UK Health Security Agency

Department for Environment, Food & Rural Affairs

Animal & Plant Health Agency

One Health vector-borne disease surveillance report 2025

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Contents

Joint foreword from CMA and CVO

The risk to the UK from vector-borne diseases (VBDs) is increasing. This is due to global resurgences of several VBDs, changing vector distributions across Europe, increased international travel and trade, and the impacts of climate change and land use change. VBDs, defined here as infections transmitted to humans and/or animals through an arthropod vector, are inherently a **One Health challenge** due to the interlinked roles of environment, animals and people. Addressing this growing risk requires a collaborative One Health approach.

Integrated One Health surveillance combining information from the environment, vectors, wildlife, domestic animals, and human health is a powerful tool for identifying and monitoring emerging and established VBD threats. This can act as an early warning system to inform timely action to protect public and animal health.

This first **One Health VBD Annual Surveillance Report** brings together animal and human health data to provide the most comprehensive overview of vectors and associated diseases in England to date. For the first time, we present an integrated assessment of the risk to the UK of VBDs affecting humans through a **VBD risk monitoring matrix**, supporting a more systematic approach to risk identification and assessment.

The report is published against a backdrop of increasing international concern. Global case numbers of several VBDs have reached record levels, with unprecedented dengue activity reported in 2023 and 2024, and chikungunya in 2025. Similar trends have been observed across Europe, where locally-acquired transmission is becoming more frequent, driven by the expansion of the invasive *Aedes albopictus* mosquito (1 to 3). At present in the UK we have no local transmission of these viruses, but cases are regularly reported in returning travellers, and incursions of invasive mosquitoes continue to be detected at UK points of entry (4). Robust surveillance is therefore essential to maintaining UK biosecurity.

West Nile virus (WNV) continues to expand northwards in Europe, and during 2025 France and Italy reported their largest outbreaks to date (5). This has implications for the UK, where native mosquito species are capable of transmission of WNV. The first evidence of WNV in mosquitoes in the UK was reported in 2025 through the Vector-Borne RADAR (VB-RADAR) project, following detections of Usutu virus (USUV) in mosquitoes and birds at multiple sites in southern England (6). This demonstrates the value of integrated One Health surveillance in identifying emerging threats early.

A number of tick-borne diseases are endemic in the UK. Lyme disease remains the most common VBD affecting humans. Additionally, a small number of cases of locally acquired Tick-Borne Encephalitis (TBE) complex have been reported since 2019 (7). Elsewhere in Europe, Crimean-Congo Haemorrhagic fever virus continues to emerge in new areas, including in Spain, Greece and France, reinforcing the need for continued vigilance (8 to 11).

Everyone can contribute to reducing the risk of VBDs in the UK. Citizens supply vital information for the Tick surveillance scheme and Mosquito recording scheme. Simple preventive actions can reduce insect bites and mitigate risk, such as wearing long sleeves and trousers, insect repellent, and being 'tick aware', and eliminating breeding sites by removing litter and standing water (12,13). People moving animals from endemic regions should be vigilant for ticks and follow recommended preventive measures, with specific requirements detailed at Taking your pet abroad and Export horses and ponies.

UKHSA, APHA and partners will continue to strengthen collaboration and integrated surveillance to support timely identification, assessment and mitigation of VBD risks protecting public and animal health in the UK.

Executive summary

Globally the burden of VBDs is increasing due to changes in climate change, land use, globalisation of trade and travel, urbanisation and changes in vector distribution. Over the last 3 years, the World Health Organization (WHO) has declared dengue as a global emergency in 2023, and in 2025 multiple outbreaks were reported across multiple WHO regions. In 2024, over three hundred million cases of malaria were reported globally, with WHO African region continuing to disproportionately contribute to the global malaria burden. In Europe, in recent years there has been an increase in locally acquired human cases of VBDs with record numbers of outbreaks of WNV and chikungunya reported in France and Italy in 2025.

This new One Health VBD surveillance report integrates data from vector, animal and human surveillance for 2025 in England. The VBD risk monitoring matrix is published for the first time, a tool which synthesises surveillance data into a composite risk level annually to systematically track the dynamic risk of VBDs to human health in England. VBDs are grouped into 4 categories, with findings in this report presented by group:

(1) Mosquito-borne pathogens with no significant animal reservoir
(2) Mosquito-borne pathogens with animal reservoir
(3) Tick-borne pathogens
(4) Pathogens transmitted by other vectors

Key findings

Overall, 40 VBDs were included in the VBD risk monitoring matrix and are under regular monitoring. The key vector species of concern are ticks and mosquitoes. To date, local transmission of VBDs to humans in England is limited to tick-borne infections, with mosquito-borne infections largely associated with travel to endemic countries. However, the risk of local transmission of mosquito-borne infections is increasing with the emergence of Usutu virus (USUV), the first detection of West Nile virus (WNV) in UK mosquitoes, and incursions of invasive mosquitoes.

Group 1. Mosquito-borne pathogens with no significant animal reservoir

Cases of mosquito-borne infections are regularly diagnosed in returning travellers from endemic countries including 1,629 cases of malaria, and 502 cases of dengue, chikungunya and Zika virus disease reported in 2025. There has been no reported local transmission of mosquito-borne infections since the 1920s to date, however the risks are increasing with regular outbreaks of dengue, chikungunya and WNV occurring in mainland Europe in the last decade. Incursions of invasive mosquitoes (*Aedes albopictus* and *Aedes aegypti*) are

generally detected in southeast England each year, but there is no evidence of establishment to date.

Group 2. Mosquito-borne pathogens with animal reservoir

USUV is now endemic in native UK mosquitoes and birds in southeast England, and the known range is expanding with the first detection in Scotland in 2025 in dead blackbirds. WNV was detected for the first time in UK mosquitoes (*Aedes vexans*) from a sample collected in 2023. The range of a key native mosquito, Culex modestus, involved in transmission of Usutu and WNV in Europe is expanding in England, with new reports of urban nuisance biting. These findings are notable due to the northerly expansion and large outbreaks of WNV and case reports of USUV in Europe, and the diagnosis of imported cases of WNV and USUV in returning travellers although there have been no locally acquired human cases reported in England to date.

Group 3. Tick-borne pathogens

Lyme disease, transmitted by the bite of an infected tick, remains the most common locally acquired VBD reported in humans in England with 1,168 acute cases reported in 2025. In addition, 2 locally-acquired cases of tick-borne encephalitis complex were reported in 2025. Other tick-borne infection risks include anaplasmosis and babesiosis although these remain rare.

Group 4. Pathogens transmitted by other vectors

There were 3 imported cases of Oropouche virus diagnosed in 2025, but there is no evidence of the main vector (*Culicoides paraensis*) in the UK.

As highlighted in our findings the risks of VBDs are changing. In response, members of the public can take measures to avoid insect bites to reduce their risk of VBDs, both in the UK and when travelling overseas. Clinicians should be aware of the changing epidemiology of VBDs in the UK and globally and take appropriate travel and exposure histories from their patients. Patients with symptoms of encephalitis and/or meningitis that have no other explanation, especially over the summer months, should be reviewed by an Infectious Diseases specialist. If no other cause is suspected, submission of samples should be discussed with the Imported Fever Service (IFS) for potential testing at the Rare and Imported Pathogens Laboratory (RIPL), irrespective of travel history. Local authorities should be aware of the risks in their areas, support vector surveillance efforts, ensure nuisance biting is reported, and have appropriate local plans in place for vector control.

