Chapter 28
Bat-Related Zoonoses

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Abstract The many emerging infectious diseases associated with Chiropteran species can have major impacts on both ecosystem and public health. As such, the scope of this chapter is to provide an overview of those potential bat-related zoonoses and their clinical relevance to people. With increased disease surveillance and a trend toward more human contact with bat populations, it is likely that additional zoonotic diseases will continue to be identified. Bat infection dynamics are driven by a complex interplay of ecological, immunological, behavioral, and anthropogenic factors. Interdisciplinary work will be needed in the future to better understand the drivers of disease emergence in bat populations and ultimately mitigate the threats that face both people and bats themselves.

Bats are increasingly implicated as hosts of zoonotic and potentially zoonotic pathogens. As a whole, chiropterans now represent the largest known reservoir of emerging viruses (Calisher et al. 2006; Wong et al. 2007). Amongst the 60 viral species currently associated with bats, 59 are RNA viruses of importance in the current generation of emerging and re-emerging human infections (Wong et al. 2007). Lyssaviruses, paramyxoviruses, filoviruses, and coronaviruses are amongst those pathogens impacting the health and well-being of both people and non-human animals around the globe. In comparison to the studies conducted on viral infections, much less attention has been paid to the non-viral pathogens of zoonotic importance within bat populations (Frick et al. 2010; Reichard et al. 2009). This is changing, however, as more research is now being conducted to detect and describe bacteria

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ranging from vector-borne to enteric pathogens, as well as protozoan parasites, and fungal agents in a variety of bat hosts.

The many emerging infectious diseases associated with chiropteran species can have major impacts on both ecosystem and public health (Calisher et al. 2006; Mühldorfer 2013; Wibbelt et al. 2010; Wood et al. 2012). As such, the scope of this chapter is to provide an overview of those potential bat-related zoonoses and their clinical relevance to people. With increased disease surveillance and a trend toward more human contact with bat populations, it is likely that additional zoonotic diseases will continue to be identified. Bat infection dynamics are driven by a complex interplay of ecological, immunological, behavioral, and anthropogenic factors (Hayman et al. 2012). Interdisciplinary work will be needed in the future to better understand the drivers of disease emergence in bat populations and ultimately mitigate the threats that face both people and bats themselves.

28.1 Viral Zoonoses

28.1.1 Rhabdoviridae

28.1.1.1 Rabies and Rabies-Related Viruses

Among bat-associated viral zoonoses, rabies (RABV) is certainly one of the most widespread in a broad range of bat species and around the world, with several new lyssaviruses identified in recent years. In several countries considered to be free of terrestrial rabies, rabid bats and human cases of bat-associated rabies have been identified in the last decades, such as in Australia where three human cases have occurred and in the United Kingdom, with one human case in Scotland (Banayrd et al. 2011; Fooks et al. 2003). In Latin America, more human rabies cases are now related to bat exposure (especially vampire bats) than to dog bites (Condori-Condori et al. 2013).

In Latin America, a review of the literature through 1990 reported 330 cases of bat-transmitted human rabies (Schneider et al. 2009). These cases, along with PAHO data to the end of 2006, revealed 637 reported cases of bat-transmitted human rabies in Latin America. Of 199 human cases transmitted by bats during the period 1996–2006, 146 (73%) were transmitted by vampire bats, 16 (8%) by non-vampire bats, and 37 (19%) with no species reported (Schneider et al. 2009). For instance, in Peru, during 2002–2007, 293 (77%) of the rabies cases diagnosed were associated with vampire bats, whereas 87 (23%) were related to dog rabies virus variants (Condori-Condori et al. 2013). It was also shown that vampire bat rabies variants spread gradually and involve different vampire bat subpopulations with different transmission cycles. Bovine paralysis caused by rabid vampire bat bites also has a major economical impact on cattle production in Mexico and several South American countries (Streicker et al. 2012). Emergence of rabies in insectivo-

rous bats in several countries in Latin America (such as Argentina, Brazil, Chile, Peru, and Uruguay) has also been reported.

In North America, rabies remains an important public health concern in the United States, with most human cases associated with bat rabies virus variants. Cases of rabies virus infection in bats are widely distributed across the continental United States (Patyk et al. 2012). Between 2001 and 2009, more than 205,439 bats were submitted for rabies virus diagnosis, and 6.7% of these bats were rabid. Increased odds of a submitted bat being rabid were associated with species that exhibit inconspicuous roosting habits, bats originating in the Southwest, and bats submitted for diagnosis during the fall (Patyk et al. 2012).

