

TBE in United Kingdom

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E-CDC risk status: affected, unknown if endemic

(Last edited in June 2026; update for 2024 and 2025: no cases)

History and current situation

Until 2019, TBE was considered only to be an imported disease to the United Kingdom. In that year, evidence became available that the TBEV is likely circulating in the country^{1,2} and a first “probable case” of TBE originating in the UK was reported.³ In addition to TBEV, louping ill virus (LIV), a member of the TBEV-serocomplex, is also endemic in parts of the UK. Reports of clinical disease in livestock, caused by LIV are mainly from Scotland, parts of North and South-West England and Wales.⁴

National deer sentinel surveillance was conducted between 2018 and 2021, initially to establish whether TBEV might be present in Great Britain, but undetected. Following confirmation of presence this was continued, to then detect the geographic extent of TBEV and any spread. In the initial samples collected between February 2018 and January 2019,¹ four percent of sera from 1,309 deer culled across England and Scotland were ELISA-positive for TBEV serocomplex. Due to the close homology between LIV and TBEV, it was not possible to differentiate between the two viruses serologically, with 73.1% of ELISA positive samples also tested by LIV hemagglutination inhibition (HAI) test being positive by both methods. Many of the seropositive samples were in areas where LIV has been reported in livestock; however, a focus of the highest seropositivity rate (47.7% by ELISA) was identified in the Thetford Forest area (South-East England), which has no previously published reports of LIV in livestock. Additionally, also seropositivity of 14.3% was detected in Hampshire (Southern England), also a county with no previous LIV reports. Five from 2,041 *I. ricinus* ticks from culled deer in ELISA-positive regions tested positive by LIV/TBE PCR⁵, all five were from the Thetford Forest area. Of the ticks removed from deer in the Thetford Forest area, 2.6% were positive by RT-PCR. A full-length genome sequence was obtained from one positive tick (figure 2). TBEV-UK Thetford was identified to be a TBEV -Eu strain, sharing 99% sequence identity with the Norwegian Mandal strain isolated from ticks in 2009.⁶

Annual tick surveys have been conducted since 2018 in areas where seropositivity in deer have been detected, additionally surveys have been conducted in localities identified through follow up of probable or confirmed TBE cases. TBEV has been confirmed over multiple years in

questing ticks in parts of Thetford Forest, the New Forest/Hampshire Dorset border and the North York Moors. The minimum infection rate detected tends to be below 1%, to illustrate, follow-up questing tick surveys were conducted in Hampshire during July and August 2018 and June 2019. Of 915 *Ixodes ricinus* ticks collected and tested in 2018 and 2,155 in 2019, one RT-PCR positive pool was identified from five adult female ticks collected from a site on the Hampshire/Dorset border². Minimum infection rate (MIR) of ticks collected from this site was estimated to be 0.17%. Sequence analysis indicates that TBEV-UK Hampshire was most closely related to TBEV-NL (LC171402.1) detected in ticks in 2017.⁷ The diversity of the Thetford and Hampshire TBEV-EU strains (Figure 2) indicates that these were a result of at least two separate importation events into the UK.^{1,2}

The first “probable TBE case” originating in the UK was in a 3-month old German infant returning from a family summer vacation in South East England in July 2019.³ Based on the timing of travel and incubation period, it is not possible that the child was infected in Germany and probable exposure was thought to be in the New Forest National Park, England, following a tick bite there. A second probable case was reported in July 2020 with exposure thought to be in in the Test Valley District of Hampshire, England, less than 20km from the first probable case¹⁵. In September 2022, a third case tested positive for TBEV by PCR was reported in England, who was likely to have acquired infection in Scotland in June 2022. In October 2022 an additional case, also confirmed by TBEV PCR, was reported in England with probable exposure in the North York Moors.⁸ There were two probable TBE serocomplex cases reported in 2025, one with likely acquisition in Dartmoor and the second either from the Peak District or the Outer Hebrides.

To summarize, overall serological evidence in deer supported by PCR detection in ticks and follow up sequence analysis of TBEV-EU RNA indicates that TBEV circulates within the Thetford Forest and the Hampshire/Dorset border and the North York Moors areas. There have been two confirmed and four probable autochthonous serocomplex cases, since TBE was first identified within the UK in 2019.

Table 1: Virus, vector, transmission of TBE in United Kingdom

Viral subtypes, distribution	TBEV-EU
Reservoir animals	Ticks, to be confirmed, but likely rodents?
Infected tick species (%)	<i>I. ricinus</i>
Dairy product transmission	Not reported
Case definition used here	Compatible clinical signs plus serological or PCR confirmation
Completeness of case detection and reporting	Unknown
Type of reporting	Acute encephalitis is a notifiable disease. ⁹ TBEV is now a notifiable organism (from August 2019) ¹⁰
Other TBE surveillance	Ongoing surveillance for possible TBE cases. Ecological studies, in addition to both sentinel and human serosurveillance studies
Special clinical features	None
Licenced vaccines	TicoVac® and TicoVac Junior® ¹¹
Vaccine recommendations	The UK Joint Committee on Vaccination and Immunisation last reviewed the situation in October 2023. It was agreed that the Green Book wording could be adjusted to highlight accessibility to vaccination for those at risk in the UK context. ¹²
Vaccine uptake	Uptake of vaccine not known
Name, address/website of TBE National Reference Center	Rare and Imported Pathogens Laboratory (RIPL) UK Health Security Agency Manor Farm Road Porton Down Wiltshire SP4 0JG www.gov.uk/guidance/tick-borne-encephalitis-epidemiology-diagnosis-and-prevention

Figure 1: Seropositive sentinel deer serum samples tested by both TBEV ELISA and LIV HAI and geographical distribution with density of samples (figure and accompanying legend are adapted and reprinted from reference)¹

