


Lack of evidence for the presence of leprosy bacilli in red squirrels from North-West Europe

Maria Tió-Coma¹  | Hein Sprong² | Marja Kik³ | Jaap T. van Dissel² | Xiang-Yang Han⁴ | Toine Pieters⁵ | Annemieke Geluk¹

¹Department of Infectious Diseases, Leiden University Medical Center, Leiden, The Netherlands

²Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands

³Faculty of Veterinary Medicine, Dutch Wildlife Health Centre (DWHC), Utrecht University, Utrecht, The Netherlands

⁴Department of Laboratory Medicine, University of Texas M. D. Anderson Cancer Center, Houston, TX, USA

⁵Division Pharmacoepidemiology and Clinical Pharmacology, Utrecht Institute for Pharmaceutical Sciences, Utrecht, The Netherlands

Correspondence

Annemieke Geluk, Department of Infectious Diseases, Leiden University Medical Center, Leiden, The Netherlands.
Email: a.geluk@lumc.nl

Funding information

This study was supported by an R2STOP Research grant from Effect hope/The Leprosy Mission Canada and the Q.M. Gastmann-Wichers Foundation (to AG).

Abstract

Leprosy is a human infectious disease caused by *Mycobacterium leprae* or *Mycobacterium lepromatosis* that can also occur in animals and even manifest as zoonosis. Recently, both mycobacteria were detected in red squirrels (*Sciurus vulgaris*) from the British Isles. To further explore the presence of leprosy bacilli in North-West Europe, we screened Belgian and Dutch squirrels. Tissue samples from 115 animals tested by qPCR were negative for both pathogens. No molecular or pathological evidence was found of the presence of these zoonotic pathogens in North-West Europe.

KEYWORDS

leprosy, *Mycobacterium leprae*, *Mycobacterium lepromatosis*, OneHealth, red squirrel, zoonosis

1 | INTRODUCTION

Leprosy, caused by *Mycobacterium leprae* or *Mycobacterium lepromatosis*, is a debilitating disease occurring in several low- and middle-income countries. Transmission is unabated as shown by stable numbers of new cases worldwide (WHO, 2018). Close contact to multibacillary patients (Moet, Meima, Oskam, & Richardus, 2004), and, to a lesser extent, infected animals and environmental sources are presumed to play a role in transmission (Tió-Coma et al., 2019; Truman et al., 2011).

Mycobacterium leprae and *M. lepromatosis* can cause leprosy-like disease in several animal hosts, including nine-banded armadillos

(Truman et al., 2011), red squirrels (Avanzi et al., 2016) and non-human primates (Honap et al., 2018).

Previously, *M. leprae* and *M. lepromatosis* have been detected in Eurasian red squirrels (*Sciurus vulgaris*) from the British Isles (Avanzi et al., 2016; Schilling, van Hooij, et al., 2019), where human leprosy has not occurred for centuries. Squirrels of other European countries and Mexico, however, were not positive for DNA of these pathogens when screened by PCR (Schilling, Avanzi, et al., 2019).

To further explore the presence of *M. leprae* or *M. lepromatosis* in continental squirrels from North-West Europe, we screened squirrels from the Netherlands and Belgium.

2 | MATERIALS AND METHODS

2.1 | Sample collection

Sixty-one wild red squirrels (*S. vulgaris*) and one Japanese squirrel (*Sciurus lis*) were found dead in the Netherlands and submitted to the Dutch Wildlife Health Centre (Figure S1). Animals died due to infection with *Toxoplasma gondii* ($n = 21$), traumatic injuries ($n = 23$) or other pathologies ($n = 18$). Skin lesions consistent with leprosy were not detected. Red squirrels ($n = 53$) victims of road traffic were collected between 2010 and 2014 in Flanders (Table S1), Belgium (Ruyts, Frazer-Mendelewska, Van Den Berge, Verheyen, & Sprong, 2017).

Necropsy included macroscopic examination, cytological analysis of liver, spleen, lungs and intestinal contents stained with HemacolorR (Hemacolor quick stain; Merck) and histological examination.

Small biopsies from liver and spleen were collected in 2 ml tubes and stored at 221220°C until further processing.

2.2 | DNA extraction

Biopsies from spleen (Dutch squirrels [$n = 62$]; Belgian squirrels [$n = 53$]) and liver (Belgian squirrels only [$n = 53$]) were used for DNA extraction.

DNA extraction was performed on 20 mg tissue using the Qiagen DNeasy Blood and Tissue Kit (Qiagen), according to manufacturer's protocol.

