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manual

# INVESTIGATING THE ROLE OF BATS IN EMERGING ZOONOSES

Balancing ecology, conservation and public health interest

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Balancing ecology, conservation and public health interest

**Edited by**
Scott H. Newman, Hume Field, Jon Epstein and Carol de Jong



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# Authors' details

*(in alphabetical order)*

**Brian R. Amman**
Viral Special Pathogens Branch, Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
e-mail: cxx1@cdc.gov

**Janine Barrett**
Queensland Centre for Emerging Infectious Diseases, Biosecurity Queensland, Brisbane, Australia
e-mail: janine.barrett@deedi.qld.gov.au

**Carol de Jong**
Queensland Centre for Emerging Infectious Diseases, Biosecurity Queensland, Brisbane, Australia
e-mail: carol.deJong@deedi.qld.gov.au

**Jonathan H. Epstein**
EcoHealth Alliance, New York, NY, United States of America
e-mail: epstein@ecohealthalliance.org

**Hume Field**
Queensland Centre for Emerging Infectious Diseases, Biosecurity Queensland, Brisbane, Australia
e-mail: hume.field@deedi.qld.gov.au

**Ivan V. Kuzmin**
Poxvirus and Rabies Branch, Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
e-mail: ikuzmin@cdc.gov

**Tammy Mildenstein**
Wildlife Biology Program, College of Forestry and Conservation, University of Montana, Missoula, United States of America
tammy.mildenstein@umontana.edu

**Scott H. Newman**
EMPRES Wildlife Health & Ecology Unit, Animal Health Service, Animal Production and Health Division, Food and Agriculture Organization of the United Nations, Rome
e-mail: scott.newman@fao.org

**Stuart Nichol**
Viral Special Pathogens Branch, Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
e-mail: stn1@cdc.gov

**Craig Smith**
Queensland Centre for Emerging Infectious Diseases, Biosecurity Queensland, Brisbane, Australia
e-mail: craig.smith@deed.qld.gov.au

**Suxiang Tong**
Gastroenteritis and Respiratory Laboratory Branch, Division of Viral Disease, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
e-mail: sot1@cdc.gov

**Jonathan Towner**
Viral Special Pathogens Branch, Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
e-mail: jit8@cdc.gov

**Lin-Fa Wang**
CSIRO Livestock Industries, Australian Animal Health Laboratory, Geelong, Australia
e-mail: linfa.wang@csiro.au

# Foreword

With over 1,150 bat species worldwide – representing about twenty percent of the biodiversity of all mammalian species – they carry out important ecological and agricultural functions such pollination and dispersion of seeds. And while many tropical plant species depend entirely on bats for the distribution of their seeds, it is true that in the tropics bats can also be carriers of important diseases such as rabies, mokola, duvenhage, hendra or nipah viruses. These are the ones we know of today, but some 40 years ago, all we knew was about rabies. Is there more we should be doing?

This manual, "Investigating the role of bats in emerging zoonoses: Balancing ecology, conservation and public health interests" is an introduction to the complex issues associated with a One Health approach to understanding the biology and ecological importance of bats, and the drivers of zoonotic disease emergence from bats to people. As an introduction, this manual will provide a basis for understanding the need to balance natural resource management, disease surveillance, prevention and control.

**Dr Juan Lubroth**,
Chief Veterinary Officer
Animal Health Service
FAO, Rome

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The bat health and safety section has been developed by the Food and Agriculture Organization, the Australian Government Department of Agriculture, Fisheries and Forestry and the Australian Wildlife Health Network. Information is based upon guidance provided in Australian AUSVETPLANs, developed by government health and agriculture agencies and bat experts in Australia; guidance within Bat Manual chapters; and information provided in the Australian Immunisation Handbook 9th Edition 2008. Lyndel Post, Wildlife Health and Environment DAFF and Tiggy Grillo AWHN collated the information.

# Preface: Scope of this manual

*Scott H. Newman* [a]

This manual has been created for capacity development in countries interested in developing bat ecology, monitoring or disease surveillance programmes. It is intended for colleagues who have minimal knowledge about these topics and may be from public health, biology, wildlife, forestry, laboratory diagnostic, veterinary or agricultural professions. The manual contributes an important body of information about bat ecology, the ecological importance of bats, field techniques for studying bats and the most important infectious agents that are non-pathogenic to bats, but pose great risk to humans as zoonotic agents when they infect non-traditional host species. While bats may pose a risk to human health, it is important to realize that in most cases, zoonotic disease exposure from bats is a result of anthropogenic activities, and the ecological benefits of bats as pollinators or insect consumers far outweigh their zoonotic disease transmission potential. Therefore, understanding the ecology of the natural host of many potential zoonotic pathogens provides an opportunity for optimum management of the biological needs of bats and their habitats, ultimately ensuring the health of humans, livestock and wildlife species. This multisectoral approach, balancing the needs of people, wildlife, livestock and the environment, is part of a broader "One Health" approach, which is rooted in ideas that evolved more than 50 years ago.