In Europe, bat rabies cases are principally attributed to two lyssaviruses, namely European bat lyssavirus-1 (EBLV-1) and European bat lyssavirus-2 (EBLV-2). Between 1977 and 2011, 961 cases of bat rabies were reported, with the vast majority (>97%) being attributed to EBLV-1, frequently isolated in The Netherlands, Northern Germany, Denmark, Poland and also in parts of France and Spain (Schatz et al. 2013). Most EBLV-2 isolates originated from the United Kingdom (UK) and The Netherlands, and EBLV-2 was also detected in Germany, Finland and Switzerland. There have been 25 suspected cases of EBLV-2, of which 22 have been confirmed. In addition, limited isolations of unique lyssaviruses from European insectivorous bats were reported in south-west Russia in 2002 (West Caucasian bat virus), in Germany in 2010 and France in 2012 (Bokeloh bat lyssavirus) (McElhinney et al. 2013; Picard-Meyer et al. 2013), and Lleida bat lyssavirus was recently identified in a bent-winged bat (*Miniopterus schreibersii*) in Spain (Aréchiga-Ceballos et al. 2013). A few human cases related to bat exposure have also been reported from Europe.

In Asia, limited reports on identification of lyssaviruses or antibodies to lyssaviruses have been published (Liu et al. 2013b). It is certainly a part of the world where new variants are likely to be identified in the near future, when better wildlife rabies surveillance will be set in this part of the world. Many aspects of the ecology of lyssaviruses in bats need still to be investigated, such as low prevalence of infection, potential survival to infection and effective shedding of the virus.

The incubation period of rabies in humans is typically 2 to 8 weeks, but can be as short as 10 days and as long as 6 years. Initial signs include headache, slight fever, malaise and pain at the bite wound. The disease which lasts from 2 to 6 days without medical support, progresses to paralysis of the muscles of deglutition, hyperesthesia and generalized convulsions. Death ensues shortly thereafter (Hoar et al. 1998). In bats, infection rate and mortality is usually low, although this has been studied in few species. Experimental studies in vampire bats indicate that a high viral load is necessary to induce mortality, with either no observable clinical signs or squeaking, tremor, paralysis and loss of appetite (Aguilar-Sétien et al. 2005). In cattle infected by vampire bats, rabies is mainly expressed by paralysis with a rather long incubation period (25–150 days or more) and lasts for 2–5 days before causing death (Hoar et al. 1998).

28.1.2 Paramyxoviridae: Henipaviruses

28.1.2.1 Hendra, Nipah, and Menangle Viruses

Several important zoonotic paramyxoviruses have been associated with animal and human deaths in Australasia since the end of the twentieth century. The henipaviruses are naturally harbored by Pteropid fruit bats (flying foxes) and some microbat species.

Hendra virus: In Australia, Hendra virus was first recognized in 1994 when 21 horses and two humans were infected, leading to the death of 13 horses and one human. As of December 2012, a total of forty-five outbreaks of Hendra virus have occurred in north-eastern Australia, all involving infection of horses (Aljofan 2013). As a result of these events, 90 animals (88 horses and two dogs) have died or been euthanized. These cases have all occurred in Queensland and in north–east New South Wales. Case fatality rate in humans is 60 % (4 of 7 recorded cases) and in horses 75 %. Human infections with Hendra virus range from mild influenza-like illness to fatal respiratory or neurological disease. Infected people initially develop fever, headaches, myalgia (muscle pain), sore throat and a dry cough. They could also have enlarged lymph nodes, lethargy and vertigo. The incubation period ranges from five to 14 days. Hendra virus is transmitted to people through close contact with infected horses or their body fluids. To date, no human-to-human transmission of Hendra virus has been documented. No specific treatment is available, but a vaccine has been developed for immunization of horses and is available since the end of 2012. The following signs have all been associated with Hendra virus cases in horses, but not all these signs will be found in any one infected horse: rapid onset of illness, increased body temperature/fever and heart rate, discomfort/weight shifting between legs, depression and rapid deterioration with either respiratory and/or nervous signs. Respiratory signs include respiratory distress, increased respiratory rates, nasal discharge at death that can be initially clear until progressing to stable white froth and/or stable blood-stained froth. Nervous signs include wobbly gait, apparent loss of vision in one or both eyes, aimless walking in a dazed state, head tilting and circling, muscle twitching, urinary incontinence and inability to rise. Horses get infected when very high concentrations of virus material are deposited directly under trees in what is call the ‘drip zone’ and almost no virus is deposited once the horses leave the perimeter of the trees. This area of the trees where the spats and the urine of feeding flying foxes will be dropped potentially poses an extremely high risk for horses (Australian Veterinary Association: http://www.ava.com.au/hendra-virus).