Overall, this report highlights the importance of integrated animal, human and arthropod vector surveillance for VBDs, and the coordinated interpretation of the findings to accurately assess the public health risk and inform a proportionate response. Robust diagnostic and surveillance systems are required to detect emerging and changing threats to protect UK public health.

Background

Climate change, land-use change, urbanisation, and the globalisation of trade and travel have altered the distribution of arthropod vectors such as mosquitoes and ticks. Alongside shifts in interactions between humans and animals, these factors have facilitated the geographic expansion of VBDs from tropical regions into urban settings worldwide in recent decades.

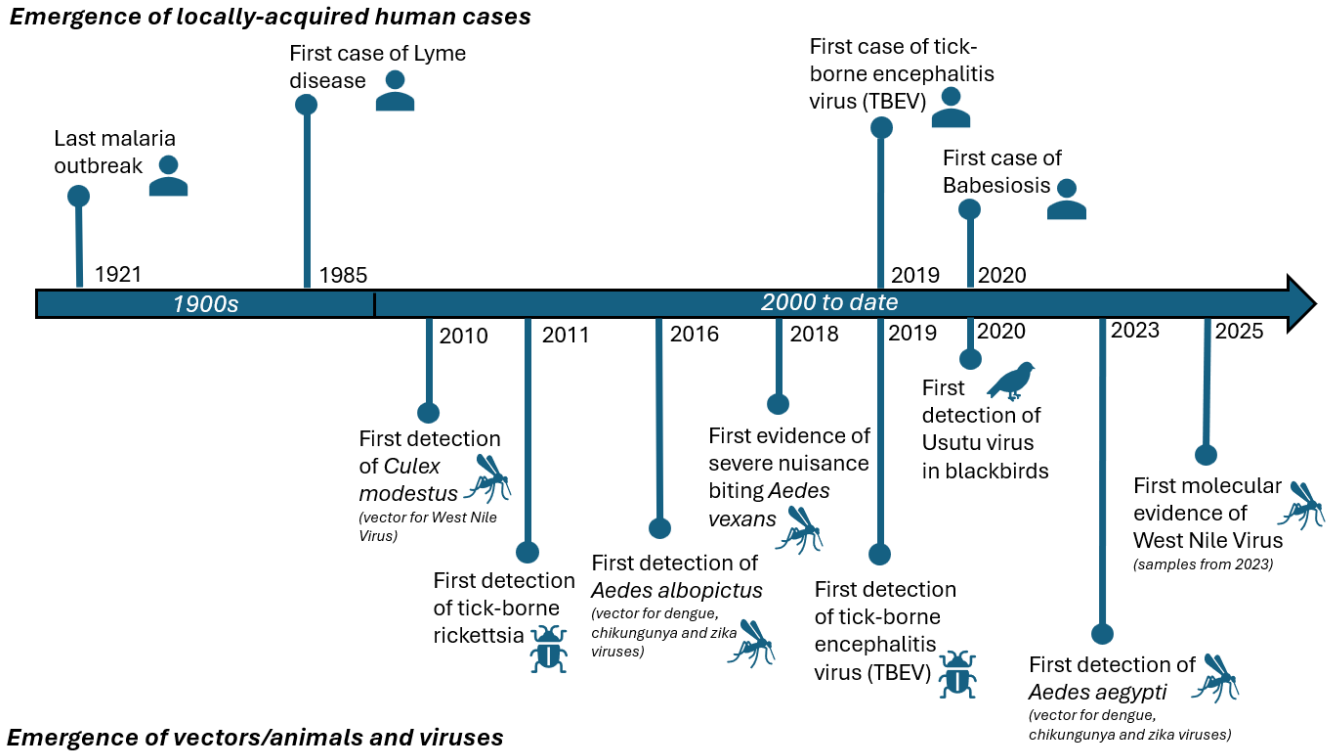
The major global VBDs (including malaria, dengue, chikungunya, WNV and Lyme disease) account for 17% of the global burden of all infectious diseases and are responsible for more than 700,000 fatal cases each year (14,15). In 2025, the World Health Organization (WHO) reported widespread outbreaks of chikungunya across multiple WHO regions including Asia, the Americas and Europe. Cases occurred in areas with previously low or no transmission, leading WHO to raise the global public health risk assessment to moderate at the end of the year (16,17). WHO also reported just over 5 million cases of dengue in 2025 globally, and although this was a decline from 14 million cases observed in 2024, sporadic locally-acquired cases were noted in Europe, including France, Croatia, Italy and Spain (3,18,19).

In recent decades, there has been a shift in the distribution and epidemiology of these major VBDs in Europe with several European countries having seen the establishment and expansion of the main vectors of concern for these diseases including mosquito species *Aedes albopictus* and *Aedes aegypti* (known to transmit dengue, chikungunya and Zika viruses) (1,2). Detections of locally-acquired human cases of VBDs have increased steadily in Europe by approximately 25% year on year, with an increasing number of outbreaks, for example of dengue, chikungunya and WNV in France and Italy (20,21). In 2025, the European Centre for Communicable Diseases (ECDC) acknowledged that “Europe is entering a phase of longer, more widespread and more intense transmission of mosquito-borne diseases which is becoming the new normal”. This poses an increasing risk of VBDs in England (22).

In England, USUV was first detected in birds and mosquitoes in 2020. Following the first detections in the south east of England, the distribution has expanded (USUV, HAIRS). In 2025, the first detections of USUV in Scotland were reported, in birds from the Isle of Arran (First detection of Usutu virus in Scotland). This highlights the continued expansion of the virus and changing risk of VBDs.

To date, travel-associated cases of VBDs are reported each year but there have been no consistent detections of locally-acquired human cases apart from cases of Lyme disease, which is the most common endemic VBD in England, and a small number of cases of tick-borne encephalitis (TBE) complex (see Figure 1 below).

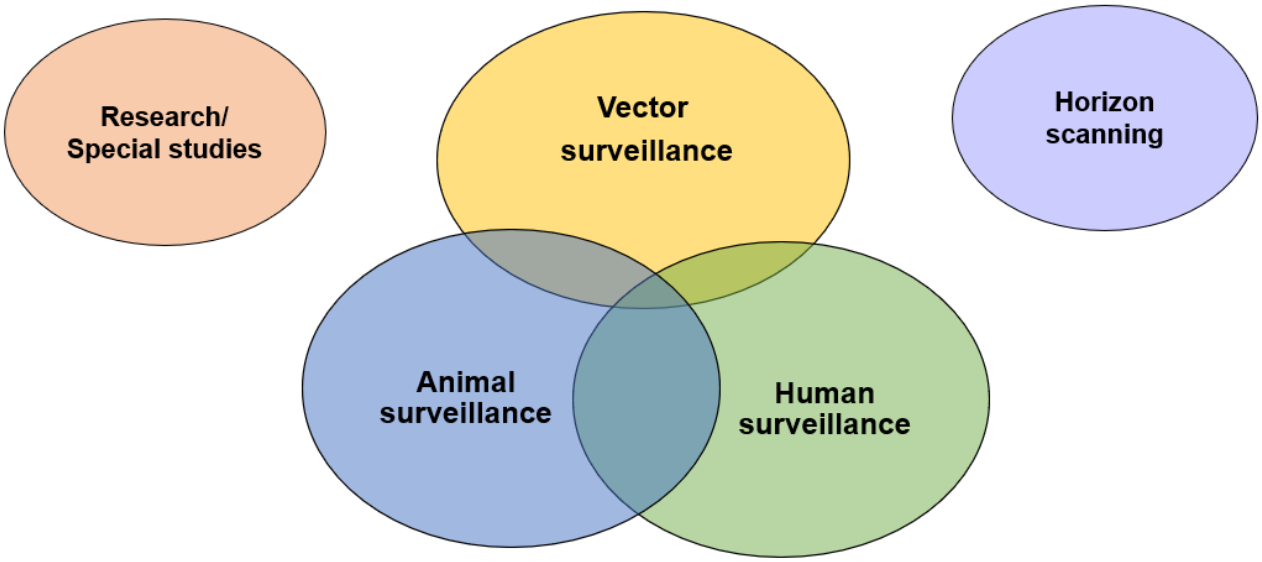
Figure 1.Timeline of the emergence of VBDs in vectors, animals and locally acquired human cases in England



VBDs have life cycles that include arthropods (insects, arachnids), animals and humans, therefore an integrated One Health surveillance approach spanning human, animal and arthropod vectors is vital to monitor and respond to the risks of VBDs as shown in European countries with endemic VBD transmission (23 to 25).

