

Acknowledgments

We gratefully acknowledge V. Adamkova, A. Becker, M. Deighton, O. Denis, J. Ferguson, A. Friedrich, Y.C. Huang, A. Ingebretsen, A. Kearns, K. Klingenberg, C. Laferrière, B. Pichon, K. Regina Netto dos Santos, J. Schrenzel, K. TaekSoo, E. Tarkka, J. Ussher, C. Vandenbroucke-Graulsfor, and L. Westblade for the timely selection and sending of *S. capitis* isolates, as well as Louise Hoden and the team at the French National Reference Center for Staphylococci for their expert technical assistance.

Dr. Butin is a pediatrician working in the neonatal intensive care unit of the Hôpital Femme Mère Enfant, Hospices Civils de Lyon, Lyon, France. Her primary research interests are the epidemiology, pathophysiology, and clinical determinants of infections in neonates, notably *Staphylococcus*-associated infections.

References

1. Liu L, Oza S, Hogan D, Perin J, Rudan I, Lawn JE, et al. Global, regional, and national causes of child mortality in 2000–13, with projections to inform post-2015 priorities: an updated systematic analysis. *Lancet*. 2015;385:430–40. [http://dx.doi.org/10.1016/S0140-6736\(14\)61698-6](http://dx.doi.org/10.1016/S0140-6736(14)61698-6)
2. Boghossian NS, Page GP, Bell EF, Stoll BJ, Murray JC, Cotten CM, et al.; Eunice Kennedy Shriver National Institute of Child Health and Human Development Neonatal Research Network. Late-onset sepsis in very low birth weight infants from singleton and multiple-gestation births. *J Pediatr*. 2013;162:1120–4, 1124.e1. <http://dx.doi.org/10.1016/j.jpeds.2012.11.089>
3. Van Der Zwet WC, Debets-Ossenkopp YJ, Reinders E, Kapi M, Savelkoul PH, Van Elburg RM, et al. Nosocomial spread of a *Staphylococcus capitis* strain with heteroresistance to vancomycin in a neonatal intensive care unit. *J Clin Microbiol*. 2002;40:2520–5. <http://dx.doi.org/10.1128/JCM.40.7.2520-2525.2002>
4. Rasigade J-P, Raulin O, Picaud J-C, Tellini C, Bes M, Grando J, et al. Methicillin-resistant *Staphylococcus capitis* with reduced vancomycin susceptibility causes late-onset sepsis in intensive care neonates. *PLoS One*. 2012;7:e31548. <http://dx.doi.org/10.1371/journal.pone.0031548>
5. Butin M, Rasigade J-P, Martins-Simões P, Meugnier H, Lemriss H, Goering RV, et al. Wide geographical dissemination of the multiresistant *Staphylococcus capitis* NRCS-A clone in neonatal intensive-care units. *Clin Microbiol Infect*. 2016;22:46–52. <http://dx.doi.org/10.1016/j.cmi.2015.09.008>
6. Ben Said M, Hays S, Bonfils M, Jourdes E, Rasigade JP, Laurent F, et al. Late-onset sepsis due to *Staphylococcus capitis* ‘neonatalis’ in low-birthweight infants: a new entity? *J Hosp Infect*. 2016;94:95–8. <http://dx.doi.org/10.1016/j.jhin.2016.06.008>
7. Goering RV. Molecular epidemiology of nosocomial infection: analysis of chromosomal restriction fragment patterns by pulsed-field gel electrophoresis. *Infect Control Hosp Epidemiol*. 1993;14:595–600. <http://dx.doi.org/10.2307/30105130>

Address for correspondence: Marine Butin, Department of Neonatal Intensive Care, Eastern Hospital Group Hospices Civils de Lyon, 59 Bd Pinel, 69500 Lyon Bron, France; email: marine.butin@chu-lyon.fr

Potentially Zoonotic *Bartonella* in Bats from France and Spain

Matthew J. Stuckey, Henri-Jean Boulouis, Florence Cliquet, Evelyne Picard-Meyer, Alexandre Servat, Nidia Aréchiga-Ceballos, Juan E. Echevarría, Bruno B. Chomel

Author affiliations University of California, Davis, USA (M.J. Stuckey, B.B. Chomel); Ecole Nationale Vétérinaire d'Alfort, Maisons-Alfort, France (H.-J. Boulouis); Agence Nationale de Sécurité Sanitaire de l'Alimentation, de l'Environnement et du Travail (ANSES), Laboratoire de la Rage et de la Faune Sauvage de Nancy, Malzéville, France (F. Cliquet, E. Picard-Meyer, A. Servat); Laboratorio de Rabia, Instituto de Diagnóstico y Referencia Epidemiológicos, Mexico City, Mexico (N. Aréchiga-Ceballos); Centro de Investigación Biomédica en Red de Epidemiología y Salud Pública (CIBERESP), Instituto de Salud Carlos III, Madrid, Spain (J.E. Echevarría)

DOI: <http://dx.doi.org/10.3201/eid2303.160934>

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*.