Nipah virus (NiV): In Malaysia and Singapore, in late 1998 and early 1999 an outbreak of human disease characterized by febrile encephalitis among pig farmers, which appeared to be linked to cases of respiratory and neurological disease in commercially farmed pigs, was described as well as in 11 employees at a slaughter plant in Singapore (Aljofan 2013; Clayton et al. 2013). There were 265 patients, of whom 105 died, reported as having NiV induced viral encephalitis, mostly among adult

males who were involved in pig farming or pork production activities. However, the reported number of patients who survived the acute NiV encephalitis was 160 with 7.5% prevalence of relapsed encephalitis (12/160 patients) more than 24 months after the outbreak. Of the 89 patients previously known to have non-encephalitic or asymptomatic Nipah virus infection, three (3.4%) developed late-onset encephalitis. Most patients presented with a severe acute encephalitic syndrome, but some also had significant pulmonary manifestations. The Malaysian outbreak was controlled by the culling of over one million pigs and strict quarantine measures on pig movements.

Nipah virus re-emerged in 2001 in outbreaks of human disease in India and Bangladesh. Since 2001, outbreaks of NiV infection have occurred almost annually in Bangladesh, with many outbreaks featuring smaller clusters of cases (Clayton et al. 2013). A second outbreak in India, close to the Bangladesh border, was reported in 2007. Sequencing and genetic characterization of these isolates revealed that they were closely related to, but distinguishable from the causative agent of disease in Malaysia. Since the emergence of NiV in Bangladesh and India, over 200 human cases have been identified, with an overall case fatality exceeding 70%. Most cases are related to consumption of unwashed fruits or palm juice contaminated by fruit bats secretions (saliva, urine, fecal materials). Outbreaks in Bangladesh and India were characterized by bat-to-human and human-to-human transmissions. *Pteropus* spp. serve as the wildlife reservoir for NiV across a wide area of South-east Asia, including countries from which no known outbreaks have emerged such as Cambodia, Thailand, Indonesia and Papua New Guinea. Seropositive bats for henipaviruses were also detected in Madagascar, Ghana and a henipavirus, or henipa-like virus, also appears to circulate in both fruit bats and microbats in China (Clayton et al. 2013).

Menangle virus: The Menangle virus, another paramyxovirus, was first identified in 1997 after a piggery in Menangle (New South Wales) experienced a high number of stillbirths (Aljofan 2013; Hoar et al. 1998). Two workers at the piggery became ill with unexplained, flu-like symptoms, but subsequently recovered. Investigations later found that the virus was transmitted from a nearby population of flying foxes, through pigs which act as a carrier of the virus. Bats appear to be an asymptomatic host, with infection caused through contact with body fluids for infected animals.

28.1.3 Filoviridae

28.1.3.1 Marburg and Ebola Viruses

Marburg virus: Marburg virus causes sporadic outbreaks of severe hemorrhagic disease in sub-Saharan Africa. Bats have been implicated as likely natural reservoir hosts based most recently on an investigation of cases among miners infected in 2007 at the Kitaka mine, Uganda, which contained a large population of Marburg virus-infected *Rousettus aegyptiacus* fruit bats (Amman et al. 2012).

In July and September 2007, miners working in Kitaka Cave, Uganda, were diagnosed with Marburg hemorrhagic fever. The likely source of infection in the cave was Egyptian fruit bats (*Rousettus aegyptiacus*) based on detection of Marburg virus RNA in 31/611 (5.1%) bats, virus-specific antibody in bat sera, and isolation of genetically diverse virus from bat tissues (Towner et al. 2009). The virus isolates were collected 9 months apart, demonstrating long-term virus circulation. The bat colony was estimated to be over 100,000 animals using mark and re-capture methods, predicting the presence of over 5000 virus-infected bats. The genetically diverse virus genome sequences from bats and miners closely matched. These data indicate common Egyptian fruit bats can represent a major natural reservoir and source of Marburg virus with potential for spillover into humans.

A study conducted at Python Cave in Uganda, where an American and a Dutch tourist acquired Marburg virus infection in December 2007 and July 2008, found that about 2.5% of more than 1600 bats captured between August 2008 and November 2009 were actively infected with the virus, seven of which yielded Marburg virus isolates (Amman et al. 2012). Moreover, Q-RT-PCR-positive lung, kidney, colon and reproductive tissues were found, consistent with potential for oral, urine, fecal or sexual transmission. The combined data for *R. aegyptiacus* tested from Python Cave and Kitaka mine indicate low level horizontal transmission throughout the year. However, Q-RT-PCR data showed distinct pulses of virus infection in older juvenile bats (~6 months of age) that temporarily coincide with the peak twice-yearly birthing seasons. Retrospective analysis of historical human infections suspected to have been the result of discrete spillover events directly from nature found 83% (54/65) events occurred during these seasonal pulses in virus circulation, perhaps demonstrating periods of increased risk of human infection.

