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Review

Public Health Awareness of Emerging Zoonotic Viruses of Bats: A European Perspective

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ABSTRACT

Bats classified in the order Chiroptera are the most abundant and widely distributed non-human mammalian species in the world. Several bat species are reservoir hosts of zoonotic viruses and therefore can be a public health hazard. Lyssaviruses of different genotypes have emerged from bats in America (Genotype 1 rabies virus; RABV), Europe (European bat lyssavirus; EBLV), and Australia (Australian bat lyssavirus; ABLV), whereas Nipah virus is the most important recent zoonosis of bat origin in Asia. Furthermore, some insectivorous bat species may be important reservoirs of SARS coronavirus, whereas Ebola virus has been detected in some megachiropteran fruit bats. Thus far, European bat lyssavirus (EBLV) is the only zoonotic virus that has been detected in bats in Europe. New zoonotic viruses may emerge from bat reservoirs and known ones may spread to a wider geographical range. To assess future threats posed by zoonotic viruses of bats, there is a need for accurate knowledge of the factors underlying disease emergence, for an effective surveillance programme, and for a rapid response system. In Europe, primary efforts should be focussed on the implementation of effective passive and active surveillance systems for EBLVs in the Serotine bat, *Eptesicus serotinus,* and *Myotis* species (i.e., *M. daubentonii* and *M. dasycneme*) Apart from that, detection methods for zoonotic viruses that may emerge from bats should be implemented. Analyses of data from surveillance studies can shed more light on the dynamics of bat viruses, (i.e., population persistence of viruses in bats). Subsequently, studies will have to be performed to assess the public health hazards of such viruses (i.e., infectivity and risk of infection to people). With the knowledge generated from this kind of research, a rapid response system can be set up to enhance public health awareness of emerging zoonotic viruses of bats. Key Words: EBLV—Lyssavirus—Bats—Hendra virus—Nipah virus—Menangle virus—Tioman virus—Ebola virus—SARS coronavirus. Vector-Borne Zoonotic Dis. 6, 315–324.

INTRODUCTION

BAT SPECIES constitute around 20% of all mammalian species and are classified in the order Chiroptera. Within this order there are two suborders, the Megachiroptera and the Microchiroptera. The Pteropodidae is the single family of the suborder Megachiroptera, the Old World fruit bats or flying foxes, and is found in tropical and subtropical Africa and east to the Western Pacific. The Microchiroptera are found throughout most of the world and are a group of generally small, insectivorous bats, a number (about 70 species) of fruit and flower feeders, a few more or less carnivorous and three species of vampire bats, all of which have the ability to echolocate. More than 30 viruses have been isolated from bats and amongst these viruses there are a number of zoonotic viruses. The actual role played by

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bats as reservoir, disseminating zoonoses, is not really defined for most zoonotic virus infections, but there is an increasing interest in this field of research. Of some zoonotic viruses, bats have been implicated as the natural host. Of others, bats may just be carriers or vectors. The aim of this paper is firstly to review the state of knowledge of important emerging zoonoses in bats, focussing on lyssaviruses, henipaviruses, SARS coronavirus (SARS-CoV), and Ebola virus (EBOV). The status of the current public health awareness in Europe for this group of viral zoonoses will be evaluated.

ZOONOTIC VIRUSES OF BATS

The most well-known and still important group of zoonotic viruses of bats are the lyssaviruses. The rabies and rabies-related viruses within the genus *Lyssavirus* of the family Rhabdoviridae, have been isolated from many insectivorous, frugivorous and haematophagous bats all over the world. In the thirties, rabies in vampire bats in the Americas was perceived and after human deaths were associated with bat rabies in North America, rabies surveillance in bats was increasingly supported (Noah et al. 1998). In a later stage, this was also the case for European bat lyssavirus (EBLV) in Europe and the Australian bat lyssavirus (ABLV) in Australia (Fig. 1).