The concept of addressing the connectivity between animal and human health is not new. In the 1960s, Calvin Schwabe, a veterinary epidemiologist and parasitologist in the United States, coined the expression "One Medicine" calling for a unified approach between veterinary and human medicine to combat zoonotic diseases – those diseases transmitted from animals to humans. The Manhattan Principles established in 2004 focus on the prevention of the emergence and re-emergence of diseases in the modern globalized world. More recently, a series of Ministerial conferences (Bamako, Mali 2006; New Delhi, India 2007; Sharm El Sheikh, Egypt 2008; Hanoi, Viet Nam 2010) resulting from the emergence and global spread of H5N1 highly pathogenic avian influenza (HPAI) have led international efforts towards addressing emerging infectious diseases at the animal-human-ecosystem interface, using the One Health approach and ensuring that health systems are capable of addressing high-impact disease threats that arise at the interface. It is recognized that to accomplish this requires inter-sectoral collaboration, timely and transparent communication, improved capacity, political commitment, regional and international cooperation, within the One Health framework.

Approximately 60 percent of emerging infectious diseases of humans are zoonotic and, since the 1940s, 70 percent originate from wildlife (often forest-dwelling) with wildlife-derived zoonotic diseases continuing to increase. These zoonotic pathogens have been identified in ungulates, carnivores, rodents, primates and non-mammal species, with important pathogens and diseases including HIV/AIDS, West Nile viruses, H5N1 HPAI, severe acute respiratory syndrome

[a] Food and Agriculture Organization of the United Nations

(SARS) and monkey pox. Most recently, bat-derived zoonotic pathogens such as Nipah and Hendra viruses, SARS-like coronaviruses, the Ebola and Marburg viruses, as well as various rabies-causing lyssaviruses, have gained notoriety as leading emerging diseases transmitted directly from bats to people, or via intermediate livestock and companion animal hosts, or fomites.

It has become clear that the emergence of infectious diseases, while complex in nature, is driven to some extent by ecosystem changes associated with growing global human population, increasing demand for animal protein by the growing middle-income class, more intensive farming systems, unsustainable natural resource consumption, biodiversity loss and habitat fragmentation, which lead to the loss of ecosystem services. Natural systems such as forests, grasslands, wetlands and oceans provide ecological services that all life depends on. Forests, for example, help purify air and water and mitigate greenhouse gas buildup in the atmosphere. Alteration in natural systems – whether in a rural, modified peri-urban or urban setting – results in decreased ecosystem services, leading to disease and increased health risks for all of the species in the ecosystem, including plants, wildlife, livestock and humans. Climate change and loss of ecosystem resilience, furthermore, are paving the road for the emergence of a series of new, multidimensional conservation and health challenges.

Approximately 70 percent of the 1.5 billion poorest people are dependent on livestock and natural resources. Poor sanitary and biosecurity conditions, in densely populated human-dominated, modified multi-species environments, provide opportunities for pathogens to transit more easily among potential host species. Subsistence bushmeat consumption, wildlife farming and trade bring people into contact with a great diversity of forest-dwelling species exposing people to novel pathogens. Intensive farming systems are also fertile breeding grounds for pathogens that can infect multiple hosts including livestock, wildlife and people.

In a globalized world where pathogens can travel the world in a day, emerging diseases, especially those affecting humans, livestock or wildlife, can have large negative socio-economic implications. Impacts can be severe for public health, livelihoods and food security, as well as for international trade and tourism. It is clear that the solution to the challenge of emerging infectious diseases relies on collaboration and integration of multiple disciplines and partners, including ministries of forestry and environment, agriculture and health. While more science is necessary to understand the complex relationships among disease emergence, transmission and ecological systems, science alone is not the solution. It is also essential to address the social and cultural dimensions of societies where issues concerning livestock, wildlife, humans and entire ecosystems intersect. Changes in thinking and behaviour must be encouraged, and future decision-making must be cognizant of the repercussions of poor natural resource management and their implications for civilization.