Ebola virus: Evidence of Ebola virus antibodies was reported in various bat species in Africa (Pourrut et al. 2009) and of Ebola-Reston virus in *Rousettus amplexicaudatus* bats from the Philippines (Taniguchi et al. 2011), respectively. In Africa, 1030 animals were captured in Gabon and the Republic of Congo, including 679 bats, 222 birds and 129 small terrestrial vertebrates, and were tested for evidence of infection by Ebola virus (Leroy et al. 2005). Of the infected animals identified during these field collections, immunoglobulin G (IgG) specific for Ebola virus was detected in serum from three different bat species (4/17 *Hypsignathus monstrosus*, 8/117 *Epomops franqueti* and 4/58 *Myonycteris torquata*). Viral nucleotide sequences were detected in livers and spleens in other bats from the same populations (4/21, 5/117 and 4/141, respectively). No viral RNA was detected in kidney, heart or lung in these animals after amplification by polymerase chain reaction (PCR) and no viral nucleotide sequences were revealed in any of the other animal species tested.

Twelve years after the Kikwit Ebola outbreak in 1995, Ebola virus reemerged in the Occidental Kasaï province of the Democratic Republic of Congo (DRC) between May and November 2007, affecting more than 260 humans and causing 186 deaths (Leroy et al. 2009). During the latter outbreak several epidemiological investigations were conducted to identify the underlying ecological conditions and

animal sources. Qualitative social and environmental data were collected through interviews with villagers and by direct observation (Leroy et al. 2009). The local populations reported no unusual morbidity or mortality among wild or domestic animals, but they described a massive annual fruit bat migration toward the southeast, up the Lulua River. Migrating bats settled in the outbreak area for several weeks, between April and May, nestling in the numerous fruit trees in Ndongo and Koumelele islands as well as in palm trees of a largely abandoned plantation. They were massively hunted by villagers, for whom they represented a major source of protein. By tracing back the initial human-to-human transmission events, it was shown that in May the putative first human victim bought freshly killed bats from hunters to eat. This study provided the most likely sequence of events linking a human Ebola outbreak to exposure to fruit bats, a putative virus reservoir. Such findings support the suspected role of bats in the natural cycle of Ebola virus and indicate that the massive seasonal fruit bat migrations should be taken into account in operational Ebola risk maps and seasonal alerts in the DRC (Leroy et al. 2009).

28.1.4 Coronaviridae

28.1.4.1 SARS- and MERS-Coronaviruses

Severe acute respiratory syndrome (SARS) was first reported in February 2003 in China. When the World Health Organization declared the outbreak over on 5 July 2003, more than 8000 cases (and almost 800 fatal) had been reported in 32 countries worldwide (Field 2009; Wang et al. 2006). Initial symptoms are flu-like and may include fever, myalgia, lethargy symptoms, cough, sore throat, and other nonspecific symptoms, leading to sever pneumonia. The only symptom common to all patients appears to be a fever above 38 °C (100 °F). Shortness of breath may occur later.

A succession of phylogenetic and epidemiological findings suggested that SARS had a wildlife origin, and that ‘wet markets’ in southern China were the origin of the outbreak. Subsequently, two groups independently identified SARS-like coronaviruses (SARS-CoV) in species of bats in China. Li et al. (2005) reported serological and molecular evidence of a cluster of SARS-like coronaviruses in several species of free-living horseshoe bats (*Rhinolophus* spp.) in southern China. They contend that the virus responsible for the SARS outbreak in humans in 2003 emerged from this cluster of viruses, and that bats are the origin of the SARS coronavirus. *Rhinolophus* species are more likely to foster host shifts of coronaviruses than other bat species; this propensity, when combined with the potential for close contact between bats, civets and humans in the wildlife trade in southern China, supports SARS-like coronaviruses as being the source of the SARS coronavirus (Field 2009). The majority of the coronaviruses originated from African, Asian and European bats (Corman et al. 2013). In addition to SARS-CoV, four human coronaviruses (HCoVs), termed HCoV-OC43, -229E, -NL63 and -HKU1 are known.