The Nipah virus (NiV) is a recently emerging virus with a megachiropteran fruit bat reservoir, and has caused a large outbreak in humans and animals in Malaysia and Singapore starting in 1998. Since that year to date more than a hundred people in Malaysia and Singapore have died of NiV encephalitis (Wong et al. 2002). Today there is increasing evidence that megachiropteran fruit bats are likely to be the reservoirs of NiV.

Hendra virus (HeV) was first identified in horses in Australia in1994 and named equine morbillivirus by that time (Field et al. 2001). In 1994–1995, three human incidences of HeV infection have been described. Few years later HeV was isolated from flying foxes and HeV seroprevalences of close to 50% were reported from various flying fox species in Australia. Menangle virus was identified in 1998 and related to infections in humans and pigs in Australia (Philbey et al. 1998). Most important clinical features in pigs consist of reproduction disorders. Humans developed unexplained febrile illness after exposure to potentially infective

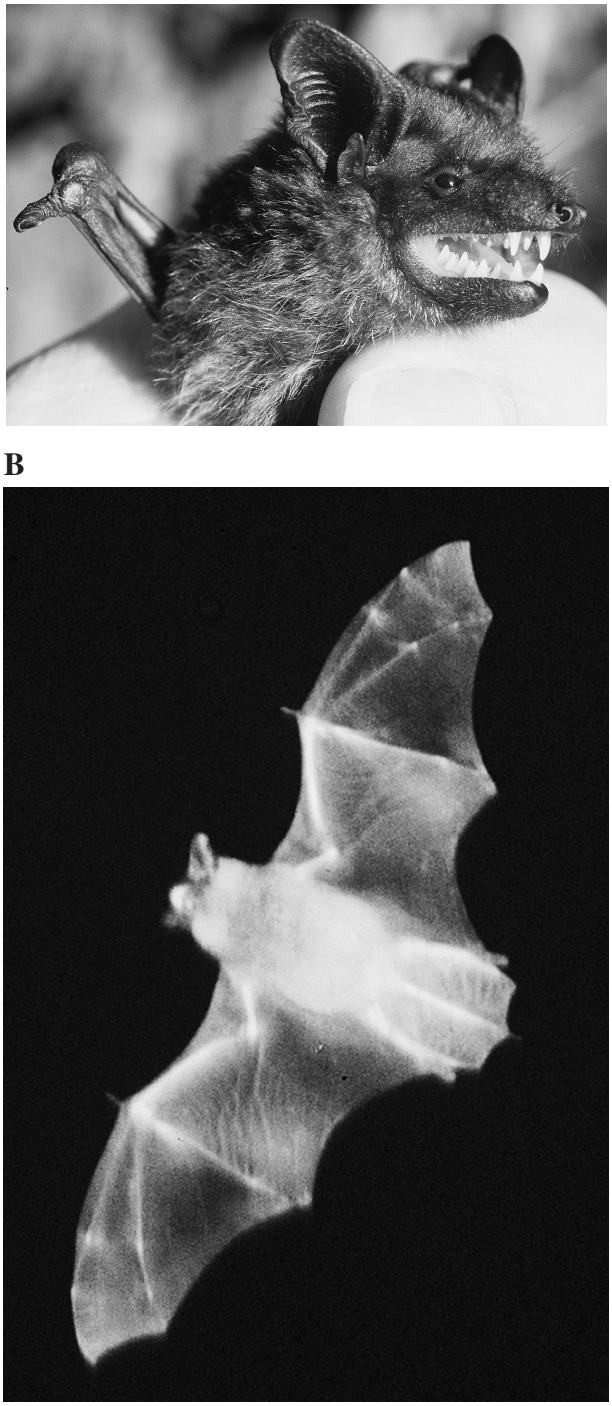

FIG. 1. (**a**,**b**) The Serotine bat, *Eptesicus serotinus*, is the main reservoir of European bat lyssavirus (EBLV) in Europe. (Photo: Z. Bruijn.)

materials (Chant et al. 1998). Antibodies to the virus were identified in several species of fruit bats in Australia (Philbey et al. 1998).

