

19.085

Potential zoonotic pathogens in bat species in South Africa

W. Markotter^{a,*}, M. Dietrich^a, M. Geldenhuys^a, T. Kearney^b, S. McCulloch^a, M. Mortlock^a, E. Seamark^c, P. Janse van Vuren^d, J. Weyer^d, J. Paweska^d

^a University of Pretoria, Centre for Viral Zoonoses, Department of Medical Virology, Pretoria/ZA

^b Ditsong National Museum of Natural History, Pretoria/ZA

^c AfricanBats, Pretoria/ZA

^d National Institute for Communicable Diseases, Centre for Emerging and Zoonotic Diseases, Pretoria/ZA

Purpose: Bats host a suite of pathogens and with several of these, the route of transmission to humans and other animals is unknown. Factors such as the availability of food resources, age, reproductive status, movement behaviour and population density have all been factors which effects the risk of infections within host populations. In addition to opportunistic short term surveillance, this study included longitudinal surveillance and the possibility of seasonal variation of pathogen prevalence. It also focus on pathogen presence in excretions to determine possible route and the risk of transmission.

Methods & Materials: In 2004 we initiated surveillance in bats with the initial objective to identify rabies-related lyssaviruses but this has since expanded to include several other pathogens. We used nucleic acid detection techniques to detect partial pathogen genomes (RT-PCR or PCR) and virus neutralization assays to test for presence of antibodies. Furthermore, excretions (saliva, faeces and urine) from insectivorous bats were evaluated to determine the pathogen composition by using next generation sequencing techniques.

Results: We reported ten new isolations of the rabies related viruses, Lagos bat (LBV) and Duvenhage virus. We indicated that frugivorous bats (*Epomophorus wahlbergii* and *Rousettus aegyptiacus*) maintain a high level (30–67%) of seropositivity against LBV and *Nycteris thebaica* and *Miniopterus natalensis* tested seropositive for Duvenhage virus, implicating these species as possible reservoir hosts. We reported the first detection of corona, paramyxovirus and filoviruses in South African bats as well as the first reports of *Bartonella* and *Rickettsia*. Longitudinal studies, specifically focused on cave dwelling fruit bats and measuring the presence of LBV antibodies over time, indicated cyclic fluctuation of antibodies with marked increases shortly after the parturition period. Metagenomic studies on excretions of insectivorous bats identified possible zoonotic pathogens such as *Leptospira*, *Rickettsia*, *Bartonella*, *Coxiella*, *Adeno-*, *Herpes-*, *Picorna-*, and *Coronaviridae*.

Conclusion: Serological evidence obtained can be used to infer periods of increased virus circulation. These caves are used for traditional activities and information can be used to identify high risk periods for entry. We identified several pathogens that are being shed into the environment, potentially infecting other species. The collective data can be used to inform prevention and control strategies.

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Tick-borne zoonotic bacteria in fallow deer (*Dama dama*) in Euganean Hills Regional Park of Italy

M.L. Menandro^a, M. Martini^{a,*}, G. Dotto^a, A. Mondin^a, G. Ziron^b, D. Pasotto^a

^a University of Padua, Department of Animal Medicine, Production and Health, Legnaro, PD/IT

^b Euganean Hills Regional Park, Este (PD)/IT

Purpose: In the last decades an increasing incidence of tick-borne zoonoses (TBZ) has been reported in Europe. This trend regards in particular pathogens transmitted by *Ixodes ricinus*, which is the main vector of several viral, bacterial, and protozoan zoonotic infections. This tick species feeds on a broad range of mammals, birds and reptiles and frequently bites human.

The aim of the study was to investigate the prevalence of zoonotic bacteria (*Borrelia burgdorferi* sensu lato, *Rickettsia* spp., *Anaplasma* spp. and *Ehrlichia* spp.) transmitted by ticks in a population of fallow deer (*Dama dama*) in the tourist area of Euganean Hills Regional Park, Veneto Region, Italy.

Methods & Materials: The study was conducted over a 13 months period from March 2014 to March 2015. The presence of *B. burgdorferi* s.l., *Rickettsia* spp., *Anaplasma* spp. and *Ehrlichia* spp. was evaluated by PCR and real time PCR assays on 61 blood samples of fallow deer culled during the population control campaigns by the park operators. PCR assays were targeted to *groEL* (*B. burgdorferi* s.l.), *gltA* (*Rickettsia* spp.) and 16S rRNA (*Anaplasma* spp. and *Ehrlichia* spp.) genes. Amplicons were purified and directly sequenced. The nucleotide sequences were analyzed using the basic local alignment search tool (BLAST).

Results: Eighteen samples (29,5%) were positive for *A. phagocytophilum* and one (1,6%) for *Ehrlichia* spp. BLAST analyses showed sequence identity ranging from 97% to 100% with those already present in the database. None of fallow deer tested carried *B. burgdorferi* and *Rickettsia* spp.

Conclusion: The results demonstrate the presence of zoonotic tick-borne pathogens in the studied area. Although the most dangerous pathogen, *B. burgdorferi*, was not detected, our results underline the risk of human recreational or professional exposure to infections during the outdoor activity or manipulation of hunted animals. Furthermore, the presence of deer populations in peri-urban areas promotes the diffusion of ticks and increases the TBZ of humans and domestic animals.

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Japanese Encephalitis outbreak among children in Mayurbhanj, Odisha-India, 2015

P. Nayak^{a,*}, A. Pradhan^b, S. Sethi^b, B. Patnaik^b, M. Pradhan^b, K.C. Dash^b

^a National Centre for Disease Control, Epidemiology, New Delhi, DELHI/IN

^b Directorate of Public Health, Odisha, Bhubaneswar/IN

Purpose: Japanese Encephalitis (JE) is one of the leading causes of viral encephalitis in Asia. Annually 50,000 cases are reported in India with 30% deaths and 75% disability, but burden may be underestimated because many suspected outbreaks are not confirmed. During September–November, 2015 a viral encephalitis epidemic among children was reported from Mayurbhanj district, Odisha,