Recently, a sixth HCoV was described, the MERS-CoV, which can cause coughing, fever, and pneumonia. This virus emerged in Saudi Arabia in 2012 and has been reported in some other Gulf States, France, Germany, Italy, Tunisia, and Britain [all cases to date can be epidemiologically linked to Saudi Arabia, Qatar, United Arab Emirates and Jordan]. The MERS virus so far (September 2013) has killed 51 people out of 135 confirmed cases of infections worldwide (ProMed, MERS-COV (71) 20130919). Close relatives of this betacoronavirus termed MERS-CoV and of HCoV-229E exist in Old World bats and HCoV-NL63 could be grown in immortalized bat cells, demonstrating the zoonotic potential of previously reservoir-bound bat CoVs. The recent description of a bat CoV related to MERS-CoV in Mexican bats (Anthony et al. 2013) and in bats from Saudi Arabia (Memish et al. 2013) emphasized the relevance of investigating neo-tropical bats for CoVs.

Identification of sequences of a group C betacoronavirus (β)-CoV in bat guano was recently reported (Wacharapluesadee et al. 2013). The detection of nucleic acid of this group C (β)-CoV and the previous isolation of viruses from bat feces and urine warrant some concerns that guano miners might be exposed to bat pathogens in fresh excreta as well as in soil substances. Therefore, bat guano miners should use preventive measures of personal hygiene and improved barrier protection to reduce the possibility of exposure to zoonotic pathogens.

28.1.5 Other Viral Pathogens

Many other viruses have been isolated or detected by molecular methods or by the presence of specific antibodies in bats, such as Hantaan virus in various bat species in Asia and Africa (Hance et al 2006; Hoar et al. 1998; Wong et al. 2007); Japanese encephalitis virus in China (Liu et al. 2013a), Venezuelan equine encephalitis virus in vampire bats and antibodies in bats from Guatemala (Hoar et al. 1998). In their review, Hoar et al. (1998) reported also detection of Chikungunya virus in African bats (*Scotophilus* sp.), Rio Bravo virus in Mexican free-tailed bats and Rift valley fever virus in bats from the Republic of Guinea.

In Uganda, four human cases of Kasokero virus isolated from *Rousettus aegyptiacus* bats living in the Kasokero cave occurred in laboratory workers (Kalunda et al. 1986). Infected laboratory workers had fever, headache, abdominal pain and diarrhea, sever myalgia and arthralgia. Signs lasted 7–10 days and were followed by complete recovery. It was demonstrated that 67 % of 74 bats from that cave were seropositive for Kasokero virus. Kyasanur virus has been isolated from bats in India and the Vesicular Stomatitis Virus (New Jersey type), which causes flu-like symptoms in infected humans, has been isolated from bats in Panama and Guatemala (Hoar et al. 1998).

28.2 Bacterial Zoonoses

28.2.1 Enteropathogenic Bacteria

28.2.1.1 Salmonella, Shigella, Yersinia, and Campylobacter

Enteric pathogens such as *Salmonella*, *Shigella*, *Yersinia* and *Campylobacter* species have occasionally been found in bats (Mühldorfer 2013). A variety of different *Salmonella* serotypes have been isolated from apparently healthy and diseased bats. Almost all of them are serotypes with a broad host-range. *Salmonella* Enteritidis and *Salmonella* Typhimurium have been frequently identified, which belong to a small group of *Salmonella* serotypes mainly associated with disease in humans and animals. Both serotypes have been isolated from organ tissues of three individual bats of the family Vespertilionidae that were found dead or severely injured near human habitations (Mühldorfer 2013). It was also reported in vampire bats (Hoar et al., 1998). In Trinidad, of 377 tested bats, representing 12 species, four bats (1.1 %) were positive for *Salmonella* spp., 49 (13.0 %) were positive for *E. coli*, and no bats were positive for *E. coli* O157 or *Campylobacter* spp. (Adesiyun et al. 2009). Isolated serotypes of *Salmonella* included Rubislaw and Molade, both from *Noctilio leporinus*, a fish-eating bat, Caracas recovered from *Molossus major*, and *Salmonella* Group I from *Molossus ater*, both insect-eating bats. Of the 49 isolates of *E. coli* tested, 40 (82 %) exhibited resistance to one or more antimicrobial agents.

Shigella, causing a dysenteric infection in humans, was isolated from a *Molossus bondae* bat in Colombia (Arata et al. 1968). *Shigella* strains of serogroups B to D have been isolated from mega- and microbats of diverse feeding habitats (Mühldorfer 2013). *Shigella flexneri* in particular was detected in more than 3 % of bats investigated.