With the global response to H5N1 HPIA, reasonable capacity for regional disease surveillance, outbreak response, control and prevention in the agriculture sector has been established. However, there is still limited wildlife surveillance capacity, limited integration of wildlife expertise into epidemiological disease assessments, and often a lack of ecological information about wildlife host or transmission species. Furthermore, disease detection or emergence in people, livestock or wildlife rarely results in a multidisciplinary integrated response to determine drivers of emergence and to implement management actions. For field programmes targeting pandemic threats to be successful, they must take into account the broad range of stakeholder concerns, thus making animal disease prevention and control integral components of more general development activities.

# Contents

# Chapter 1
# Emerging infectious diseases

*Carol de Jong* [a], *Hume Field* [a], *Scott H. Newman* [b] *and Jonathan H. Epstein* [c]

## WILDLIFE AND EMERGING INFECTIOUS DISEASES

Although the current focus on emerging diseases in scientific literature and the popular press might suggest otherwise, novel diseases have occurred throughout history. By definition, every newly identified disease is novel. Today's endemic disease was yesterday's novel disease. This observation is not meant to invoke any complacency regarding the inevitability of disease emergence, nor to downplay the need for surveillance or discount the challenges associated with investigating and managing the outbreak of new diseases. Rather, it offers a window into the lessons of history.

Emerging infectious diseases (EIDs) are defined as infections that have newly appeared in a population or have existed previously but are rapidly increasing in incidence or geographic range (Morens, Folkers and Fauci, 2004). Emerging infections have been a familiar threat since ancient times, with pandemics of cholera, influenza, smallpox and measles causing the deaths of millions of people worldwide. Since the 1940s, the incidence of EIDs has risen significantly and more than 300 infectious diseases have emerged (Jones *et al.*, 2008), most of which are viruses (Taylor, Latham and Woolhouse, 2001). More than 60 percent of EIDs are of zoonotic origin (Jones *et al.*, 2008), and in the last decade of the twentieth century zoonotic EIDs constituted 52 percent of all EID events (Taylor, Latham and Woolhouse, 2001).

Of all EIDs, zoonoses from wildlife represent the most significant, growing threat to global health. Among the zoonotic EIDs to emerge since the 1940s, the majority of EID events have originated in wildlife (71.8 percent) and their incidence has continued to increase (Jones *et al.*, 2008). Emerging zoonotic pathogens have been identified in ungulates, carnivores, rodents, primates, bats and other mammal and non-mammal species (Woolhouse and Gowtage-Sequeria, 2005). The best known EID of modern times, acquired immunodeficiency syndrome (AIDS), emerged from non-human primates around the early twentieth century (Worobey *et al.*, 2008). AIDS, which is caused by infection with one of two types of the human immunodeficiency virus (HIV), now threatens to surpass the Black Death of the fourteenth century and the 1918 to 1920 influenza pandemic, each of which killed 50 million people (Morens, Folkers and Fauci, 2004). Other recently emerged diseases, including Ebola virus, hantavirus, Nipah virus, West Nile virus, severe acute respiratory syndrome (SARS) coronavirus and highly pathogenic avian influenza (HPAI) virus, are examples of emerged or emerging zoonoses that have had (or threaten to have) a significant impact on human health.

[a] The State of Queensland, Department of Employment, Economic Development and Innovation (2011)

[b] Food and Agriculture Organization of the United Nations

[c] EcoHealth Alliance

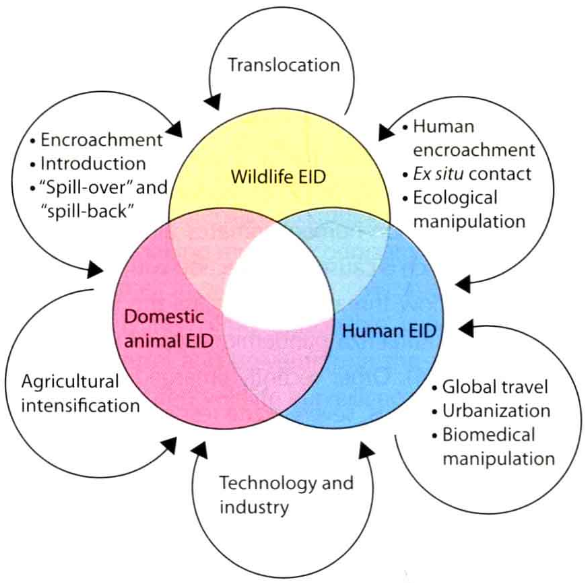
Understanding the factors that lead to pathogens jumping species or to increased contact among wildlife, livestock and humans is critical to understanding how diseases emerge from wildlife.