2.3 | RLEP and 202 qPCR

A qPCR amplifying an *M. leprae*-specific repetitive sequence (RLEP) was performed (Martinez et al., 2009). For *M. lepromatosis*, primers and probe (202-qPCR) were designed based on criteria for TaqMan PCR reactions to amplify a 168 bp fragment in contig 202 which has two copies in the genome and is specific of *M. lepromatosis*. Amplification was carried in a final volume of 25 μ l by addition of GoTaq™ Probe qPCR Master Mix (Promega), 22.5 μ M primers (Table 1), 6.25 μ M TaqMan probe (Table 1) and 5.0 μ l sample using the following profile: 2 min at 95°C, 40 cycles of 15 s at 95°C and 1 min at 60°C. Nuclease-free water was used as negative control and *M. leprae* or *M. lepromatosis* DNA as positive controls. DNA of *M. leprae* Br4923 and Thai53, *M. bovis* BCG P3 and *M. tuberculosis* H37DNA was used to assess 202qPCR specificity. A C_t of 38.5 was taken as the limit for positivity.

Statistical analysis was performed in R (version 3.4.1).

3 | RESULTS

To study whether leprosy bacilli are presented in Dutch and Belgian squirrels, we performed qPCR analysis on 115 red squirrels none

TABLE 1 Primers and probes for repetitive sequence and 202 qPCR

Primer/probe	Sequence 5'-3'
RLEP qPCR F	GCAGCAGTATCGTGTAGTGAA
RLEP qPCR R	CGCTAGAAGTTGCCGTAT
RLEP qPCR Probe FAM	CGCCGACGGCCGATCATCGA
qPCR 202 F	CTGATCGCACACCTTGATGAGAG
qPCR 202 R	GTTAGGTTGATCGACATCTTCGGTGC
qPCR 202 Probe VIC	CACCACTAGCGCACCACGTCAGACAGGC

Note: Forward (F) primers, reverse (R) primers and probes with dyes used to detect presence of *Mycobacterium leprae* (RLEP) and *Mycobacterium lepromatosis* (202) by TaqMan qPCR.

of which showed clinical signs of leprosy. DNA samples were negative for both RLEP-qPCR (*M. leprae*) and 202-qPCR (*M. lepromatosis*). Thus, *M. leprae*- and *M. lepromatosis*-specific DNA was not detected in the Dutch or Belgian red squirrel populations with a 95% confidence interval (CI) of 0.0%–4.1%. Part of these samples has been tested successfully for the presence of tick-borne pathogens by qPCR (Ruyts et al., 2017), and 45% were positive for the presence of Bartonella DNA (Von Loewenich et al., 2019).

4 | DISCUSSION

Since the discovery of Eurasian red squirrels suffering from leprosy-like disease in the British Isles (Avanzi et al., 2016), there has been an increased interest to screen other squirrels for *M. leprae* and *M. lepromatosis*. We examined 114 animals from the red squirrel population in the Netherlands and Belgium.

In Brownsea Island, *M. leprae* DNA was found in 25 out of 25 red squirrels (eight with leprosy-like lesions; Avanzi et al., 2016). In Scotland and Ireland, *M. leprae* was not detected, but *M. lepromatosis* was identified. The authors calculated that 21% of the squirrel population without clinical signs and all squirrels with clinical signs from the British Isles carried either *M. leprae* or *M. lepromatosis*.

As recently described (Schilling, Avanzi, et al., 2019), in a squirrel population showing no disease manifestations and with the same prevalence of leprosy as the British Isles (21%), a sample size of 19 should suffice to identify minimally one case with a 95% CI. Since our sample size (53 Belgian squirrels, 62 Dutch squirrels) was 2 to 3-fold larger, we should have identified leprosy bacilli in the Dutch and Belgian squirrel population, if present, in at least the same prevalence as in the British Isles. When taking into account also previously tested continental European Eurasian red squirrels ($n = 96$; Schilling, Avanzi, et al., 2019), the prevalence in mainland Europe is less than 2.2% with a 95% CI.

Our findings are consistent with previous observation in other European countries (France, Italy, United Kingdom, Germany and Switzerland) and Mexico (Schilling, Avanzi, et al., 2019) where *M. leprae*- or *M. lepromatosis*-specific DNA was not detected.

Pinnae samples have been reported to be the optimal tissue for molecular screening. Spleen and liver have also been successfully used to detect *M. leprae* and *M. lepromatosis* DNA in squirrels (Avanzi et al., 2016); however, the sensitivity might differ from pinnae samples. The lack of positive PCR results could be due to a lower prevalence of the leprosy bacilli in the Dutch and Belgian red squirrel population compared to the reference UK population. It is conceivable that red squirrels in UK could be more susceptible due to reduced immunity as a consequence of squirrelpox transmitted by grey squirrels (McGowan et al., 2014). Alternatively, the animals could carry a bacillary load below the detection limit, or our tissue sampling might have been suboptimal. However, animals with leprosy-related lesions have not been observed in these populations suggesting that the absence of the pathogen is a more-plausible scenario. As we did not find evidence of the presence of *M. leprae* or *M. lepromatosis*, our results endorse the recent hypothesis (Schilling, Avanzi, et al., 2019) that Eurasian red squirrels in the British Isles are the only known wild rodent up to date carrying the leprosy bacilli.