A high prevalence of different Yersinia species (~35 %) was detected in the feces of 70 insectivorous *Myotis myotis* collected from natural populations in Poland (Mühldorfer 2013). Most of the *Yersinia* species isolated from bats are widely distributed in the environment and rarely associated with disease in mammals and birds. Cases of systemic *Y. pseudotuberculosis* infection have been described once in an adult insectivorous bat *(M. myotis)* found dead in Germany after hibernation (Mühldorfer 2013) and a bat in England (Hoar et al. 1998), respectively.

28.2.2 Vector-Borne Bacteria

28.2.2.1 Borrelia, Bartonella and Neorickettsia

Several *Borrelia* and *Bartonella* species and the causative agent of Potomac horse fever disease *Neorickettsia risticii* have been detected in blood and organ tissues of bats (Mühldorfer 2013). The majority of infected animals appear to be healthy, only

two vespertilionid bats (*Pipistrellus* sp. and *Natalus tumidirostris*) revealed severe borrelial spirochetemia.

In recent years, many new *Bartonella* species have been isolated or detected from bats around the world, including the United Kingdom, Kenya, Guatemala, Peru (Bai et al. 2012) Taiwan (Lin et al. 2012), France and Mexico (Stuckey et al. unpublished data). Phylogenetic analyses of *Bartonella* strains derived from bats identified several distinct phylogroups indicating the presence of a variety of novel *Bartonella* species in bats. It is notable that bats of the same species as well as bats of the same geographic origin and ecological niche (i.e. *Desmodus rotundus*, members of the family Vespertilionidae) shared closely related strains of *Bartonella*. It is not known if these *Bartonella* species are zoonotic. Furthermore, soft ticks (family Argasidae) and other ectoparasites commonly found on bats or in bat habitats are infected with *Bartonella*, *Borrelia* and *Rickettsia* species, posing a potential risk of intra- and interspecies transmission cycles between bats, humans and domestic animals (Mühldorfer 2013).

28.2.3 Other Bacterial Pathogens

A variety of pathogenic *Leptospira* species have been identified in bats in Asia, Europe, Australia and the Americas (Hoar et al. 1998; Mühldorfer 2013). The prevalence of leptospiral infections in bats varied from almost 2–35% depending on the sample size of the respective study. The family Phyllostomidae comprised the majority of microbats infected with *Leptospira*, whereas in obligate insectivorous species (i.e. families Vespertilionidae and Molossidae) leptospiral infection with pathogenic strains has occasionally been found. In Australia, native flying fox populations (genus *Pteropus*) were suggested as possible carriers of pathogenic *Leptospira* responsible for infections in humans and other animals because of high bacterial detection rates in kidney (11%) and urine samples (39%) and high seroprevalences (18, 28%) (Mühldorfer 2013). Similarly, bats from Madagascar and Comoros islands harbor a notable diversity of *Leptospira* spp.; a finding similar to the diversity found in a comparable investigation of bats in the Amazon region (Lagadec et al. 2012; Matthias et al. 2005). Leptospirosis incubation is 1–32 days (median 9 days) and median duration is 14 days. Most symptomatic patients develop a mild illness consisting of fever, chills, headache and myalgia. Severe forms of the disease may manifest in acute renal failure, hepatitis, jaundice, myocarditis and meningoencephalitis and outbreaks of severe pulmonary hemorrhagic leptospirosis have occurred resulting in high morbidity and mortality (Leshem et al. 2011).

A few other zoonotic agents, such as *Coxiella burnetii*, the agent of Q fever or *Mycobacterium bovis* were isolated from bats in Morocco and southern USSR and from captive Indian fruit bats in England, respectively (Hoar et al. 1998). Agglutinin antibodies against *Brucella* were detected in 5 of 53 vampire bats captured in areas of Brazil where incidence of brucellosis in cattle was high (Ricciardi et al. 1976). Several *Pasteurella* species (i.e. *P. multocida*, *P. pneumotropica* and *Pasteurella*

species B) have been identified as primary pathogens in bats responsible for a variety of localized and systemic infections in European bat species; most *Pasteurella* strains isolated from organ tissues of 29 vespertilionid bats represented *P. multocida* ssp. *septica* (85 %) and capsular type A (75 %) (Mühldorfer 2013).

28.3 Protozoan Parasites

28.3.1 Trypanosoma, Toxoplasma, Coccidia, and Leishmania

Few parasites of bats are known to be pathogenic to humans and are usually transmitted mechanically via an intermediate vector (Hoar et al 1998). Many species of trypanosomes can infect bats, but one of main concern is *Trypanosoma cruzi*, the agent of Chagas disease. Recently a new genotype of *T. cruzi*, associated with bats from anthropic areas and which could be a potential source of infection to humans was described (Marcili et al. 2009). Chagas disease is commonly transmitted by reduviid bed bugs. In humans, the disease is characterized by high fever, adenitis, anemia and facial edema in the acute form and myocarditis in the chronic form. Pathogenicity of bat trypanosomes for humans is not clearly established. *T. cruzi* has been detected in vampire bats, *Desmodus rotundus*, which can be of concern in term of zoonotic transmission, as these bats feed on mammals, including humans (Ramirez et al. 2013).