## DRIVERS OF EMERGENCE

Wildlife populations constitute a large and often unknown reservoir of infectious agents (Chomel, Belotto and Meslin, 2007), playing a key role in emergence by providing a "zoonotic pool" from which previously unknown pathogens may emerge (Morse, 1995). The emergence of many zoonoses can be attributed to predisposing factors such as global travel, trade, agricultural expansion, deforestation and urbanization; such factors increase the interface and/or the rate of contact among human, domestic animal and wildlife populations, thereby creating increased opportunities for spill-over events to occur (Daszak, Cunningham and Hyatt, 2000; 2001). Lederberg, Shope and Oaks (1992) describe these changes as providing an "epidemiological bridge" that facilitates contact between the agent and the naive population. Daszak, Cunningham and Hyatt (2000) suggest that disease emergence from wildlife sources is primarily an ecological process, with emergence frequently resulting from a change in the ecology of the host or the agent or both. They suggest that most emerging diseases exist within a finely balanced host-agent continuum among wildlife, domestic animal and human populations. Any changes in the environment or host behaviour provide agents with favourable new ecological niches, allowing them to reach and adapt to new hosts and spread more easily between them (Morens, Folkers and Fauci, 2004).

FIGURE 1.1

**The host-parasite continuum: most emerging diseases exist in a host-parasite continuum among wildlife, domestic animal and human populations**




*Source:* Daszak, Cunningham and Hyatt, 2000

Pathogen adaptation and virulence are additional dynamics that have direct linkages to the ecological systems in which they occur. Regardless of whether the system is natural or agricultural, the key to pathogens' survival is their ability to adapt to the ever-changing environment. In natural systems, loss of biodiversity, changes in landscape ecology, climate change and other variables pose innate adaptation challenges for pathogens. In agricultural settings, farming modifications including intensification, changes in animal density or husbandry practices, use of pharmaceuticals and marketing create the adaptation challenges for pathogens. The pathogens that exist in wildlife or livestock hosts are therefore constantly challenged to adapt to new environmental circumstances for their survival, resulting in the emergence of "super pathogens" that can cross sectors such as the wildlife-livestock interface, and can ultimately infect humans when the opportunity arises.

Table 1.1 lists a range of drivers for the emergence of infectious disease identified by Daszak, Cunningham and Hyatt (2000), Morens, Folkers and Fauci (2004), Woolhouse and Gowtage-Sequeria (2005) and Chomel, Belotto and Meslin (2007). At the macro

TABLE 1.1
**Drivers of emerging zoonoses**

| **Human behaviour*** |
|---|
| Cultural preference and celebrations |
| Food choices (bushmeat, live-animal markets, freshly killed) |
| Traditional medicine |
| Consumption instead of conservation |
| Ecotourism |
| Petting zoos |
| Exotic pet ownership |
| **Modifications to natural habitats*** |
| Communities and settlement encroaching on natural habitat |
| Development and construction |
| Water resource management (dams, redirecting river or ocean flow patterns) |
| Deforestation |
| Fragmentation of habitat |
| Loss of biodiversity and species |
| Waste and garbage management |
| Climate change |
| **Changes in agricultural practices*** |
| Expansion of livestock farming and encroachment |
| Intensification of production systems resulting in overcrowding, stress, and faster growing and input/ output periods |
| More wastewater and faecal runoff into the environment |
| Farming of new species, including wildlife, without proper medical care, husbandry or biosecurity |
| Globalized international market chains |

* The impacts are amplified by human demographics and socio-economic advancement from poverty towards middle income.

*Source:* Adapted from Chomel, Belotto and Meslin, 2007.

level, closer human contact with wildlife habitats, primarily caused by human population expansion into and modification of wildlife habitat, is considered a major driver in the emergence of zoonotic infections (Cunningham, 2005). At the microbial level, molecular changes may contribute to emergence, when mutation, recombination or reassortment occur or microbes switch from animal to human hosts (Morens, Folkers and Fauci, 2004).