Ebola virus (EBOV) first emerged in 1976 in two outbreaks in Sudan and the Democratic Republic of Congo (formerly Zaire). After the period from 1979 to 1997 in which no cases were reported, the virus re-emerged in 1997 in Ivory Coast. Mortality rates in humans were high in all occasions: always over 50% and up to 90% in some outbreaks (Pourrut et al. 2005). Analyses of animal carcasses and serologic survey have shown that the great apes are particularly at risk from Ebola. There is increasing evidence that African fruit bat species are important reservoirs of Ebola virus.

Severe acute respiratory syndrome (SARS) first appeared in Guangdong, China in November 2002, and it subsequently spread to other parts of the world, making it a major infectious disease outbreak. The rapid spread of the disease and the relatively high mortality rates, were a serious public health threat and resulted in important economic losses. The etiologic agent was a newly emerged and previously unrecognized coronavirus, now known as SARS-coronavirus (Marra et al. 2003). In 2005, SARS coronavirus-like sequences were detected in several bat species in China and it was suggested that some insectivorousbat species may be an important reservoir for the virus.

For several other zoonotic viruses it has been suggested that bats might be a reservoir. Examples of this group of viruses are West Nile virus (WNV) and St. Louis encephalitis virus. Both of these viruses are arthropod borne viruses causing encephalitis in humans. WNV has been isolated from a number of animal species and WNV neutralizing antibodies and RNA sequences have been detected in bats (Marfin et al. 2001, Pilipski et al. 2004), but the actual role of bats in the WNV transmission cycle is unknown. In a study performed in the Netherlands WNV RNA was not detected in the brains of any of seventy Serotine bats (unpublished observation). Corvid bird species are regarded the main reservoir but at least some bat species seem to be able to carry the virus and might play a role in WNV transmission to terrestrial animals and humans.

In this review, the arthropod-borne viruses, like WNV, will not be discussed any further. The other zoonotic viruses mentioned, will be discussed in more detail below.

BAT LYSSAVIRUSES

Lyssaviruses (genus *Lyssavirus*, family Rhabdoviridae) are RNA viruses with a single-stranded, negative-sense genome that infect a variety of mammals often resulting in rabies. Although rabies is generally associated with carnivorous mammals, there is growing evidence that bats are now a major viral reservoir, particularly in North America and Europe (Amengual et al. 1997, Noah et al. 1998).

The lyssaviruses' negative-sense EBLV genome encodes five proteins: the nucleoprotein (N), phosphoprotein (P), matrix protein (M), glycoprotein (G), and RNA polymerase (L) in the order 3′-N-P-M-G-L-5′. Molecular epidemiological studies of lyssaviruses have tended to focus on the N, a well-conserved structural protein, and the G, which contains domains responsible for host-cell receptor recognition and membrane fusion, and is the major target for host neutralising-antibody responses (Badrane et al. 2001).

Currently, there are seven recognised genotypes of lyssavirus defined on the basis of their genetic similarity (Bourhy et al. 1993, Gould et al. 1998): rabies virus (RABV; genotype 1), Lagos bat virus (LBV; genotype 2), Mokola virus (MOKV; genotype 3), Duvenhage virus (DUVV; genotype 4), European bat lyssavirus type 1 (EBLV-1; genotype 5), European bat lyssavirus type 2 (EBLV-2; genotype 6) and Australian bat lyssavirus (ABLV; genotype 7). All genotypes except MOKV have bat reservoirs, suggesting that lyssaviruses originated from these mammals. Additionally, four new lyssavirus genotypes that infect bats in central Asia have been proposed: Aravan virus, Khujand virus (Kuzmin et al. 2003), Irkut virus, and West Caucasian bat virus (WCBV) (Botvinkin et al. 2003). Genotype 1 is responsible for rabies in terrestrial mammals throughout the world, in a number of different bat species on the American continent, as well as for most of the human deaths worldwide (Badrane et al. 2001). Australian bat lyssavirus has

been associated with two human fatalities caused by two different strains. One of these strains was found in some Pteropid species (fruit bats) and the other one in one microchiropteran insectivorous species.

