

# Bats, bacteria and their role in health and disease



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**Bats are ancient and among the most diverse mammals in terms of species richness, diet and habitat preferences, characteristics that may contribute to a high diversity of infectious agents. During the past two decades, the interest in bats and their microorganisms largely increased because of their role as reservoir hosts or carriers of important pathogens. Rapid advances in microbial detection and characterisation by high-throughput sequencing technologies have led to large genetic data sets but also improved our possibilities and speed of identifying unknown infectious agents. Assessing the risk of infectious diseases in bats and their pathological manifestation, however, is still challenging because of limited access to appropriate material and field data, and continuing limitations in wildlife diagnostics and the interpretation of genetic results. As a consequence, emerging pathogens can suddenly appear with devastating effects as happened for the white nose syndrome. To date, much research on bats and infectious agents still focusses on viruses, whilst the knowledge on bacteria and their role in disease is comparatively low.**

Some bacterial pathogens, such as *Bartonella* and *Leptospira*, have been more intensively studied and it seems that bats have a remarkably high diversity of bacterial species<sup>1,2</sup>. Interestingly, genetic analyses provide continuous evidence of yet-undescribed bacterial sequences and clades that might be associated with different species of bats, their habitats, ectoparasites (only for *Bartonella*) or geographic origins. It is very likely that they represent novel species within the families Bartonellaceae and Leptospiraceae but need to be further characterised.

Novel bacteria belonging to the family of Pasteurellaceae were isolated from three different species of vespertilionid bats from

Europe<sup>3</sup>. They were classified as members of the genus *Vespertiliobacter* and provide some evidence for species-specific adaptations in bats. Three further isolates that also belong to this genus have been collected recently from Nathusius's pipistrelles (*Pipistrellus nathusii*) confirming the presence of diverse bacterial strains in different species of insectivorous bats (family Vespertilionidae) (Figure 1).

*Bartonella*, *Leptospira* and many Pasteurellaceae species are known pathogens that can cause serious bacterial infections in mammals. Infected bats, however, appear to be healthy or do not show specific disease symptoms suggesting that these bacteria might possibly have co-evolved with their hosts<sup>4</sup>. To date, bacterial diseases are rarely described in wild bats<sup>5</sup>. They often represent individual cases that have been caused by well-recognised bacterial pathogens such as *Pasteurella multocida*, *Escherichia coli*, *Salmonella* and *Yersinia* species. The only exception known so far is an outbreak of acute systemic pasteurellosis caused by *P. multocida* in a colony of wild big brown bats (*Eptesicus fuscus*) in Wisconsin, USA, which resulted in high mortality<sup>6</sup>. In fruit bats kept in captivity sporadic infections associated with different opportunistic bacteria (e.g. *Staphylococcus aureus*, *Listeria* or alpha-hemolytic *Streptococcus* spp.) (Lisa L Farina, pers. comm.) and serious outbreaks of *Yersinia pseudotuberculosis*<sup>7</sup> are known to occur.

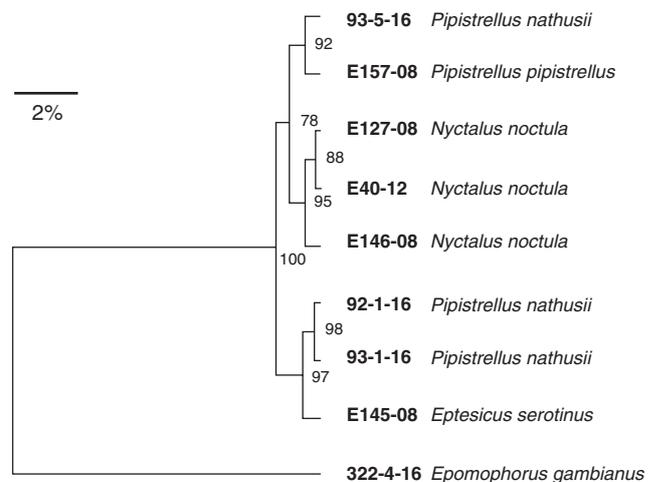


Figure 1. Phylogenetic tree based on partial 16S rRNA gene sequences. Sequences of *Vespertiliobacter* strains isolated from wild insectivorous bats of five different vespertilionid species were compared to a sequence of an unknown Pasteurellaceae-like bacterium isolated from a Gambian epauletted fruit bat kept in a zoo. The tree was built in Bionumerics v. 7.0 (Applied Maths) using the UPGMA method. Bootstrap values of 500 replicates are indicated at the branch points. The bar represents 2% sequence divergence.

The limited number of studies and literature available on infectious diseases of bats most probably reflect challenges we face in wildlife health investigations. For example, bats roosting and foraging in close proximity to humans are more likely to be found than bats that inhabit remote areas. Predation, scavenging and the fast decomposition of bat carcasses limit the access to diseased or dead animals and strongly affect wildlife diagnostics. High-throughput sequencing has markedly enhanced our abilities to detect unknown, non-culturable infectious agents or to study host-associated microbial communities in bats<sup>8</sup>. The genetic analyses are complex and generate large amounts of sequencing data that represent numerous bacterial taxa (host microbiota, unknown bacterial species, ingested and environmental bacteria) and require judicious interpretation of results. Clearly, they provide valuable insights into the composition of the microflora and the bacterial diversity in different species of bats<sup>9,10</sup>. In perspective, basic knowledge about bats and their microorganisms will enhance our understanding of existing bacteria-host interactions and their role in health and disease.

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## Biography

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