Acknowledgments

We thank Laurent Arthur, Michèle Lemaire, Alvaro Aguilar Setién, Noël Tordo, Janet Foley, Deana Clifford, Rickie Kasten, Philip Kass, Daniel Greenia, Tristan Burgess, José M. Berciano, Annick Suzor-Weiner, Nadia Haddad, Martine Monteil, Elisabeth Petit, Thibaud Dugat, and Jean-Philippe Buffet for help with the study design, bat sampling, laboratory diagnostics, manuscript preparation, and general guidance. We also thank the Société Française pour l'Étude et la Protection des Mammifères (SFEPM) group for their participation in the passive bat rabies surveillance in France.

M.J.S. was funded by a Chateaubriand STEM (Science, Technology, Engineering & Mathematics) Fellowship (French Ministry of Foreign Affairs) with matching funds from Mériat, Lyon, France.

Dr. Stuckey works in the Department of Population Health and Reproduction at the University of California Davis School of Veterinary Medicine. His research interests include disease ecology and epidemiology of zoonoses.

References

- McKee CD, Hayman DT, Kosoy MY, Webb CT. Phylogenetic and geographic patterns of *Bartonella* host shifts among bat species. *Infect Genet Evol*. 2016;44:382–94. <http://dx.doi.org/10.1016/j.meegid.2016.07.033>
- Lei BR, Olival KJ. Contrasting patterns in mammal–bacteria coevolution: *Bartonella* and *Leptospira* in bats and rodents. *PLoS Negl Trop Dis*. 2014;8:e2738. <http://doi.org/10.1371/journal.pntd.0002738>
- Judson SD, Frank HK, Hadly EA. Bartonellae are prevalent and diverse in Costa Rican bats and bat flies. *Zoonoses Public Health*. 2015;62:609–17. <http://dx.doi.org/10.1111/zph.12188>
- Mühldorfer K. Bats and bacterial pathogens: a review. *Zoonoses Public Health*. 2013;60:93–103. <http://dx.doi.org/10.1111/j.1863-2378.2012.01536.x>
- Veikkolainen V, Vesterinen EJ, Lilley TM, Pulliainen AT. Bats as reservoir hosts of human bacterial pathogen, *Bartonella mayotimonensis*. *Emerg Infect Dis*. 2014;20:960–7. <http://dx.doi.org/10.3201/eid2006.130956>
- Lin EY, Tsigrelis C, Baddour LM, Lepidi H, Rolain JM, Patel R, et al. *Candidatus Bartonella mayotimonensis* and endocarditis. *Emerg Infect Dis*. 2010;16:500–3. <http://dx.doi.org/10.3201/eid1603.081673>
- Kamani J, Baneth G, Mitchell M, Mumcuoglu KY, Gutiérrez R, Harrus S. *Bartonella* species in bats (Chiroptera) and bat flies (Nycteribiidae) from Nigeria, West Africa. *Vector Borne Zoonotic Dis*. 2014;14:625–32. <http://dx.doi.org/10.1089/vbz.2013.1541>
- Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, et al. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*. 2012;28:1647–9.
- Concannon R, Wynn-Owen K, Simpson VR, Birtles RJ. Molecular characterization of haemoparasites infecting bats (Microchiroptera) in Cornwall, UK. *Parasitology*. 2005;131:489–96. <http://dx.doi.org/10.1017/S0031182005008097>
- Lilley TM, Veikkolainen V, Pulliainen AT. Molecular detection of *Candidatus Bartonella hemsundetiensis* in bats. *Vector Borne Zoonotic Dis*. 2015;15:706–8. <http://dx.doi.org/10.1089/vbz.2015.1783>

Address for correspondence: Bruno B. Chomel, VM3B Room 1020, 1089 Veterinary Medicine Dr, University of California, Davis, CA 95616, USA; email: bbchomel@ucdavis.edu