One Health is defined as a unifying approach to sustainably balance and optimise the health of people, animals (domestic and wild) and ecosystems (plants and the environment) by recognising that all 3 of these are closely linked and interdependent (26). Recognising the importance of a One Health approach, this report outlines the multisectoral collaborations (between research and special studies, vector surveillance, animal surveillance, human surveillance and horizon-scanning) involved in monitoring and assessing the current risk of VBDs to human health in England (see Figure 2 below).

Figure 2. Components of One Health VBD surveillance



This report focuses on reporting surveillance data from pathogens from each category of the VBD risk monitoring matrix where data is available and there were detections reported through human, vector or animal surveillance between January and December 2025. It also provides an overview of existing surveillance systems for vectors, humans, and animals, which is summarised in Appendix B to D.

Human case numbers are reported for England only, whereas animal case numbers are reported for England, Scotland and Wales as the Animal and Plant Health Agency (APHA) remit is for Great Britain.

Recognising that VBDs are an active area of research, the report also highlights research studies led or co-led by UKHSA, the Department for Environment, Food and Rural Affairs (Defra), and the APHA in collaboration with academic partners that inform ongoing situational assessments. These include modelling approaches used to generate predictive maps of vector species distributions and to assess the suitability of current and projected UK temperatures for VBD transmission.

One Health VBD coordination

An integrated One Health approach is key to preparing, monitoring and responding to the risks of vector-borne diseases (VBDs) in England, and there are several multi-agency groups and networks which help to coordinate this in the UK.

The longest standing of these is the Human Animal Infections and Risk Surveillance (HAIRS) group, a multi-agency cross-government horizon scanning and risk assessment group, established in 2004. HAIRS identifies and risk assesses emerging zoonotic infections which may pose a threat to UK public health. HAIRS activities are to monitor hazards, produce risk statements or formal risk assessments, depending on the level of risk (see HAIRS risk assessment process). During 2025, HAIRS published updated risk assessments for USUV and WNV. A number of other HAIRS risk assessments for VBDs were updated during 2025, and will be published during 2026, including chikungunya virus, dengue virus, Zika virus and tick-borne bacterial infections. A working group has been established on Oropouche virus.

A new UKHSA-led VBD horizon scanning group was convened in 2023 as part of a systematic approach to detect early signs of changes in risk to the UK from infectious diseases. Technical specialists from UKHSA, APHA, Malaria and Parasitology Reference Laboratories, and Food, Water and Environmental laboratories identify and review signals that may indicate changing risk to the UK from VBDs, and these are discussed at monthly meetings. During 2025, 49 signals were discussed.

During 2025, a joint WNV One Health surveillance group was convened, comprised of APHA, NHSBT and UKHSA, that met monthly during the transmission season, and monitored all relevant surveillance and research data. The group considered data for humans (case-based, blood donor, and syndromic surveillance), animals (dead and live bird, and equine surveillance) and vector (mosquito surveillance and research, modelling).

Building on the success of this approach, the group will reconvene for the 2026 transmission season and broaden the focus to include additional VBDs under monitoring.

The group worked together with multi-agency partners to update the West Nile virus surveillance and response plan, and to keep UK Blood Services informed.

UKHSA, Defra and APHA also collaborated on the Invasive Mosquito National Contingency plan update. In 2026, a working group is being established to coordinate One Health work on ticks.

Vector-borne disease risk monitoring matrix

The UKHSA-led VBD horizon scanning group, assess and monitor the risk level to human health using a risk monitoring matrix. This synthesises data from vector, animal and human disease surveillance into a composite risk level which is used to inform prevention, preparedness and response activities. This matrix is kept under continual review and will be published as part of this report annually.

To compile the matrix, a list of initial VBDs for consideration were identified through a literature search, and surveillance and epidemiological intelligence reports. The inclusion and exclusion criteria for the pathogen to be included in the VBD risk monitoring matrix were:

- inclusion – reporting of a human case in the UK or Europe, and/or the pathogen had led to an outbreak or event of public health significance anywhere in the world within the last 10 years
- exclusion – if the pathogen was already monitored by one of the other UKHSA-based horizon-scanning groups based on mode of transmission (for example, *Yersinia pestis* is monitored by the contact horizon-scanning group)

VBDs were grouped into 4 categories:

- Group 1 – mosquito-borne pathogens with no significant animal reservoir
- Group 2 – mosquito-borne pathogens with animal reservoir
- Group 3 – tick-borne pathogens
- Group 4 – pathogens transmitted by other vectors

This risk-monitoring matrix is used to systematically inform horizon-scanning, surveillance and potential mitigations, and enhance capabilities for VBD diagnostics.

Each VBD was assigned a domestic transmission level based on UK vector and reference laboratory surveillance data, as summarised in Table 1 below (see Appendix A for sources of evidence). The transmission risk levels are kept under continual review by the VBD horizon scanning group (see One Health VBD coordination). The 2025 surveillance findings for pathogens in each group are described in the subsequent chapters of this report.

Based on data up to 31 December 2025, a total of 40 VBDs of human health significance were identified for inclusion in the VBD risk monitoring matrix (16 mosquito-borne, 10 tick-borne, 13 transmitted by other vector species, and one with multiple modes of transmission).

By transmission level, only Lyme disease causes widespread locally acquired cases across England (level 4). There is limited local transmission of other tick-borne pathogens with

human cases remaining rare and sporadic, including TBEV, louping ill virus, *Anaplasma phagocytophilum, Babesia divergens*, and *Francisella tularensis* (level 3).

There is no local transmission of mosquito-borne viruses to humans currently, however USUV has been identified in mosquitoes and birds, and there has been a detection of WNV in mosquitoes in one locality (level 2). At level 1, competent vector species have been detected transiently in the UK (1a) or are established (1b), but there is no evidence of local disease transmission to date. A number of pathogens have never had the main vector species detected in the UK (level 0) but remain under monitoring.