Infection of bats with *Toxoplasma gondii* has been reported based on serological studies and more recently on its isolation from bats in Brazil (Cabral et al. 2013; Sun et al. 2013). Therefore, consumption of undercooked bats could be a source of human infection. In bats, systemic toxoplasmosis caused by *T. gondii* was diagnosed in two juvenile, captive flying-foxes (*Pteropus conspicillatus* and *P. scapulatus*), which died following respiratory distress. One animal displayed clinical signs suggestive of neurological disease (Sangster et al. 2012).

Coccidia of the genus *Eimeria* have been isolated from several species of bats in many parts of the world (Hoar et al. 1998). Many new *Eimeria* species have been reported (McAllisher et al. 2012). Prevalence in bats is usually low (< 1–5 %) and it is not known if they are pathogens for humans (Hoar et al. 1998).

Leishmaniasis is a zoonotic disease caused by parasites of the genus *Leishmania*. It has expanded beyond its natural range and is becoming increasingly urban (Shapiro et al. 2013). Using PCR and PCR-RFLP, *Leishmania* (Viannia) *braziliensis* was detected in two bats (Chiroptera) in Mato Grosso do Sul, Brazil, an endemic area. The animals testing positive were found in both a rural site and an urban site. These results indicate the need for further research into the viability of *Leishmania* in bats. It could have implications for public health in that part of Brazil, given the large populations of urban bats, their mobility, and their ability to roost at close proximity to humans within residences and other buildings (Shapiro et la. 2013).

28.4 Fungal Pathogens

28.4.1 Histoplasma, Coccidioides and Other Fungal Infections

Despite the emergence of white nose syndrome caused by *Pseudogymnoascus destructans,* which destroyed an estimated 6–7 million bats in North America in recent years (first reported in 2007 in some New York state caves), the main zoonotic fungal diseases related to bats are histoplasmosis and to a lesser extend coccidioidomycosis and a few other fungal infections also identified in bats (Hoar et al. 1998).

Histoplasmosis: Histoplasmosis is caused by *Histoplasma capsulatum*, a dimorphic fungus that is endemic in the Americas and parts of Asia and Africa (Hoar et al. 1998). There are two varieties that are pathogenic to humans, var. *duboisii* and var. *capsulatum*. The former exists only in Africa, while var. capsulatum is most prevalent in regions of North, Central, and South America, but has also been reported from parts of Africa, Southern and Eastern Europe, Eastern Asia, and Australia (Cottle et al. 2013). It grows as a mold in soil enriched with bird or bat guano; human infection occurs after inhalation of the dust generated when such soil is disturbed. Visiting caves, collecting or being exposed to bat guano are the main sources of human contamination from bats (CDC 2012; Cottle et al. 2013; Hoar et al. 1998; Jülg et al. 2008; Kajfasz and Basiak 2012; Schwarz and Kauffman 1977). The threat of *Histoplasma capsulatum* infection in bat-inhabited caves should be emphasized to travelers and also to physicians (Kajfasz and Basiak 2012). Bats usually are healthy carriers and shed the fungus in their feces. In humans, clinical manifestations in humans vary according to host immunity and exposure intensity, ranging from asymptomatic infection (in most healthy persons exposed to a low inoculum; about 80 % of the time) to life-threatening pneumonia with respiratory failure (Cottle et al. 2013; Hoar et al 1998). Between these extremes, clinical presentations include acute or subacute pulmonary disease, pericarditis, rheumatological syndromes with erythema nodosum, progressive disseminated disease, and mediastinal complications. Acute pulmonary histoplasmosis in returning travelers typically presents as a flu-like illness with high-grade fever, chills, headache, nonproductive cough, pleuritic chest pain, and fatigue. Chest radiographs often show diffuse reticulonodular infiltrates and mediastinal lymphadenopathy. Symptom onset is usually 1–3 weeks following exposure and most individuals recover spontaneously within 3 weeks. Disseminated disease is a rare complication, more likely to occur in persons with severely impaired cellular immunity (Cottle et al. 2013). The African species, *H. capsulatum* var *duboisii,* is associated with cutaneous lesions and occasionally infection of long bones (Hoar et al. 1998).