In Europe, lyssaviruses isolated from bats belong to EBLV-1 and EBLV-2 (Amengual et al. 1997). EBLV was first isolated in Germany and Yugoslavia in 1954. Since that time, more than 600 bat cases have been reported throughout Europe, most commonly in Denmark and the Netherlands, although this is likely to reflect more extensive surveillance in these localities rather than major differences in epidemiology. EBLV-1 infection has also been reported in a small number of terrestrial mammals, including five sheep in Denmark (Rønsholt et al. 1998, Tjørnehøj et al. 2006)) and a Stone marten, *Martes foina*, in Germany (Müller et al. 2004). These animals exhibited clinical symptoms consistent with rabies and were killed. In addition, five human deaths due to EBLV have been reported (Fooks et al. 2003, Selnikova et al. 2006). The overall rarity of EBLV-associated death in terrestrial animals may be because the transmission of EBLV between bats and other mammals is infrequent, the virulence of EBLV is low compared to rabies virus, or simply because cases go undetected. There is some evidence that EBLV is less pathogenic than other lyssaviruses. In particular, EBLV only causes clinical symptoms in cats and dogs when injected intracerebrally and not intramuscularly, suggesting virulence may be low (Fekadu et al. 1988). Furthermore, it is possible that bats develop persistent EBLV infection, manifesting as the long-term carriage of viral RNA without overt disease. In particular, some wild-caught bats have antibodies to EBLV for up to three years and viral RNA has been detected in the saliva of apparently healthy bats (Arguin et al. 2002, Badrane et al. 2001, Serra-Cobo et al. 2002, Wellenberg et al. 2002). On the other hand it is also possible that bats experience an inapparent acute infection and are subject to continual re-infection.

HENDRA VIRUS

Hendra virus is a single stranded, negative sense RNA virus. Based on biological properties and genomic organization, Hendra virus and Nipah virus are classified into the new genus *Henipavirus* of the *Paramyxovirinae* subfamily within the *Parmyxoviridae* family. Most viruses in the *Paramyxovirinae* subfamily have genomes of around 15,500 nucleotides that encode seven to nine proteins of which two or more are derived from overlapping reading frames in the P gene. Members of the *Paramyxovirinae* subfamily have three nucleocapsid associated proteins: an RNA binding protein (NP), a phosphoprotein (P), and a putative polymerase protein, and three membrane associated proteins, including an inner membrane or matrix protein (M) and two glycosylated envelope proteins, comprising a fusion protein (F) and an attachement protein (G, or H, or HN) (Lamb et al. 2000).

Hendravirus is the type species of the new genus *Henipavirus* and was first identified in 1994 from a disease outbreak in horses in the Brisbane suburb of Hendra. Thirteen out 20 horses in the outbreak died of hyperacute respiratory disease (Murray et al. 1995). The horse-trainer and a stable-boy suffered from respiratory disease a few days after the death of the horse index case. The stable-boy recovered, but the horse-trainer died. In September 1995 another human case of Hendra virus infection occurred in a farmer in Brisbane. In contrast to the first case the farmer showed mainly neurological signs. First manifestation of his disease was in August 1994 with a mild meningoencephalitis, and he subsequently experienced a persistent fatigue. In a later stage he developed epileptic seizures and coma, and died in September 1995. All reported human cases had had close contact with diseased horses. Human to human transmission has never been reported. A serosurvey in horses in Queensland did not reveal any seropositives (1964 horses tested), indicating the virus had not spread in the horse population (Murray et al. 1995). A wildlife serosurvey was started in 1995 and within a year positive results in ELISA and serum neutralization test were reported from flying foxes. Since then HeV antibodies have been demonstrated in over 20% of flying foxes in Eastern Australia and the virus has been isolated from three of four flying fox species,

from foetal tissues and from blood (Halpin et al. 1999).