Table 1. UKHSA vector-borne disease risk monitoring matrix 2025

Transmission level	Group 1 Mosquito-borne pathogens with no significant animal reservoir	Group 2 Mosquito-borne pathogens with animal reservoir	Group 3 Tick-borne pathogens	Group 4 Pathogens transmitted by other vectors
Level 0 – Vector not detected				
Level 0		Equine encephalitis viruses Ross river virus		*Oropouche virus* *Leishmania spp* (leishmaniasis) *Trypanosoma spp* Filaria: *Onchocerca volvulus*, *Wuchereria bancrofti, Brugia spp* *Loa loa, Mansonella spp* Sand fly fever viruses *Orientia tsutsugamushi* (*Rickettsiaceae* family)
Level 1 – Vector present				
Level 1a – Detected defined as competent vector detected transiently in single setting or linked to importation (for example freight) or otherwise without evidence of being established				
Level 1a	Dengue virus Chikungunya virus Zika virus Yellow fever virus	Japanese encephalitis virus Inkoo virus	Other spotted fever group rickettsioses (*R. rickettsia, R. conorii conorii, R. conorii indica, R. africae*)****	

	Mayaro virus		Crimean-Congo Haemorrhagic Fever virus	
Level 1b – Established defined as continued detection of competent vector in single or multiple sites over time				
Level 1b	*Plasmodium* spp (malaria)	Rift Valley virus Ťahyňa virus *Dirofilaria* spp Sindbis virus	*Neoehrlichia mikurensis*	*Rickettsia typhi* (Murine typhus) *Borrelia recurrentis* (Louse-borne relapsing fever) *Rickettsia prowazekii* (Epidemic typhus) *Thelazia callipaeda* *Babesia venatorum*
Level 2 – Pathogen detected in vector or animals				
2a Pathogen detected in vectors only	N/A	West Nile virus Usutu virus	*Rickettsia raoultii* *Rickettsia massiliae* *Rickettsia helvetica* *Borrelia miyamotoi* (Tick-borne relapsing fever) *Spiroplasma ixodetis*	*Rickettsia felis* (Flea-borne spotted fever)
2b Pathogen detected in animals*	N/A	Usutu virus		
Level 3 – One or more autochthonous human case(s) in single geographical area or **single sporadic cases in unrelated geographical areas****				
Level 3	*Francisella tularensis* (tularaemia)***	*Francisella tularensis* (tularaemia)	*Francisella tularensis* (tularaemia)	*Francisella tularensis* (tularaemia)

			Babesia divergens *Anaplasma phagocyto philum* Louping ill virus Tick-borne encephalitis virus	
Level 4 – Geographically spread autochthonous transmission to humans				
Level 4			*Borrelia burgdorferi* (Lyme disease)	

*Excluding travel-associated infections with no local transmission
** Excluding infections with clear non-UK vector related route (for example transfusion acquired, travel acquired)
*** *Francisella tularensis* (tularaemia) can be transmitted in a number of ways including via ticks, mosquito, animal contact, ingestion, and airborne routes
**** Not *R. massiliae, R. raoultii, R. helvetica* or *R. felis*

Summary of human cases of VBDs in England, 2025

In 2025, human cases of locally-acquired VBDs in England were limited to those transmitted by ticks (VBD risk monitoring matrix: Group 3), with Lyme disease remaining the most common in England (Table 2). There were also 2 cases of probable tick-borne encephalitis (TBE) complex reported in patients without a history of international travel.

There were no locally acquired human cases of mosquito borne-borne infections reported in 2025. However, there were travel-associated cases of malaria (1,629 cases), dengue (336 cases), chikungunya (159 cases), rickettsioses (37 cases), Zika virus disease (7 cases) and WNV (2 cases) reported in England (Table 2).Three cases of imported Oropouche virus and one case of USUV infection were reported, representing the first cases diagnosed in England. An overview of human surveillance methods is provided in Appendix D.

There were no reports of human cases of the following VBD risk monitoring matrix pathogens in England:

- Group 1 (mosquito-borne pathogens with no significant animal reservoir) – Mayaro virus, yellow fever virus
- Group 2 (mosquito-borne pathogens with animal reservoir) – Japanese encephalitis virus, equine encephalitis viruses, Ross River virus, Inkoo virus, Rift Valley fever virus, Ťahyňa virus, Dirofilaria spp
- Group 3 (tick-borne pathogens) – Crimean-Congo haemorrhagic fever virus, *Neoehrlichia mikurensis*, *Spiroplasma ixodetis*, *Anaplasma phagocytophilum*
- Group 4 (pathogens transmitted by other vectors) – *Borrelia recurrentis* (louse-borne relapsing fever), sand fly fever viruses

Table 2. Number of cases of locally acquired and travel-associated vector-borne diseases reported in England, in 2025

Vector-borne disease/organisms		Number of cases in England, 2025*	
VBD risk monitoring matrix group		**Travel-associated**	**Locally-acquired**
1: Mosquito-borne pathogens with no significant animal reservoir in UK	Chikungunya	159	0
	Dengue	336	0
	Malaria (*Plasmodium* species) †	1,629	0
	Zika virus disease	7	0
2: Mosquito-borne pathogens with animal reservoir	Usutu virus (USUV)	1	0
	West Nile virus (WNV)	2	0
3: Tick-borne pathogens	Lyme disease (*Borrelia burgdorferi*) ‡	-	1,168
	Rickettsial infections§	37	0
	Tick-borne encephalitis (TBE) complex	2	2
4: Pathogens transmitted by other vectors	Oropouche virus disease	3	0

Note: case numbers are reported, except for malaria (Plasmodium species), for England only; the travel-associated infection reports include data for England, Wales and Northern Ireland

* Data reported by Rare and Imported Pathogens Laboratory (RIPL) for all pathogens except malaria which is reported by the Malaria Reference Laboratory (MRL). Data for chikungunya, dengue, Oropouche virus disease, rickettsial infections, tick-borne encephalitis complex and Zika virus disease includes confirmed and probable cases.

† Data for malaria is provisional numbers of imported malaria cases for 2025 in the UK (Imported malaria in the UK: statistics). Additionally, data for cryptic cases of malaria is summarised in the Malaria in the UK annual reports.

‡ Data is reported for acute Lyme disease cases in 2025, including acute neurological cases. Travel history is not always available for laboratory diagnosed cases, 52 cases had a travel history reported but the country of recent travel does not necessarily reflect where the infection occurred; this will mean that although all 1,168 Lyme cases are currently reported as locally acquired this may still include some travel-associated cases.

§ Rickettsial infections have been reported under Section 3, tick-borne pathogens, but transmission can also occur by different arthropod vectors including mites, lice and fleas

Summary of VBD incident responses in England, 2025

In 2025, UKHSA responded to several VBD-related incidents. Case studies of 3 incidents are included as follows.

Case study 1. Detection of invasive mosquitoes

Single adult *Aedes albopictus* and *Aedes aegypti* were detected at Heathrow baggage terminal on 2 separate occasions. The local Health Protection Team convened an Incident Management Team in line with the National contingency plan for invasive mosquitoes. The Medical Entomology and Zoonoses Ecology (MEZE) team implemented enhanced surveillance working in conjunction with the local authority and airport management to assess the extent of the incursion, mitigate the risk of establishment, and advise on appropriate control measures. All identified larval habitats were removed or appropriately treated. Enhanced surveillance was conducted for 2 weeks, during which no further invasive mosquito eggs or adults were detected.

Case study 2. First molecular evidence of WNV in UK mosquitoes

The MEZE group has supported a local authority in Nottinghamshire to respond to nuisance biting caused by *Aedes vexans* mosquitoes along the Trent Catchment on the River Idle near Gamston (Retford) in Nottinghamshire from 2018. During 2024 and 2025, the local authority organised larvicidal control and landscape remodelling to reduce mosquito breeding funded by a Natural England Nature Recovery grant. During 2025, mosquitoes collected from this site in 2023 were tested for West Nile virus as part of the VB-RADAR project. From this, APHA identified WNV genetic material in 2 pools of *Aedes vexans* mosquitoes, the first reported detection of WNV in UK mosquitoes. An incident management team was established. Enhanced mosquito surveillance and virus testing was implemented and public communications undertaken. The numbers of nuisance biting mosquitoes were extremely low compared to previous years. All mosquitoes collected both at this site and at all other sites sampled in England were negative for WNV RNA, showing that there was no evidence of WNV circulating during 2025.