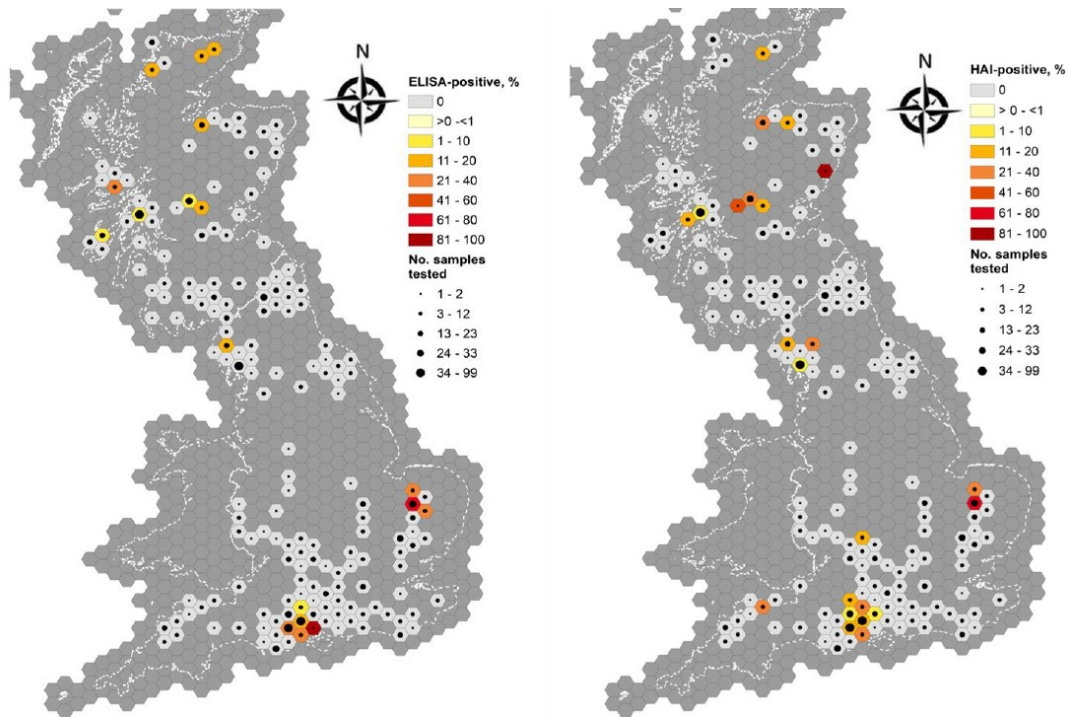
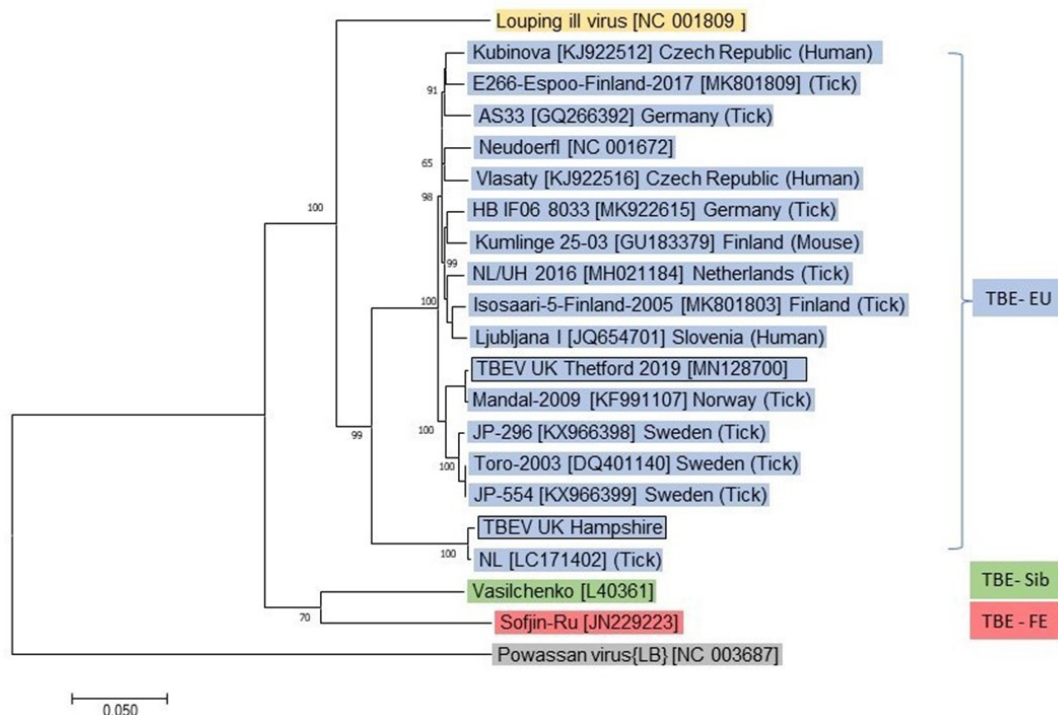


Figure 2: Phylogenetic tree highlighting the TBEV UK-Thetford and TBEV-UK Hampshire strains (figure and accompanying legend are adapted and reprinted from reference)²



The boxes highlight the TBEV strains from a tick removed from deer in Thetford 2018 and questing ticks collected in Hampshire in 2019. The tree was constructed with a maximum-likelihood analysis of full length genomes and is rooted with the tick-borne Powassan virus. European TBEV strains are highlighted in blue, Siberian TBEV in green, Far Eastern in pink, and louping ill virus in yellow. Strains are identified with the name, GenBank accession numbers, country location and host.

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