ACKNOWLEDGEMENTS

We thank Ir. M.G.E. Montizaan (DWHC, Utrecht University, The Netherlands) for creating the map of the Dutch squirrel location.

CONFLICTS OF INTEREST

The authors declare that they have no conflict of interest.

ETHICAL APPROVAL

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to. No ethical approval was required as wild animals were found dead and offered for necropsy.

ORCID

Maria Tió-Coma  <https://orcid.org/0000-0002-3594-1156>

REFERENCES

- Avanzi, C., Del-Pozo, J., Benjak, A., Stevenson, K., Simpson, V. R., Busso, P., ... Meredith, A. L. (2016). Red squirrels in the British Isles are infected with leprosy bacilli. *Science*, 354(6313), 744–747. <https://doi.org/10.1126/science.aah3783>
- Honap, T. P., Pfister, L.-A., Housman, G., Mills, S., Tarara, R. P., Suzuki, K., ... Stone, A. C. (2018). *Mycobacterium leprae* genomes from naturally infected nonhuman primates. *PLoS Neglected Tropical Diseases*, 12(1), e0006190. <https://doi.org/10.1371/journal.pntd.0006190>
- Martinez, A. N., Lahiri, R., Pittman, T. L., Scollard, D., Truman, R., Moraes, M. O., & Williams, D. L. (2009). Molecular determination

of *Mycobacterium leprae* viability by use of real-time PCR. *Journal of Clinical Microbiology*, 47(7), 2124–2130. <https://doi.org/10.1128/jcm.00512-09>

- McGowan, N. E., Marks, N. J., McInnes, C. J., Deane, D., Maule, A. G., & Scantlebury, M. (2014). Effects of parasitism and morphology on squirrelpox virus seroprevalence in grey squirrels (*Sciurus carolinensis*). *PLoS ONE*, 9(1), e83106. <https://doi.org/10.1371/journal.pone.0083106>
- Moet, F. J., Meima, A., Oskam, L., & Richardus, J. H. (2004). Risk factors for the development of clinical leprosy among contacts, and their relevance for targeted interventions. *Leprosy Review*, 75(4), 310–326.
- Ruyts, S., Frazer-Mendelewska, E., Van Den Berge, K., Verheyen, K., & Sprong, H. (2017). Molecular detection of tick-borne pathogens *Borrelia afzelii*, *Borrelia miyamotoi* and *Anaplasma phagocytophilum* in Eurasian red squirrels (*Sciurus vulgaris*). *European Journal of Wildlife Research*, 63(3), 1–43. <https://doi.org/10.1007/s10344-017-1104-7>
- Schilling, A.-K., Avanzi, C., Ulrich, R. G., Busso, P., Pisanu, B., Ferrari, N., ... Cole, S. T. (2019). British red squirrels remain the only known wild rodent host for leprosy bacilli. *Frontiers in Veterinary Science*, 6(8), <https://doi.org/10.3389/fvets.2019.00008>
- Schilling, A.-K., van Hooij, A., Corstjens, P., Lurz, P. W. W., DelPozo, J., Stevenson, K., ... Geluk, A. (2019). Detection of humoral immunity to mycobacteria causing leprosy in Eurasian red squirrels (*Sciurus vulgaris*) using a quantitative rapid test. *European Journal of Wildlife Research*, 65(3), 49. <https://doi.org/10.1007/s10344-019-1287-1>
- Tió-Coma, M., Wijnands, T., Pierneef, L., Schilling, A. K., Alam, K., Roy, J. C., ... Geluk, A. (2019). Detection of *Mycobacterium leprae* DNA in soil: Multiple needles in the haystack. *Scientific Reports*, 9(1), 3165. <https://doi.org/10.1038/s41598-019-39746-6>
- Truman, R. W., Singh, P., Sharma, R., Busso, P., Rougemont, J., Paniz-Mondolfi, A., ... Cole, S. T. (2011). Probable zoonotic leprosy in the Southern United States. *New England Journal of Medicine*, 364(17), 1626–1633. <https://doi.org/10.1056/NEJMoa1010536>
- von Loewenich, F. D., Seckert, C., Dauber, E., Kik, M. J. L., de Vries, A., Sprong, H., ... Brandstetter, M. (2019). Prosthetic valve endocarditis with *Bartonella washoensis* in a human European patient and its detection in red squirrels (*Sciurus vulgaris*). *Journal of Clinical Microbiology*. <https://doi.org/10.1128/JCM.01404-19>
- WHO (2018). Global leprosy update, 2017: Reducing the disease burden due to leprosy. *Weekly Epidemiological Record*, 93, 11.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

How to cite this article: Tió-Coma M, Sprong H, Kik M, et al. Lack of evidence for the presence of leprosy bacilli in red squirrels from North-West Europe. *Transbound Emerg Dis*. 2020;67:1032–1034. <https://doi.org/10.1111/tbed.13423>