Case study 3. TBE complex cases

In August 2025, 2 unrelated cases of probable TBE complex infections with no international travel history were notified to UKHSA. Diagnostic tests were unable to distinguish between TBEV and a closely related orthoflaviviruses, louping ill virus (LIV), a tick-borne infection

which commonly affects sheep but on rare occasions can result in human infections. These were therefore described as probable TBE complex cases. The first case was diagnosed in an individual who reported being bitten by a tick while visiting Dartmoor. The second case did not recall a tick bite but had visited the Outer Hebrides and Peak district during their incubation period. An incident management team was established to investigate both cases. Further tick surveillance was undertaken in Dartmoor and the Peak district. Virus testing was completed, however no evidence of TBEV was detected in tick samples collected. Tick prevention messaging was promoted in the areas where the potential exposures occurred.

Mosquito-borne pathogens with no significant animal reservoir (Group 1)

Overview

This section reports on 2025 cases of the Group 1 pathogens dengue, chikungunya, and Zika viruses (all transmitted by *Aedes* mosquito species, which are potentially invasive), and malaria. Table 3 provides a short summary of activity in 2025 for these pathogens by surveillance type.

Table 3. Group 1 Surveillance summary, England, 2025

Group 1 Surveillance summary, England 2025	
Vector (mosquitoes)	• In 2025, there were 2 detections of invasive *Aedes* mosquito species identified through mosquito traps at London Heathrow airport, with no evidence of established populations • In 2025, 3 native *Anopheles* species detected • Between 2010 and 2015, there were no detections of invasive *Aedes* mosquito species however, from 2016 onwards, there has been one or 2 detections in most years
Animal	• Not applicable

Human	• To date, there have been no locally acquired cases of dengue, chikungunya and Zika virus disease in England and due to the absence of the main vector (*Aedes* mosquito species) the risk to human health is very low for all 3 pathogens. In 2025, a total of 502 travel-associated cases were reported
	• From 2021:
	  • travel-associated cases of dengue in England have increased yearly with a record number of cases noted in 2024 (876 cases) which was in line with global trends. In 2025, there was a decrease in cases of dengue in England with a total of 336 cases
	  • travel-associated cases of chikungunya have increased year on year with a total of 159 cases reported in 2025
	  • a small number of travel-associated cases of Zika virus have been reported with the highest number (15) noted in 2024 and 7 cases reported in 2025

Group 1 Surveillance summary, England 2025	
	• In 2025, there were 1,629 travel-associated cases of malaria (*Plasmodium* species) in the UK, this is a decrease in comparison to cases reported across the UK in 2024 • Cryptic malaria cases, reported in the Malaria annual reports, are uncommon in the UK and make up less than 1% of all cases

Dengue, chikungunya and Zika virus disease

Dengue, chikungunya and Zika are mosquito-borne viral diseases transmitted to humans by the bite of an infected female *Aedes albopictus* or *Aedes aegypti* mosquito. Additionally, Zika virus transmission is possible through sexual contact and in utero.

Dengue, chikungunya and Zika virus disease may present with similar symptoms including fever, rash, headache, and muscle or joint pains, however symptoms can range from mild to severe. More information about these viruses can be found in the Travel-associated infections in England, Wales and Northern Ireland: 2025 report.

Vector surveillance

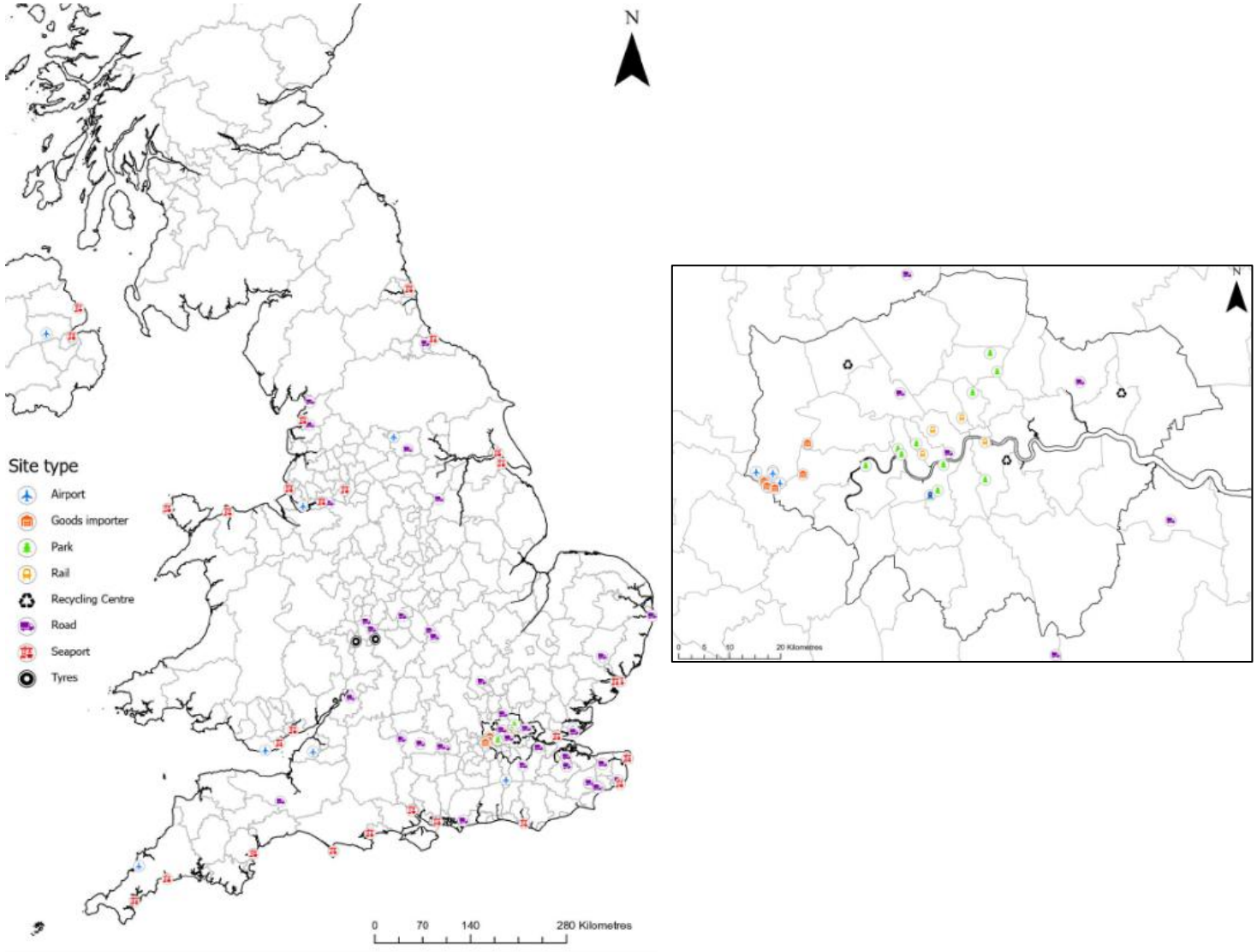
The UKHSA invasive mosquito surveillance scheme monitors for species *Aedes albopictus* and *Aedes aegypti* which, in addition to the virus listed above, can also transmit Yellow fever virus (see Appendix C Overview of vector surveillance section for details).

