



HAL
open science

Difficulties in schistosomiasis assessment, Corsica, France

Hélène Moné, M. C. Holtfreter, Gabriel Mouahid, J. Richter

► **To cite this version:**

Hélène Moné, M. C. Holtfreter, Gabriel Mouahid, J. Richter. Difficulties in schistosomiasis assessment, Corsica, France . *Emerging Infectious Diseases*, 2016, 22 (4), pp.762-763. 10.3201/eid2204.160110 . hal-01311074

HAL Id: hal-01311074

<https://sde.hal.science/hal-01311074v1>

Submitted on 3 May 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

glycoprotein-specific antibodies are present at high levels concurrent with the longitudinal detection of genomic RNA. A large-scale seroprevalence and cross-neutralization study is ongoing.

We used complete genome and H gene sequences in a comprehensive phylogenetic analysis. FeMV^{US1} is closely related to viruses from Asia, highlighting the global distribution of FeMV (Figure, panel A). Compared with the sequence for the FeMV^{776U} H gene, sequences for FeMV^{US1} and FeMV^{US5} were 98% and 81% similar, and the glycoproteins were 98% and 86% identical. The complete H gene of the most divergent US strain (FeMV^{US5}) clustered phylogenetically in a basal sister relationship with all other viruses from Asia and the United States (Figure, panel B), suggesting a long evolutionary association of FeMV in feline hosts.

Ecologic surveys continue to identify novel viruses that are homologous to known paramyxoviruses in many wildlife species, including bats and rodents (6). Investigating closely related viruses in domestic species is warranted, given the substantial number of animals that cohabit with humans. Switches from natural to unnatural host species can result in enhanced pathogenicity (e.g., receptor switching has caused feline panleukopenia virus to infect dogs as canine parvovirus) (7). Given the high degree of antigenic relatedness of morbilliviruses, understanding evolutionary origins and trajectories and conferring cross-protection through immunization are critical. Although no evidence for FeMV transmission to humans or other animals exists, the propensity for noncanonical use of signaling lymphocytic activation molecule 1 F1 (CD150) should be investigated because epizootic transmission of morbilliviruses can occur (8).

The detection of FeMV sequences in a clinically healthy animal after 15 months is a novel and surprising observation but is consistent with the known propensity for morbilliviruses to persist *in vivo* (9). All known morbilliviruses cause acute infections, and the typical long-term clinical manifestations occur in the central nervous system, not the urinary system (1). These observations should prompt additional research because the prevalence of CKD in cats is high and because CKD decreases the quality of life of affected animals and is the ultimate cause of death for approximately one third of cats (10).

Acknowledgments

We thank Florence Lee, Diane Welsh, Karen Greenwood, Graeme Bainbridge, Betsy Galvan, and Rik de Swart for helpful suggestions, critical reading of the manuscript, and technical support. We thank the Winn Foundation for previous support.

Funding for this study was provided by Boston University and Zoetis LLC.

References

1. Woo PC, Lau SK, Wong BH, Fan RY, Wong AY, Zhang AJ, et al. Feline morbillivirus, a previously undescribed paramyxovirus associated with tubulointerstitial nephritis in domestic cats. *Proc Natl Acad Sci U S A*. 2012;109:5435–40. <http://dx.doi.org/10.1073/pnas.1119972109>
2. Furuya T, Sassa Y, Omatsu T, Nagai M, Fukushima R, Shibutani M, et al. Existence of feline morbillivirus infection in Japanese cat populations. *Arch Virol*. 2014;159:371–3. <http://dx.doi.org/10.1007/s00705-013-1813-5>
3. Nambulli S, Sharp CR, Acciardo AS, Drexler JF, Duprex WP. Mapping the evolutionary trajectories of morbilliviruses: what, where, and whither. *Curr Opin Virol*. In press 2016.
4. Simmonds P. SSE: a nucleotide and amino acid sequence analysis platform. *BMC Res Notes*. 2012;5:50. <http://dx.doi.org/10.1186/1756-0500-5-50>
5. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol*. 2011;28:2731–9. <http://dx.doi.org/10.1093/molbev/msr121>
6. Drexler JF, Corman VM, Müller MA, Maganga GD, Vallo P, Binger T, et al. Bats host major mammalian paramyxoviruses. *Nat Commun*. 2012;3:796. <http://dx.doi.org/10.1038/ncomms1796>
7. Parrish CR, Kawaoka Y. The origins of new pandemic viruses: the acquisition of new host ranges by canine parvovirus and influenza A viruses. *Annu Rev Microbiol*. 2005;59:553–86. <http://dx.doi.org/10.1146/annurev.micro.59.030804.121059>
8. Ludlow M, Rennick LJ, Nambulli S, de Swart RL, Duprex WP. Using the ferret model to study morbillivirus entry, spread, transmission and cross-species infection. *Curr Opin Virol*. 2014;4:15–23. <http://dx.doi.org/10.1016/j.coviro.2013.11.001>
9. Rima BK, Duprex WP. Molecular mechanisms of measles virus persistence. *Virus Res*. 2005;111:132–47. <http://dx.doi.org/10.1016/j.virusres.2005.04.005>
10. Lawler DF, Evans RH, Chase K, Ellersieck M, Li Q, Larson BT, et al. The aging feline kidney: a model mortality antagonist? *J Feline Med Surg*. 2006;8:363–71. <http://dx.doi.org/10.1016/j.jfms.2006.06.002>

