stellenbosch University, Medical Virology (Department of Pathology), Cape Town/ZA

<sup>2</sup> University of KwaZulu Natal, School of Life Sciences, Durban/ZA

<sup>3</sup> Stellenbosch University & National Health Laboratory Service Tygerberg, Medical Virology (Department of Pathology), Cape Town/ZA

**Purpose:** Coronaviruses are RNA viruses encompassing four genera. The alpha- and betacoronaviruses commonly cause mild disease in humans. However, outbreaks of severe respiratory disease in 2002 and 2012 led to the identification of highly pathogenic human betacoronaviruses, SARS- and MERS-CoV, respectively. Bats are believed to be the reservoir host from which all mammalian coronaviruses emerged.

Few studies have been published on South African bat coronaviruses; only 16 bat alphacoronavirus and two betacoronavirus sequences have been reported. Phylogenetic inference shows that the betacoronavirus sequences belong to the same viral species as MERS-CoV. Through a One Health approach, this study aimed to describe coronavirus diversity within South African bat populations as well as factors that might influence bat-coronavirus ecology.

**Methods & Materials:** During a general surveillance effort, 404 bat faecal pellets were screened using PCR assays targeting conserved regions of the coronavirus genome. An additional 183 faecal pellets, collected from *Neoromica capensis* bats, were screened as part of a species-specific surveillance study. Using mixed effects logistic regression analyses, collected ecological sampling data were collated with screening results to identify possible predictors of coronavirus infection in *N. capensis* bats.



**Results:** Based on putative coronavirus species classification criteria, the general surveillance effort detected nine coronavirus species, eight alphacoronaviruses and one MERS-related betacoronavirus, from eight different bat species.

The species-specific surveillance detected three coronavirus species, including MERS-related betacoronaviruses, and identified several instances of coinfection with two different coronaviruses. The mixed effects logistic regression analyses indicated that female *N. capensis* bats and bats trapped at low altitude sites with low body condition scores were most likely to be coronavirus positive.

**Conclusion:** This study demonstrates that diverse coronaviruses are present in different South African bat species and lends additional support to an ongoing circulation of MERS-related betacoronaviruses in this region. The observed cases of coinfection indicate the potential for recombination that could lead to the emergence of a new coronavirus that might have zoonotic potential. The collation of ecological data with screening results revealed that both host and environmental factors may influence coronavirus ecology. These findings could assist the development of improved wildlife surveillance sampling strategies for better detection of novel bat coronaviruses.

<https://doi.org/10.1016/j.ijid.2018.11.026>

03.007

#### Long-term wildlife and human disease surveillance in northern Congo: a model for the detection of Ebola virus disease epizootics

E. Kuisma<sup>1,\*</sup>, S. Olson<sup>2</sup>, P. Reed<sup>3</sup>, A. Ondzie<sup>4</sup>, V. Munster<sup>5</sup>, C. Goma Nkoua<sup>6</sup>, H.-J. Parra<sup>7</sup>, W. Karesh<sup>8</sup>, J.-V. Mombouli<sup>7</sup>

<sup>1</sup> Wildlife Conservation Society, Wildlife Health Programme, Brazzaville/CG

<sup>2</sup> Wildlife Conservation Society, Wildlife Health Program, New York/US

<sup>3</sup> Field Veterinarian, Cape Town/ZA

<sup>4</sup> Wildlife Conservation Society Congo, Brazzaville/CG

<sup>5</sup> Rocky Mountain Laboratories NIAID, Laboratory of Virology, Hamilton, MT/US

<sup>6</sup> Laboratoire National de Santé Publique, Service d'Epidémiologie Moléculaire, Brazzaville/CG

<sup>7</sup> Laboratoire National de Santé Publique, Brazzaville/CG

<sup>8</sup> EcoHealth Alliance, New York, NY/US

**Purpose:** We examine if local communities reporting great ape and other mammal carcasses are able to act as an effective wildlife mortality surveillance network for Ebola virus disease (EVD) with wide-coverage and low financial commitment.