NIPAH VIRUS

Nipah virus is a single stranded RNA virus of the subfamily Paramyxovirinae in the Paramyxovirus family, classified in the genus *Henipavirus* together with Hendra virus (Wang et al. 2000). The virus genome encodes five proteins: The nucleoprotein (N), the phosphoprotein (P), the attachment protein (G) and the fusion protein (F), of which the latter two are incorporated in the lipid bilayer envelope (Chua et al. 2000, Wang et al. 2000, Chan et al. 2001).

Nipah virus emerged in 1998 in Malaysia. A major disease outbreak in pigs and humans resulted in the death of 105 humans and about 45% of all pigs in Malaysia were culled (Chua 2003, Mohd Nor et al. 1999, 2000). Predominant signs in pigs were acute fever and respiratory disease. In humans disease symptoms were encephalic of nature, including fever, headache, myalgia, dullness and coma. Around 50% of clinically apparent cases die. The primary mode of transmission between pigs is via the respiratory route and animal handlers working with infected pigs are at greatest risk for attracting the disease. Transmission from animal to human requires close contact with contaminated tissue or body fluids from infected animals. According to a WHO release the incubation period of the virus is between 4 and 18 days. During the outbreak in Malaysia there was no clear evidence for person to person transmission, but in 2004 during a second outbreak in Bangladesh epidemiological investigations showed evidence for a person to person transmission within households and families (ICDDR 2004).

Nipah virus appeared to be closely related to HeV and for that reason investigations into the natural host of the virus were focussed on bat surveillance. In Malaysia there are at least 13 species of megachiropteran fruit bats. NiV neutralizing antibodies were found in 21 bats of 5 species (Field et al. 2001). In addition peridomestic animals including rats, dogs, chicken, ducks, pigeons and jungle fowl were tested for antibody to NiV. A fair NiV seroprevalence was found in dogs, especially in endemic areas, but the low prevalence in dogs outside the outbreak areas, indicated that NiV did not seem to spread horizontally in dogs (Field et al. 2001). Nowadays there is increasing evidence that some fruit bat species, such as *Pteropus hypomelanus*, *P. vampyrus* (Malaysia), and *P. giganteus* (Banglasdesh), are natural reservoirs of NiV.

The emergence of NiV into the pig population and subsequently into the human population, is believed to be due to changes in ecological conditions. Deforestation and drought resulting in a lack of resources for bat populations can make bats move from their natural habitats into agricultural areas. The increase in pig farming together with the roaming around of bats probably has resulted in a transmission of the virus from bats to pigs, and then to humans (Bengis et al. 2004). In 2001 and 2003 NiV re-emerged in Bangladesh; at least 8 laboratory confirmed cases have been documented (Hsu et al. 2004). Contacts with infected patients and sick cows appeared to be the most important risk factors for contracting the disease. There was no clear history of exposure to bats or any other specific animal species, although bats in the region had serologic evidence of infection (Hsu et al. 2004). In the beginning of 2004, new clusters of NiV encephalitis were reported from Bangladesh, and recently in January 2005, a new NiV outbreak was confirmed with 20 patients and five deaths involved. This indicates that there is a need to enhance NiV outbreak investigations and NiV surveillance in order to further clarify how the virus is maintained in its reservoir hosts and via what routes the virus is transmitted to humans.

MENANGLE VIRUS AND TIOMAN VIRUS

The antigenetically closely related Menangle virus (MenV) and Tioman virus (TiV) are also members of the *Paramyxovirus* family. Their classification in the *Paramyxoviridae* family has not yet been finally defined (Zhu et al. 2003), but based on a study of the genome structure and phylogenetic analyses of the structural

gene sequences it has been proposed to classify these viruses as members of the genus *Rubulavirus* (Bowden et al. 2001). In the genomes of MenV and TiV, the fusion protein F and the attachment protein HN, two envelope glycoproteins, are present.