Address for correspondence: W. Paul Duprex, Department of Microbiology, Boston University School of Medicine, 620 Albany St, Boston, MA 02118, USA; email: pduprex@bu.edu

Difficulties in Schistosomiasis Assessment, Corsica, France

Hélène Moné, Martha C. Holtfreter, Gabriel Mouahid, Joachim Richter

Author affiliations: University of Perpignan, Perpignan, France (H. Moné, G. Mouahid); Heinrich-Heine-University Düsseldorf, Düsseldorf, Germany (M.C. Holtfreter, J. Richter)

DOI: <http://dx.doi.org/10.3201/eid2204.160110>

To the Editor: We would like to add some specification and clarification to the discussion regarding the diagnostics and case definitions for urinary schistosomiasis in travelers to Corsica, France (1–3). Evidence for a *Schistosoma*

haematobium infection typically depends on the detection of viable ova in the urine. However, in regard to *S. haematobium* infections acquired in Corsica, several ova excreted by the first 2 published case-patients (i.e., the 12-year-old boy and his father) exhibited atypical morphology (4). Therefore, we supplemented our morphologic study with a molecular study of miracidia by using cytochrome c oxidase mitochondrial DNA barcoding and the internal transcribed spacer 2 gene.

The results indicated that the schistosome responsible for the infection of the first case-patient reported in Corsica was *S. haematobium* that had been introgressed by genes of zoonotic *S. bovis* through a hybridization process. *S. bovis* is the cause of bovine intestinal schistosomiasis and uses the same intermediate host (*Bulinus truncatus* snails) that *S. haematobium* uses (5). Such interactions between *S. haematobium* and *S. bovis* have also been reported in Benin (5). These findings imply that the clinical course of case-patients and diagnostic test results might be affected by atypical schistosomiasis. Whereas the boy in our study experienced a clinically typical schistosomal infection of the bladder, his father and his siblings, who had identical histories of exposure, were seropositive for *S. haematobium* but were asymptomatic (4).

We recommend that clinicians treat any suspected case of *S. haematobium* infection, whether or not the patient excretes ova, given that the disease is potentially serious and the indicated drug for treatment (praziquantel) is safe. Epidemiologic analyses should take into account the role of zoonotic *S. bovis* infection and supplement parasitological investigations with molecular analyses (5,6).

References

1. Beltrame A, Zammarchi L, Zuglian G, Gobbi F, Angheben A, Marchese V, et al. Schistosomiasis screening of travelers to Corsica, France. *Emerg Infect Dis*. 2016;22:159–60. <http://dx.doi.org/10.3201/eid2201.151590>
2. Beltrame A, Zammarchi L, Zuglian G, Gobbi F, Angheben A, Marchese V, et al. Schistosomiasis screening of travelers from Italy with possible exposure in Corsica, France. *Emerg Infect Dis*. 2015;21:1887–9. <http://dx.doi.org/10.3201/eid2110.150869>
3. Gautret P, Mockenhaupt FP, von Sonnenburg F, Rothe C, Libman M, Van De Winkel K, et al. Local and international implications of schistosomiasis acquired in Corsica, France. *Emerg Infect Dis*. 2015;21:1865–8. <http://dx.doi.org/10.3201/eid2110.150881>
4. Holtfreter MC, Moné H, Müller-Stöver I, Mouahid G, Richter J. *Schistosoma haematobium* infections acquired in Corsica, France, August 2013. *Euro Surveill*. 2014;19:20821. <http://dx.doi.org/10.2807/1560-7917.ES2014.19.22.20821>
5. Moné H, Holtfreter MC, Allienne JF, Mintsá-Nguéma R, Ibikounlé M, Boissier J, et al. Introgressive hybridizations of *Schistosoma haematobium* by *Schistosoma bovis* at the origin of the first case report of schistosomiasis in Corsica (France, Europe). *Parasitol Res*. 2015;114:4127–33. <http://dx.doi.org/10.1007/s00436-015-4643-4>
6. Berry A, Fillaux J, Martin-Blondel G, Boissier J, Iriart X, Marchou B, et al. Evidence for a permanent presence of schistosomiasis in Corsica, France, 2015. *Euro Surveill*. 2016;21:30100. <http://dx.doi.org/10.2807/1560-7917.ES.2016.21.1.30100>

Address for correspondence: Joachim Richter, Tropical Medicine Unit, Department of Gastroenterology, Hepatology and Infectious Diseases, Heinrich-Heine-University Düsseldorf, Moorenstr 5, Dusseldorf, D-4B225, Germany; email: joachim.richter@med.uni-duesseldorf.de

Correction: Vol. 21, No. 11

Cryptococcus was misspelled in the title of Climatic Influences on *Cryptococcus gattii* Populations, Vancouver Island, Canada, 2002–2004 (C.K. Uejio al.). The article has been corrected online (http://wwwnc.cdc.gov/eid/article/21/11/14-1161_article).



Get the content you want delivered to your inbox.

- Table of Contents
- Podcasts
- Ahead of Print Articles
- CME
- Specialized Content

Online subscription: wwwnc.cdc.gov/eid/subscribe.htm