## IMPACT OF EIDs

EIDs are a significant threat to global public health, particularly considering that more than 25 percent of annual deaths worldwide are estimated to be directly related to infectious diseases (Morens, Folkers and Fauci, 2004). Economic losses associated with livestock morbidity and mortality threaten not only agricultural industries, but also wildlife-based economies such as wildlife tourism or the bushmeat trade (Chomel, Belotto and Meslin, 2007). Historically, wildlife diseases have been considered important only when agriculture or human health are threatened (Daszak, Cunningham and Hyatt, 2000). However EIDs are also a significant threat to species conservation and biodiversity. While wildlife species can be considered reservoirs of pathogens with the potential to infect humans and livestock, wildlife populations are themselves also threatened by introduced pathogens. Spill-over of infectious agents to wildlife populations is a particular threat to endangered species, where the presence of infected reservoir hosts can lower the pathogen's threshold density and lead to local population extinction (Daszak, Cunningham and Hyatt, 2000). For example, white nose syndrome, an emerging fungal pathogen of hibernating bats in northeastern North America first observed in 2006, has caused unprecedented bat mortality leading to losses of up to 95 percent in some hibernacula (Blehert *et al.,* 2009; Wibbelt *et al.,* 2010). Another (non-bat) example of the impact of EIDs on wildlife populations is high-pathogenicity avian influenza. While low pathogenic avian influenza was probably introduced from free-ranging waterfowl into poultry, the change from low to high pathogenicity occurred in poultry and spill-back into wildlife populations. This scenario has been responsible for a population-level impact on bar-headed geese (*Anser indicus),* as more than 6 000 individuals died during a single outbreak at Qinghai Lake in 2005 (Chen *et al.,* 2006; Zhou *et al.,* 2006).

## BATS AND EIDs

In recent years, bats have been implicated in numerous EID events and are increasingly recognized as important reservoir hosts for viruses that can cross species barriers to infect humans and other domestic and wild mammals (Calisher *et al.,* 2006). Bats are second only to rodents in numbers of living genera and species, and are the largest order of mammals in overall abundance (Sulkin and Allen, 1974). They are unique in their vagility (potential for long-distance travel), and often aggregate in very large colonies (Turmelle and Olival, 2010). However, despite their abundance, relatively little is known about the species from which zoonotic viruses emerge to cause human disease (Calisher *et al.,* 2006). Much of the information gathered on the role of bats in the maintenance and spread of viruses has been from species of Microchiroptera (insectivorous bats), and there is relatively little information available for members of the suborder Megachiroptera (flying foxes and fruit bats) (Mackenzie, Field and Guyatt, 2003).

The role of bats in viral disease is well established (Sulkin and Allen, 1974), particularly their role as hosts for alpahviruses, flavirviruses, rhabdoviruses and arenaviruses (Mackenzie, Field and Guyatt, 2003). Calisher *et al.* (2006) report on 66 viruses that have been isolated from or detected in bat tissues of 74 species (Table 1.2). Some viruses have been isolated from bats of only one species, and one from bats of 14 species. There are also many viral infections for which only serological evidence is available. Perhaps one of the highest-profile EID events in recent years – for which flying foxes have been identified as the natural host – is Nipah virus, which was identified as the cause of a major outbreak of disease in pigs and humans, resulting in 265 human cases of viral encephalitis (with a 38 percent mortality rate) and the eventual culling of 1.1 million pigs (Chua *et al.*, 2000). It is recognized that this catastrophic disease event was probably the result of several major ecological and environmental changes associated with deforestation and the expansion of non-industrial pig farming in association with the production of fruit-bearing trees. This combination created circumstances that led to the infection of pigs following indirect exposure to virus shed from fruit bats (Chomel, Belotto and Meslin, 2007). The highly infectious virus subsequently led to human cases (Daszak, Cunningham and Hyatt, 2001), most of which involved pig farmers or people associated with pig farming.

Bats possess certain characteristics that may maximize their effectiveness as reservoir hosts for viruses. Natural history features such as high species diversity, long life span, the capacity for long-distance dispersal, dense roosting aggregations (colony size), social behaviours and population structure, the use of torpor and hibernation, unique immunology and spatial population structure (Calisher *et al.*, 2006; Turmelle and Olival, 2009) have been suggested for the association of bats and EIDs. Evolutionary adaptations such as conserved

FIGURE 1.2
**A property quarantined during an outbreak of Hendra virus in Queensland, Australia**


HUME FIELD; © THE STATE OF QUEENSLAND (DEEDI)

FIGURE 1.3
**Dense roosting behaviour of little bent-wing bats (*Miniopterus australis*) facilitating the transmission of virus among individuals**


CAROL DE JONG; © THE STATE OF QUEENSLAND (DEEDI)

cellular receptors and pathways may also enhance the capacity for transmission of bat-associated viruses to other mammals (Calisher *et al.*, 2006).

So why are these diseases emerging now? When attempting to answer this question, it is appropriate to distinguish between emergence and detection. The identification of bat species as probable natural hosts of some recently described EIDs can be attributed