Menangle virus was isolated in 1997 from stillborn piglets in New South Wales, Australia, and caused reproductive disease in pigs (Philbey et al. 1998). Serological evidence indicated that two humans in close contact with infected pigs had contracted influenza like illness following infection with MenV (Chant et al. 1998). This indicates a zoonotic potential but the real public health hazard of MenV is not clear yet. Tioman virus was first isolated in 1999 from pooled urine samples of Island flying foxes, *Pteropus hypomelanus*, during the search for the reservoir host of Nipah virus. The infectivity to livestock and the zoonotic potential of Tioman virus are unknown.

SARS CORONAVIRUS

SARS coronavirus is classified within the order *Nidovirales*, family *Coronaviridae*, genus *Coronavirus* (Xu et al. 2003). Coronaviruses are positive stranded RNA viruses and have a genome 29–32 kb long. The genomes' open reading frames (ORFs) encode five proteins: the replicase polyproteins (ORF1a and ORF1ab), the spike (S), envelope (E) and membrane (M) glycoproteins, and the nucleocapsid protein (N) (Xu et al. 2003).

On the basis of antigenic and genetic analyses coronaviruses are subdivided into three groups (groups 1–3). Group 1 viruses include human coronaviruses, canine coronavirus (CCoV), porcine transmissible gastroenteritis virus (TGEV), porcine epidemic diarrhea virus (PEDV), and feline infectious peritonitis virus (FIPV). Group 2 viruses include human coronaviruses, bovine coronaviruses (BCoV), and murine hepatitis virus (MHV). Group 3 viruses are avian viruses, such as avian infectious bronchitis virus (IBV) and turkey coronavirus (TCoV).

In humans coronaviruses are associated with respiratory and gastrointestinal disease. SARS coronavirus was identified in 2003 as the causative agent of the SARS (severe acute respiratory syndrome) outbreak in the winter of 2002-2003 and fully sequenced soon after (Marra et al. 2003). Since that time a lot of efforts have been made to search for a natural SARS-CoV reservoir, and the identification of SARS-CoV in civet cats and other wild animals in live animal markets suggests that this novel human pathogen emerged as a result of an interspecies transmission (Guan et al. 2003). However, subsequent surveys failed to find the virus in either farmed or wild civets, suggesting that civets may have served only as an amplification host for SARS-CoV. In a surveillance study for SARS-CoV in wildlife in Hong Kong a CoV closely related to SARS-CoV was identified in Chinese horseshoe bats, *Rhinolophus sinicus*. Twenty-three of 59 anal swabs were found positive by RT-PCR (Lau et al. 2005). In another survey in bats in Hong Kong, group 1 coronavirus sequences were detected in faecal and respiratory samples of three other microchiropteran bat species. In particular, 63% (12/19) of fecal samples from *Miniopterus pusillus* were positive for the virus. Few positives were found in *Miniopterus magnater* and *Miniopterus schreibersii* and deducted viral sequences were highly similar to those from *M. pusillus*. All CoV sequences found in bats were group 1 CoVs (Poon et al. 2005). It is uncertain which bat species is the natural host of SARS-CoV, but the high incidences found in Chinese horseshoe bats and *M. pusillus* suggest that these species are likely to be major reservoirs of these viruses. More recent papers report a wide diversity of Corona viruses in bats in China (Woo et al. 2006). Direct or indirect transmission routes of SARS-CoV from bats to humans are unidentified. It is speculated that Palm civets, *Paguma larvata*, might eat fruits or fruit remnants discarded by bats, but to our knowledge this is not supported by data.