Coccidioidomycosis: *Coccidioides immitis*, causing coccidioidomycosis, also known as valley fever in California, has been isolated from bat guano (Krutzsch and Watson 1978). Coccidioidomycosis is a systemic disease caused by *Coccidioides immitis* and *C. posadasii* spp., which are predominant in arid zones of the American continent, mainly in the Southwestern United States and the northern states of Mexico, as well as other regions with different environmental conditions

(Welsh et al. 2012). Some countries of Central and South America are also endemic zones. Most infected patients are asymptomatic. Disseminated disease develops in less than 5 % of clinically affected individuals. Culture, biopsy, and DNA probes are used for fungus identification. Prognosis is related to low antibody detection and a positive intradermic skin reaction to coccidioidin. Immunosuppressed patients and pregnant women require special attention in diagnosis, therapy, and prognosis. Amphotericin B in its different forms, itraconazole, and fluconazole, are the most frequently used treatments. Both fungi have been detected in bats and bat guano (Krutzsch and Watson 1978; Cordeiro et al. 2012). In Brazil, *Coccidioides posadasii* was recovered from *Carollia perspicillata* bat lungs (Cordeiro et al. 2012). Immunologic studies detected coccidioidal antibodies and antigens in *Glossophaga soricina* and *Desmodus rotundus* bats.

Candidiasis: Candida albicans, which causes mucocutaneous candidiasis ("thrush" or oropharyngeal candidiasis) in the mouth or throat of humans, was isolated from liver, kidney, spleen and intestinal content of several bats captured in Nigeria (Oyeka 1994). The most common symptom of oral thrush in humans are white patches or plaques on the tongue and other oral mucous membranes. It was indicated that bat consumption is common in that country and people could get infected by improper handling of bats or consumption of raw or undercooked bat meat (Oyeka 1994). In a recent study conducted in Brazil, 7 (12.3 %) of 57 bats showed yeasts in their feces. Five species of the genus *Candida* were isolated: *C. guilliermondii*, *C. krusei*, *C. lusitaniae*, *C. parapsilosis*, and *C. pelliculos* (Botelho et al. 2012).

Other fungal infections: Other fungal infections have been described in bats, some of which could potentially be transmitted to humans. Bats are susceptible hosts and reservoirs for *Histoplasma capsulatum, Paracoccidioides brasiliensis*, and *Sporotrichum schenckii* (Raymond et al. 1997). *Sporothrix schenckii, Scopulariopsis* sp. and *Cryptococcus neoformans* have been isolated from bats or bat guano in the Americas (Hoar et al. 1998; Kajihiro, 1965). Blastomycosis is a granulomatous disease of mucous membranes. *Blastomyces dermatitidis* has been isolated from the lungs of an asymptomatic insectivorous bat (*Rhinopoma hardwickei hardwickei*) from India, and insectivorous bats orally inoculated with *B. dermatitidis* transiently shed viable organisms in their feces. Mexican free-tailed bats (*Tadarida brasiliensis*) intraperitoneally injected with *B. dermatitidis* developed systemic blastomycosis and excreted viable fungi in their feces. Apparently, bats can serve as both hosts and vectors for *B. dermatitidis* and may be potential sources for human infection (Raymond et al. 1997).

28.5 Summary

Bats themselves have an undeniable impact on our planet; with over 1200 chiropteran species identified to date, bats comprise one-fifth of all mammalian species globally and provide critical ecosystem services ranging from pollination to insect control (Wibbelt et al. 2010). Their vast numbers, capability of flight, and a variety

of ecological, immunological, and socioeconomic factors also enable bats to transmit an increasingly recognized spectrum of pathogens (Calisher et al. 2006; Mühldorfer 2013; Wibbelt et al. 2010; Wood et al. 2012). The potential for the emergence of zoonoses in particular will continue to increase as human development encroaches on bat populations. As such, future research will be needed to monitor infection and better understand those underlying drivers of disease.

Addendum Since this chapter was written, the largest outbreak of Ebola virus ever reported occurred in West Africa (Guinea, Liberia and Sierra Leone) with more than 5,300 human cases and more than 2600 deaths by mid September 2014 and another unrelated outbreak occurred since July 2014, with 66 cases including 37 deaths in the area of Djera, Equateur Province in the Democratic Republic of Congo. In both outbreaks, the index case was a person who had been exposed to bushmeat (WHO, 2014).

As far as Bartonella and bats, a recent publication linked Bartonella mayotimonensis, which had been described as a cause of human endocarditis in North America (Lin et al., 2010) to a bat reservoir, as this Bartonella species was isolated from several bats from Finland (Veikkolainen et al. 2014). It clearly indicate that bats can be the reservoirs of zoonotic Bartonella species.

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