**Methods & Materials:** Partnering with the Congolese Ministry of Health (MoH), the Wildlife Conservation Society (WCS) conducted wildlife mortality surveillance and community outreach campaigns in the Cuvette and Sangha regions of the Republic of Congo (RoC). As several recorded EVD epidemics have been preceded by epizootics and physical contact with wildlife carcasses, residents in the rural communities are visited by members of the WCS Wildlife Health Program for educational campaigns. The team meets with the community and provides information on the dangers of EVD and other zoonotic diseases, including how to reduce the risk of human exposure by changing behaviour. Advice includes avoiding contact with carcasses and building awareness of the best practice in the case of illness. The hunters and women foraging in the forest are then encouraged to report observations of carcasses to a hotline and posters are affixed to prominent locations in the

village. Carcass notifications trigger a follow-up visit to reinforce the initial messaging, sampling, testing, and a return visit to relay the test results.

**Results:** Since 2006, our network engaged over **5,800** hunters in more than **290** villages, effectively covering more than **140,000** km<sup>2</sup> of landscape within Ebola endemic areas and high levels of human-wildlife cohabitation. To date, the network has safely sampled carcasses from 41 gorillas, 10 chimpanzees, and 6 mortalities of other species. In total, **16** national and international field staff have been trained in safe carcass sampling methods.

**Conclusion:** This decade-long disease surveillance effort continues to function as an early but untested warning system for epizootics and zoonotic spillover. The last positive detection of Ebola virus in RoC was June 2003. Surveillance of wildlife mortality, coupled with community education are fundamental tools that public health agencies can use to protect against future outbreaks.

<https://doi.org/10.1016/j.ijid.2018.11.027>

03.008

#### Review of brucellosis in Albania: disease frequency in humans and animals, and one health efforts to control the disease, 1925 to present

K. Mersini<sup>1,\*</sup>, L. Alla<sup>2</sup>, A. Juma<sup>3</sup>, X. Koleci<sup>4</sup>, J. Crilly<sup>3</sup>, S. Bino<sup>5</sup>

<sup>1</sup> South East European Centre for Disease Surveillance and Control, Tirana/AL

<sup>2</sup> Institute of Public Health, Surveillance and Control of Infectious Diseases, Tirana/AL

<sup>3</sup> Food Safety and Veterinary Institute, National Veterinary Epidemiology Unit, Tirana/AL

<sup>4</sup> Agricultural University of Tirana, Faculty of Veterinary Medicine, Tirana/AL

<sup>5</sup> Institute of Public Health, Tirane/AL

**Purpose:** The aim of the current review is to provide frequency estimates and spatial distribution of brucellosis in humans and animals over a century.

**Methods & Materials:** Descriptive epidemiology of brucellosis in humans and animals is elucidated by a combined approach utilizing official data and literature review. Official data on disease occurrence from 1990 to present were collected from the Institute of Public Health and Food Safety and Veterinary Institute. A total of 77 national publications on brucellosis from 1938 to 2016 were reviewed and data were extracted.

**Results:** Results are divided in different time periods according to disease patterns and control measures applied on animal populations. The first period 1925 – 1960 was marked by a rapid increase of cases both in humans and animals. The prevalence in small ruminants was 4% – 8% and 0.2% – 9% in cattle, meanwhile average annual incidence in humans was 23 cases per 100,000. During the next period 1960 – 1990, the disease was almost eradicated due to intensive test and slaughter and massive vaccination of animals. As a result the prevalence in small ruminants in 1989 has fallen to 0.02% and 0.001% in small ruminants and cattle respectively. During the 80s only sporadic cases were recorded in humans. In the third period 1991 – 2004 a comeback of brucellosis has been documented with similar trend like in the 60s. Interestingly the number of cases in 2004 was 1.139 which is almost the double of 614 cases in 1960, however the incidence was identical with 37 cases per 100,000 pop which is explained by rapid demographic changes that occurred in the country. The fourth period 2005 – 2015 is characterized by a rapid decline with 5 cases per 100,000 pop