EBOLA VIRUS

Ebola virus, family Filoviridae, has a negative non-segmented RNA genome. Filoviruses are the causative agent of regular outbreaks of hemorrhagic fever in humans in Africa, with mortality rates up to 88%. Since 1976 there have

been a number of outbreaks in Central Africa, particularly in Sudan (1976), the Democratic Republic of Congo (1976, 1995, 2001, 2002, 2003), Gabon (1994, 1996, 1997) (Pourrut et al. 2005) and Angola (2005). Long time the animal reservoir of Ebola virus was unknown, and lots of vertebrates and invertebrates around epidemic foci have been tested, often without any positive result. Bats have more than once been suggested as candidate reservoirs for Ebola virus, and several researchers reported the identification of this virus in wild bats (Pourrut et al. 2005). An extensive survey to find the natural Ebola reservoir was carried out by Leroy et al. (2005). During trapping expeditions in Gabon and in the Democratic Republic of Congo, 1,030 wildlife animals were captured, including 679 bats. Immunoglobulin G (IgG) specific for Ebola virus was detected in serum from three different fruit bat species: four of 17 *Hypsignathus monstrosus*, eight of 117 *Epomops frangueti*, and four of 58 *Myonycteris torquata*. Viral nucleotide sequences were detected in organs of other bats from the same species. These findings suggest megachiropteran fruit bats may act as reservoirs for Ebola virus. To date there is no evidence of direct transmission of EBOV from bats to human. However, mortality among great apes from Ebola infection can increase during dry seasons when fruit is scarce in the forest and contacts between apes and fruit bats may be fostered as they compete for food. Ebola virus may be transmitted via fruits partly eaten by bats.

VIRUS DETECTION AND VIRUS MAINTENANCE IN BATS

The lyssaviruses as well as the group of paramyxoviruses and Ebola virus can readily be propagated in cell culture. For European bat lyssaviruses cell cultures in neuroblastoma cells, and for the paramyxoviruses, Nipah virus and Hendra virus cell cultures in MDCK (Madin-Darby canine kidney) cells, vero cells and HeLa (human cervical cancer) cells have been described (Moll et al. 2004, Wong et al. 2002). Cell cultures of Ebola virus and SARS-CoV have been described in vero cells (Neumann et al. 2002, Vincent et al. 2005).

Using immunohistochemistry in infected animals, Nipah viral antigen is seen in blood vessels of most organs. In the CNS, apart from the bloodvessels, viral antigen can be identified in neurons and some glial cells (Wong et al. 2002). Immunoperoxidase staining of brain tissues of EBLV infected bats, clearly and exclusively showed viral antigen bodies in the cytoplasm of neurons (Van der Poel et al. 2000). For Ebola virus antigen detection assays and immunohistochemistry have been used in wild animals and in humans and based on the positive immuno-histochemical staining, the virus was detected in muscle and bone marrow (Rouquet et al. 2005). The use of immuno-histochemical staining has also been described for SARS-CoV (Xu et al. 2005) and in the cases of SARS-CoV infection indeed the lung tissues seem to be the primary target showing high concentrations of the virus.

For rapid and specific antigen detection conventional and real time RT-PCR assays are the most indicated, and test protocols for these assays have been described extensively for bat lyssaviruses, Nipah virus, Hendra virus, Ebola virus as well as SARS-CoV (Guillaume et al. 2004, Heaton et al. 1997, Prosniak et al. 2003, Smith et al. 2001, Towner et al. 2004, Keightley et al. 2005). Based on the results of the antigen staining studies of the described viruses, brain tissues would be the primary choice for collection of samples for RT-PCR analyses for lyssaviruses and Hendra virus. Muscle tissue or bone marrow could be sampled for Ebola virus PCR detection and nasopharyngeal swabs have been successfully used for detection of CoV sequences in bats (Lau et al. 2005).

For serological diagnosis in bats, neutralizing plaque or titration assays have been successfully used for Nipah virus (Olson et al. 2002), EBLV (Wellenberg et al. 2002) as well as Ebola virus (Towner et al. 2004) and SARS-CoV (Lau et al. 2005). Apart from the virus neutralization assays and virus plaque assays used for these viruses, a large number of ELISA tests have been developed and partly compared to SNT (Eshagi et al. 2004, Chan et al. 2001, Kashiwazaki et al. 2004, Ksiazek et al. 1999).