During 2025, 110 localities ran 1,070 invasive mosquito traps, with the locations shown in Figure 2. Isolated incursions of single adult mosquitoes of *Aedes albopictus* and *Aedes aegypti* were detected at London Heathrow Airport on 2 separate occasions (see Summary of VBD incidents section). No invasive mosquitoes were detected at any other sites surveyed across the country. All detections of invasive mosquitoes in the UK to date are summarised in Table 4 below.

Table 4. Detections of invasive mosquitoes in UK, 2010 to 2025

Detection	Year	Species	Life stage	Location type
-	2010 to 2015	No detections		
1	2016	*Aedes albopictus*	Eggs	Lorry stop
2	2017	*Aedes albopictus*	Eggs	Lorry stop
3	2018	*Aedes albopictus*	Eggs	Lorry stop
4	2018	*Aedes albopictus*	Eggs	Fresh fruit and vegetable importer
5	2019	*Aedes albopictus*	Eggs	Lorry stop
6	2019	*Aedes albopictus*	Eggs	International Importer Warehouse
-	2020 to 2022	No detections		
7	2023	*Aedes aegypti*	Eggs	International Importer Warehouse
8	2024	*Aedes albopictus*	Eggs	M20 Service station
9	**2025**	***Aedes albopictus***	**Adult**	**Airport**
10	**2025**	***Aedes aegypti***	**Adult**	**Airport**

Figure 3. Map showing location of targeted UKHSA invasive mosquito adult and ovitraps June to October 2025, with London inset



Human surveillance

In 2025, global case numbers of dengue fell substantially following the record surge in 2024. However, WHO reported several significant chikungunya outbreaks globally, including large outbreaks in countries across the Indian Ocean region, increased transmission in Asia and the Americas, as well as locally acquired cases in France and Italy.

In England, there were no locally acquired cases of dengue, chikungunya or Zika virus disease in 2025; however, there were a total of 502 travel-associated cases (see Figure 4 below).

Dengue remained the most frequently reported pathogen, but cases declined sharply from a peak of 876 in 2024 to 336 cases in 2025 (see Figure 4 below). Comparing travel-associated dengue cases in England to global case numbers highlights that travel-associated cases follow a similar trend over time (see Figure 5 below).

In 2025, the number of travel-associated chikungunya cases continued to rise, increasing from 105 in 2024 to 159 in 2025, the highest annual total since 2014 (see Figure 4 below). Seven cases of Zika virus disease were reported, compared to 15 in 2024 (see Figure 4 below).

Given the small numbers, caution is required in interpretation of trends. Some potential factors that may influence numbers reported include traveller numbers to affected regions, changes in awareness in clinicians and travellers, and testing referral patterns.

Detailed case demographics, travel history and data for England, Wales and Northern Ireland can be found in the Travel-associated infections in England, Wales and Northern Ireland: 2025 report.

Figure 4. Number of travel-associated chikungunya, dengue and Zika virus disease cases by year, England, 2021 to 2025

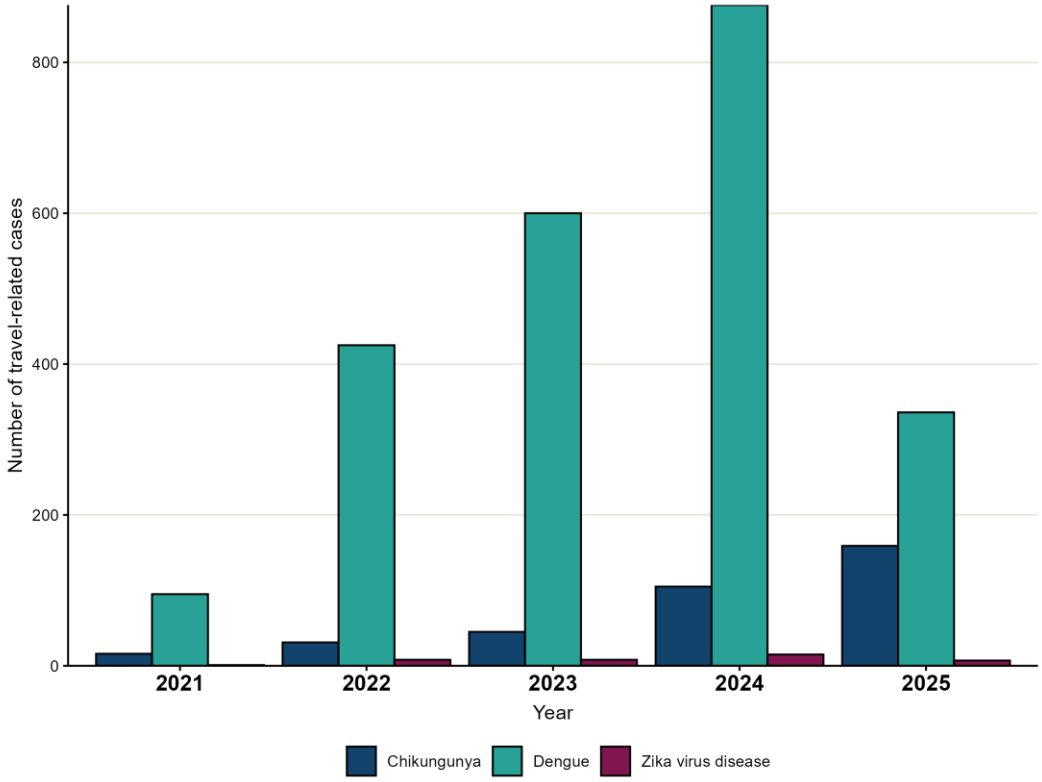
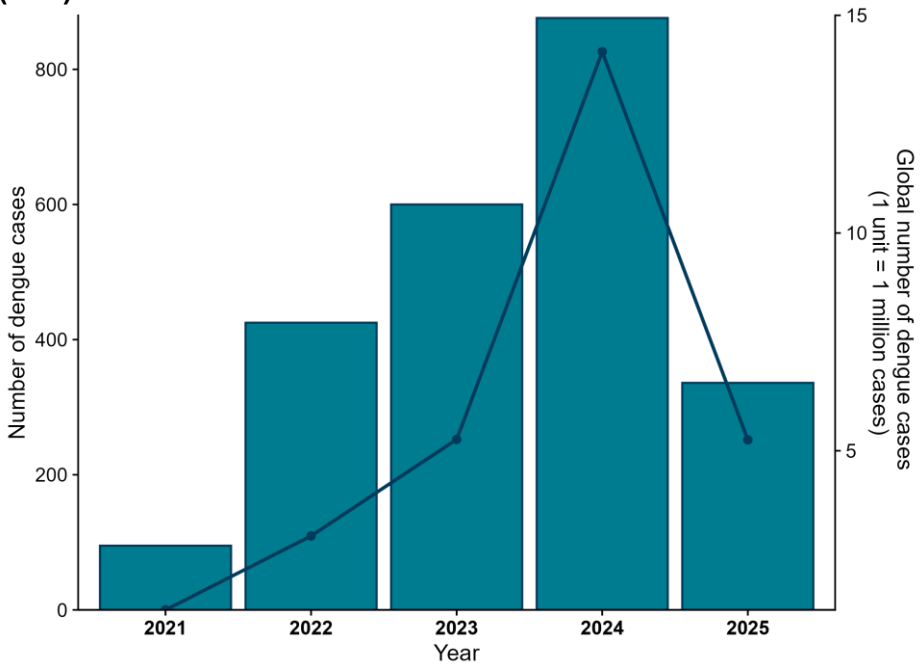


Figure 5. Number of travel-associated dengue cases by year (bar), England, 2021 to 2025, compared to global case numbers reported to the World Health Organization (line)



Data source: Global Dengue Surveillance Dashboard

Malaria (*Plasmodium* species)

Malaria is a serious and potentially life-threatening febrile illness caused by infection with protozoan parasites of the genus *Plasmodium*. It is transmitted to humans by the bite of the female *Anopheles* mosquito in tropical and subtropical regions.

