

# The role of wild deer in the epidemiology of cattle TB: A review

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## Background

- In Great Britain (GB), bovine tuberculosis (bTB) causes large **economic loss in the livestock industry**, and poses as a **public health risk**.
- Having a bTB wildlife reservoir makes it increasingly difficult for countries to eradicate this disease, as they are a source of reinfection to livestock [1].
- Examples where wildlife species have been shown to be maintenance hosts of bTB include: badgers (*Meles meles*) in the UK, white-tailed deer (*Odocoileus virginianus*) in the United States, and brushtail possums (*Trichosurus vulpecula*) in New Zealand [2].
- bTB has been found in at least 14 species of deer globally, and **five of the six deer species in GB have been found to be bTB positive** [3].



## Main Objective

- In certain parts of GB, questions are being raised about whether deer are a main sylvatic reservoir or a spill-over host of bTB, and whether more measures need to be put in place to control for the bTB transmission risk from deer to the livestock industry.
- In order to assess this risk, a literature review was conducted to assess the current evidence on the role wild deer play in the spread of bTB.

## Methods

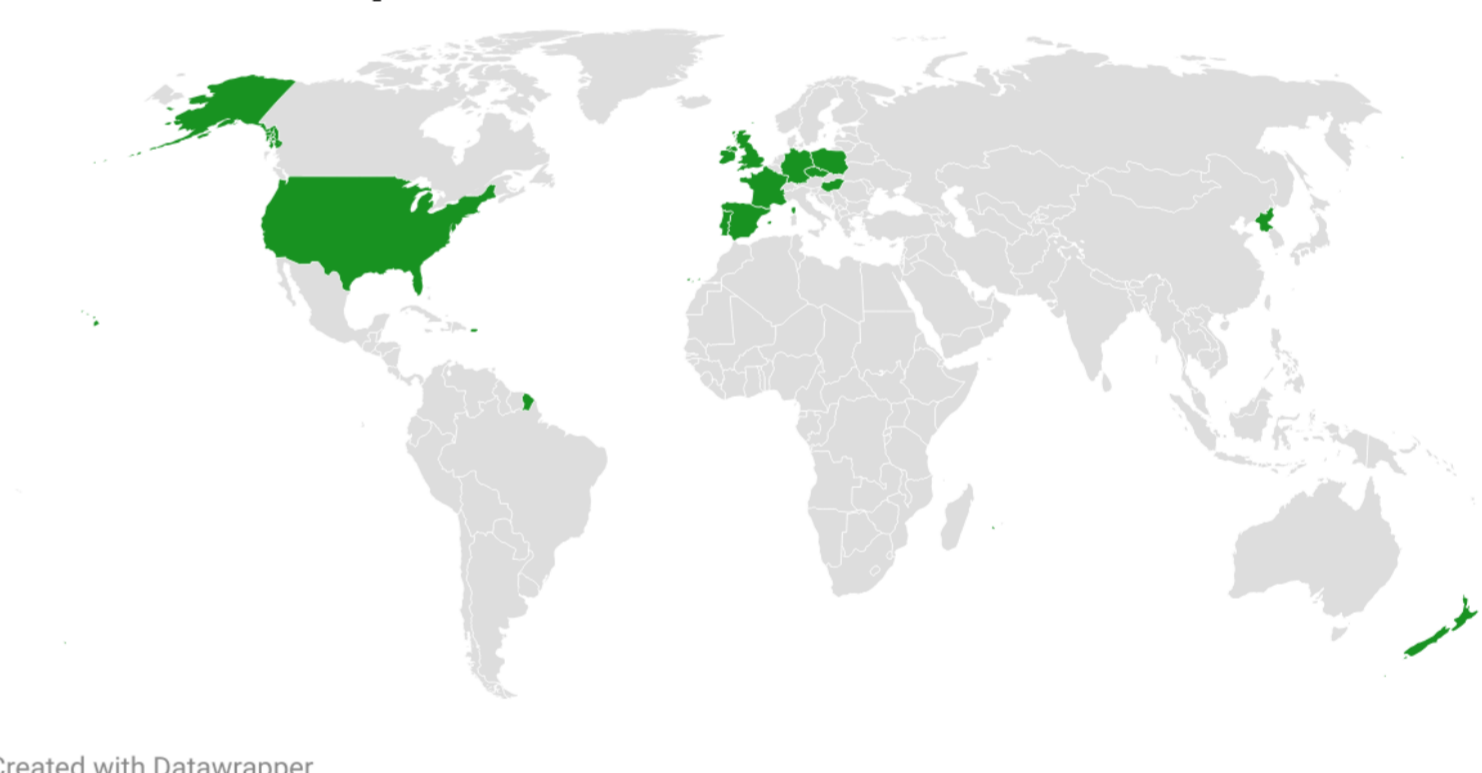
- A literature search was conducted on Scopus on the 17<sup>th</sup> of January 2022.
- Search terms used focused on epidemiology and whole-genome sequencing of bTB in wild deer and cattle, excluding badgers, bison, elk and pet deer.
- This search resulted in 54 papers, with **39** deemed as relevant to the topic.
- An additional **11** relevant papers were found as references in the initially identified publications.

## Common Themes

**Table 1.** A summary of the key findings from the literature review.

<b>Occurrence and prevalence</b>	<ul style="list-style-type: none"><li>• Evidence of bTB in deer was found in <b>12 countries</b>, spanning <b>four continents</b>.</li><li>• <b>Prevalence estimates</b> of deer with bTB in South-West England range from 0.00-5.17 (95% CI), <b>dependant on species</b> [4].</li></ul>
<b>Potential risk factors identified</b>	<ul style="list-style-type: none"><li>• <b>Density:</b> Increased deer density is linked to an increase in bTB, resulting in a ban of supplementary feeding in Michigan US in order to reduce population numbers [5]. However this risk is likely to be localised to certain areas [4].</li><li>• <b>Species:</b> fallow deer (<i>Dama dama</i>) were estimated to pose a higher bTB risk to cattle in England and Wales compared to other species [4, 6].</li><li>• <b>Age:</b> Juveniles have been found to have a much lower prevalence of bTB compared to adults [4].</li><li>• <b>Super-Shedders:</b> evidence of red deer (<i>Cervus elaphus</i>) super-shedders has been seen in Europe [7].</li></ul>
<b>Genomic evidence</b>	<ul style="list-style-type: none"><li>• Spoligotyping and whole-genome sequencing has provided initial evidence of bTB transmission between cattle and deer. In the US cattle and deer were found to have the same single bTB mutations [8], and in Ireland deer had a similar bTB genome to cattle, however the genomic diversity was higher in deer suggesting that they are acting as a source of infection [9]. This literature search did not find any molecular evidence of transmission from publications in GB.</li></ul>

Countries with published evidence of bTB in deer



## Key Messages

- This literature review has highlighted that **deer can become maintenance hosts of bTB if certain conditions are met**. However, the transmission risk to livestock and other wildlife species is likely to be localised.
- More genomic evidence, particularly whole-genome sequencing, should be prioritised in GB to assess the risk wild deer may pose as a bTB infection source for cattle.



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