It has been suggested that bats are unique in their response to viral infections because bat species seem to be able to sustain viral infec-

tions without overt disease (Sulkin et al. 1974). Indeed a wide range of viral infections have been identified in bats, but in fact for most of these viruses it is unknown in what number of eventualities bats themselves are victims of the infection. Moreover, for the viruses described in this paper that have bat species as their reservoir hosts, the definite mechanism of long-term maintenance is unknown. Since both continuous circulation as well as persistent infection in individual bats can result in a virus maintenance in the bat reservoir, pathogenity itself actually does not play a crucial role on the population persistence in bats. Even in case of a high fatality rate of infection of a specific virus in bats, this species may still be an important reservoir host for the virus. The reproduction rate of a specific virus in a specific population will determine if the pattern of circulation (Roberts et al. 2003) supports the persistence of the virus in the population. Continuous or intermitting circulation in a specific bat population as well as reactivation from a persistently infected bat can lead to shedding of infectious virus and in case of a zoonotic virus result in a public health hazard.

CONCLUSION

Emerging zoonotic viruses pose an increasing concern to public health and several bat species are known to be associated with some of these viruses. Lyssaviruses and Henipaviruses are probably the most definite examples of this group of zoonotic viruses (Ghatak et al. 2000). Lyssaviruses of different genotypes have emerged from bats in America (RABV), Europe (EBLV), and Australia (ABLV). Hematophagous bats, insectivorous bats, and megachiropteran fruit bats, respectively, are regarded the main natural reservoirs of these viruses. A separated cluster of ABLVs is found in insectivorous bats. Nipah virus is probably the most important recent zoonosis of bat origin in Asia. In the case of NiV as well as for the other zoonotic paramyxoviruses of bat origin in Asia, some megachiropteran bat species seem to be natural hosts. Recently it has been suggested that Chinese horseshoe bats and some other insectivorous bat species could be the reservoirs for SARS-CoV. But to date there is no evidence for a direct transmission of ccoronaviruses from bats to humans. In the case of EBOV there seems to be some circumstantial evidence for a direct transmission of the virus from megachiropteran fruit bats to primates. Thus far, EBLV is the only zoonotic virus that has been detected in bats in Europe.

New zoonotic viruses may emerge from bat reservoirs and old ones may spread to a wider geographical range. To assess future threats posed by zoonotic viruses of bats, there is a need for accurate knowledge of the factors underlying disease emergence, an effective surveillance programme and a rapid response system. Concerning virus research in bats, primary efforts should be focussed on the implementation of effective surveillance systems for a selected group of viruses depending on specific bat species and viruses. In a number of countries such surveillance systems have been put in place, and have shed some light on the dynamics of some viruses in bats. In Western Europe at present, EBLVs are the viruses of primary focus. Several European countries have a passive surveillance of EBLVs bats in place (Echevarria et al. 2001). To generate a good picture of the actual state of EBLVs in bats in Europe, such surveillance should be implemented in all European countries where EBLVs are endemic in native bats. To gain more insight in the dynamics of EBLVs in bats there is also a need for active surveillance of bats. Such active surveillance studies could consist of longitudinal sampling of bats and testing sera and excreta for virus and antibodies. Besides EBLVs, active surveillance could also be targeted on emerging viruses of which Nipah virus, Ebola virus, and SARS coronavirus seem to be the most likely choices. Nipah virus, Ebola virus, or SARS coronavirus emergence in native bats in Europe does not seem likely since thus far all reported detections of Nipah virus, EBOV, and SARS-CoV in bats, were in species exotic to Europe. However, emergence in native species can not be excluded. Still it is more indicated to focus an active surveillance of Nipah virus, SARS-CoV, and EBOV in bats in Europe on imported exotic species.

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