Vector surveillance

In 2025, traps run as part of the Nationwide Wetland Mosquito Survey, recorded 3 native *Anopheles* species (*Anopheles. claviger, Anopheles. plumbeus* and *Anopheles. maculipennis s.l.*) between June and October 2025. These species are all relatively common, across a range of habitats and there is no evidence of nuisance biting caused by these species in normal circumstances.

Human surveillance

WHO produce annual global estimates of malaria cases and deaths. The most recent data available is for 2024, when there were an estimated 282 million malaria cases and more than 600,000 malaria related deaths, a slight increase compared to 2023 (27).

In 2025, there were 1,629 cases of imported malaria reported in the UK in the provisional annual statistics, this was lower compared to the provisional number of imported malaria cases reported in 2024 (1,812 imported malaria cases). Cryptic malaria cases are cases where there is no history of recent travel to a malaria-endemic area and for which epidemiologic investigations cannot identify a plausible mode of acquisition. Cryptic malaria cases are reported in the Malaria in the UK annual reports and are uncommon in the UK, making up less than 1% of all cases.

A review of malarial PCR positive blood donors in England from January 2020 to August 2025 identified 17 positive donors (28).

Mosquito-borne pathogens with significant animal reservoir (Group 2)

Overview

This section reports on Group 2 pathogens, Usutu (USUV) and West Nile (WNV) viruses which are transmitted by *Culex spp.* mosquitoes and maintained in a mosquito-bird transmission cycle, detected in 2025. Table 5 provides a short summary of activity in 2025 for these pathogens by surveillance type.

Table 5. Group 2 Surveillance summary, England 2025

Group 2 Surveillance summary, England 2025	
Vector (mosquitoes)	• The bridge vector for Group 2 pathogens, *Culex modestus* was first detected in 1944 and again in 2010 in the North Kent marshes. Between 2010 and 2025, *Culex modestus* further expanded in sites in coastal and estuarine Essex, Suffolk, Hampshire and West Sussex. • In 2025, *Culex modestus* was detected in four new locations, Kent, Cambridgeshire, Northamptonshire and Lincolnshire. • In 2025, the first molecular detection of WNV in a UK mosquito was reported in a sample collected in 2023, with no further detections in subsequent samples collected during 2025 • In 2020, USUV was detected for the first time in mosquitoes in England and has since increased in its geographic range across England
Animal	Birds • As noted through vector surveillance, there have been no detections of WNV in birds in 2025 • There has been an increasing range of USUV detections in birds in southeast England Equines • In 2025 and in prior years, there were no detections of locally acquired WNV in equines
Human	• To date, there have been no locally acquired cases of WNV or USUV reported • In 2025, there were 2 travel-associated cases of WNV and a travel-associated case of USUV was reported for the first time, detected in a blood donor

West Nile virus and Usutu virus

WNV and USUV are closely related viruses which are maintained in a mosquito to bird transmission cycle but can infect certain mammals as dead-end hosts.

Most infections with WNV and USUV are asymptomatic, and when symptoms occur, they are typically mild. WNV commonly presents with flu-like illness, whereas USUV is characterised by fever, myalgia, headache, asthenia, and rash. In rare cases, both viruses can lead to severe neurological disease: fewer than 1% (about 1 in 150) of WNV infections involve the brain and central nervous system, causing meningitis, encephalitis, or acute flaccid paralysis, while only a small number of severe neurological cases of USUV have been reported, mainly in immunocompromised individuals (29, 30). The incubation period of WNV ranges from 2 to 21 days, while that of USUV in humans is shorter, at 3 to 12 days. There is currently no vaccine available for humans for WNV.

Vector surveillance

The principal bridge vector implicated in transmission of WNV and USUV to mammals in Europe that occur in the UK are *Culex modestus* (found in wetland habitats and drainage ditches) and *Culex pipiens molestus,* hereafter referred to as *Culex molestus* (urban habitats associated with flooded basements or underground habitats) [including *molestus pipiens* hybrids]. *Culex modestus* was first detected in the UK on Hayling Island in 1944 and was found again in 2010 in the North Kent marshes. Prior to 2025, the known range included sites in coastal and estuarine Essex, Suffolk, Hampshire and West Sussex.

USUV was first detected in mosquitoes and birds in the UK in the London region in 2020 where it was associated with a reduction in blackbirds (31).

National Wetland Mosquito Survey

During 2025, 25 traps were run at 30 wetland systems across England and Wales between June and October as part of nationwide wetland mosquito surveillance. Over 7,000 mosquitoes were collected from 12 different species, and *Culex modestus* was detected in Lincolnshire.

Snapshot Wetland Mosquito Survey

The Snapshot Wetland Mosquito Survey included participation from 73 of the 81 50km grids squares in England, with contributions from 87 separate wetland sites during 2024 and 2025. In total, 2,298 mosquitoes were captured, representing 14 native UK species: most being primarily bird biting wetland-associated species. *Culex modestus* breeding sites at Farlington Marshes (Cambridgeshire) and Pannel Valley NR (East Sussex) were detected for the first time.

The detection of *Culex modestus* in 4 new locations (Kent, Cambridgeshire, Northamptonshire and Lincolnshire) in 2025 suggests ongoing range expansion in the UK which may increase the risk of emerging WNV cases in the UK (see Figure 6 below) (32).

