

Potentially Zoonotic Bartonella in Bats from France and Spain

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We detected *Bartonella* in 11 of 109 insectivorous bats from France and 1 of 26 bats from Spain. These genetic variants are closely related to bat-associated *Bartonella* described in Finland and the United Kingdom and to *B. mayotimonensis*, the agent of a human endocarditis case in the United States.

Bartonellae have been identified in bats sampled in locations around the world where diverse chiropteran host species can interact with numerous *Bartonella* variants and potential arthropod vectors (1–3). Many *Bartonella* species are zoonotic, potentially affecting human and bat health (4). *Bartonella* spp. in bat populations of Europe are of particular interest because some variants described in Finland and the United Kingdom are closely related to *Bartonella mayotimonensis*, a species detected in the resected aortic valve of a 59-year-old endocarditis patient in the United States (5,6). To determine if potentially zoonotic bat-associated bartonellae are circulating elsewhere in Europe, we tested insectivorous bats from France and Spain for the presence of *Bartonella* spp.

We performed necropsies on 26 bats from Spain and 109 from France to collect heart tissue for *Bartonella* spp. diagnostics (online Technical Appendix Table 1, <https://wwwnc.cdc.gov/EID/article/23/3/16-0934-Techapp1.pdf>). Bats from Spain were originally collected during active surveillance for rabies at the Unidad de Aislamiento y Detección Virus, Instituto de Salud Carlos III, Madrid, Spain. Of the bats from France, 97 were originally submitted for passive rabies surveillance to the Agence Nationale de Sécurité Sanitaire

We detected *Bartonella* DNA in 12 (8.9%) of 135 bat heart tissue samples (online Technical Appendix Table 2); 11 of the tissues were from bats from France, and 1 was from an unidentified bat captured in Torreferrusa, Catalonia, Spain. The 11 *Bartonella*-positive bats from France belonged to only 4 of the 13 sampled species: *N. noctula* (2/15 bats [13.3%, 95% CI 1.7%–40.5%]), *P. nathusii* (6/24 bats [25%, 95% CI 9.8%–46.7%]), *M. daubentonii* (2/3 bats [66.6%, 95% CI 9.4%–99.1%]), and *M. mystacinus* (1/4 bats [25%, 95% CI 0.6%–80.6%]).

All 12 *Bartonella* variants (GenBank accession nos. KY041981–KY041992) clustered closely with zoonotic *B. mayotimonensis* (Figure). Two sequences obtained from *M. daubentonii* bats sampled in Lorraine (GenBank accession no. KY041985) and Upper Normandy (GenBank accession no. KY041989), France, shared 100% nt identity with *Bartonella* strains previously isolated from bats of the same species in Finland and the United Kingdom (5,9). None of the *Bartonella* variants were closely related to *Candidatus Bartonella naantaliensis* or *Candidatus Bartonella hemsundetiensis*, which were also described in bats sampled in Finland (5,10). The absence of variants resembling these bartonellae from northern Europe suggests a spatial heterogeneity in the distribution of *Bartonella* spp. across bat populations and selective adaptations to specific host reservoirs.

Further research is needed to better evaluate the prevalence of zoonotic *Bartonella* species in western Europe and to determine if *B. mayotimonensis*, the agent of a US case of human endocarditis, is present across a broader range than currently documented. Future studies should consider specifically focusing on *Nyctalus*, *Pipistrellus*, and *Myotis* bat species, from which we most frequently detected variants similar to *B. mayotimonensis*.

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