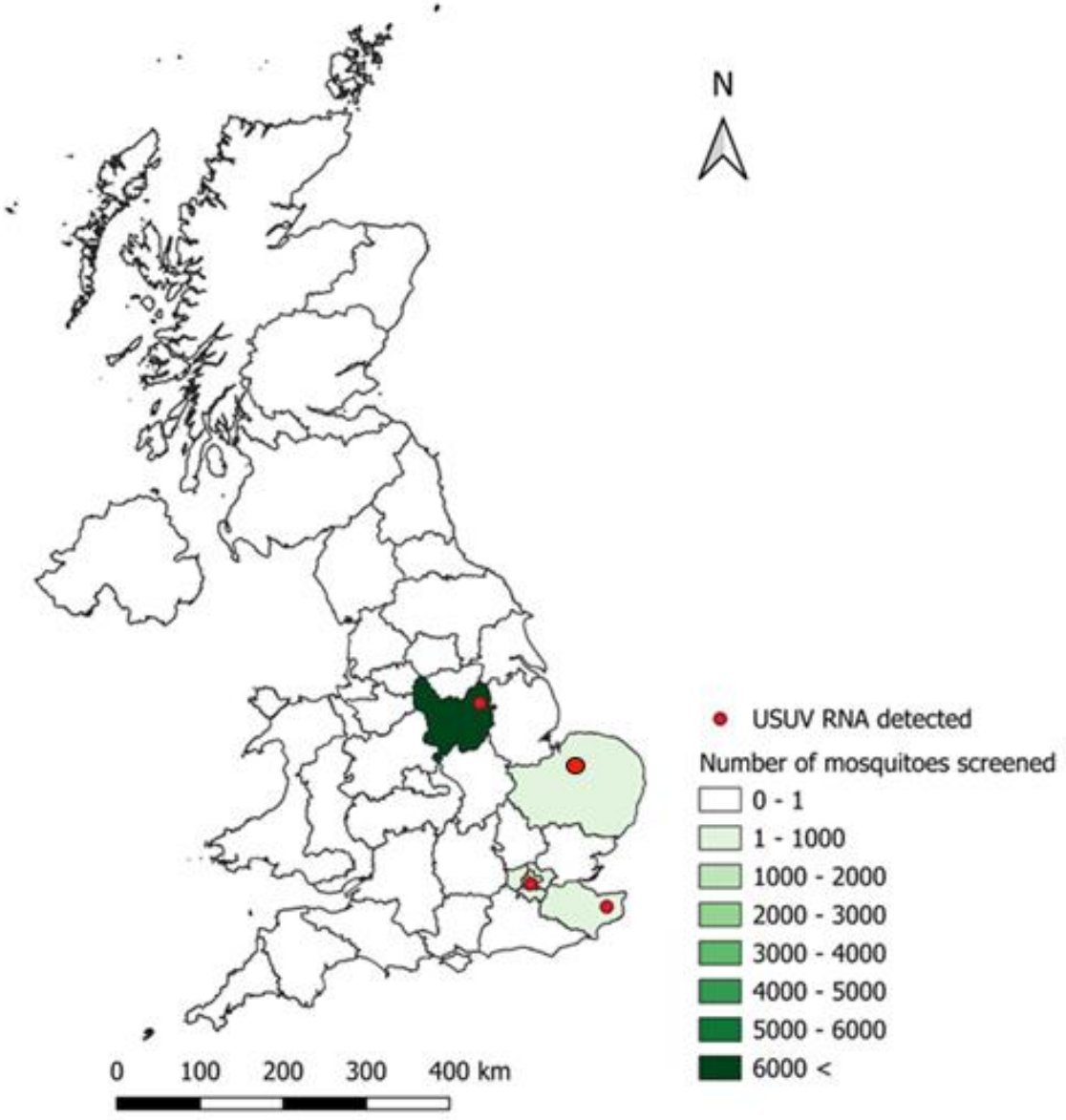
Figure 6. Map showing locations of *Culex modestus* through the Snapshot Wetland Mosquito Survey

Grey triangles represent historic records, teal circles represent new 2024 records, orange squares represent new 2025 records

Vector-borne Real-time Arbovirus Detection And Response (VB-RADAR) project

Mosquito screening for WNV and USUV continued as part of the VB-RADAR research project, with mosquito sampling from a range of wetland, rural and urban habitats across southern England. The first detection of WNV RNA in UK mosquitoes was reported in 2025 in mosquitoes collected from Nottinghamshire during 2023 (33). Enhanced surveillance at this site during 2025 found no further evidence of WNV. Overall, in 2025, around 8,000 mosquitoes were screened, including the WNV index site in Nottinghamshire. USUV RNA was detected at all locations where mosquitoes were collected, while also being detected in overwintering female *Culex pipiens s.l.*, providing evidence of viral persistence during winter months (see Figure 7 below).

Figure 7. Mosquito surveillance conducted as part of the VB-RADAR project



Red points indicate the detection of USUV RNA in mosquito pools. The shaded regions indicate the number of mosquitoes collected and screened in each region.

Animal surveillance

In 2025, WNV circulation continued to expand across Europe in birds and animals with persistent endemic activity and periodic epidemics, frequently affecting new areas. Outbreaks in birds and or equids were reported in 11 countries, and 14 countries reported human outbreaks (5). Northerly expansion was evident, with Belgium reporting WNV outbreaks in wild birds, the Netherlands reporting their first outbreak in equids, and human outbreaks reported in Northern France for the first time (5). USUV was first detected in mosquitoes and birds in the UK in the London region in 2020 where it was associated with a reduction in blackbirds (31).

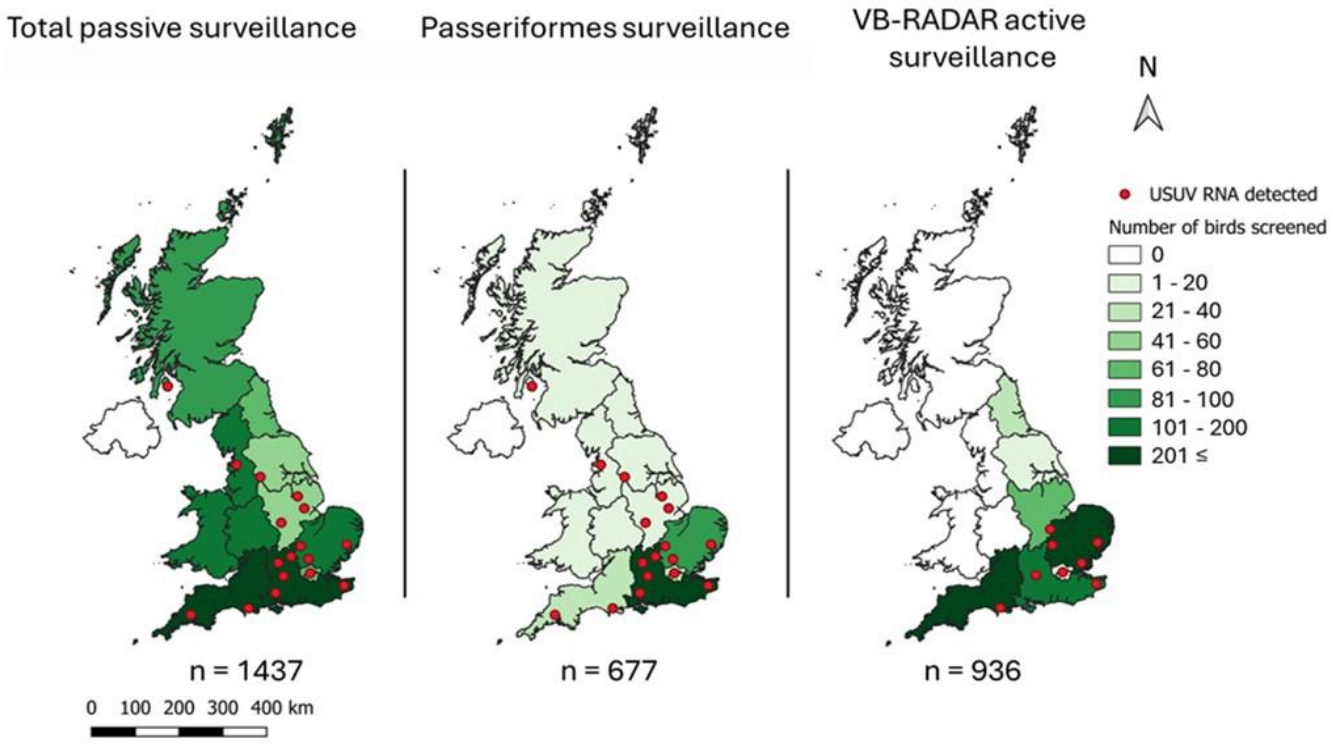
Birds

During 2025, the Arbovirus National Reference Laboratory (NRL) at APHA received pooled brain and kidney tissue samples from 1,221 dead wild birds from passive orthoflavivirus surveillance. Of these, samples from target bird species were tested for WNV and USUV, and all were negative for WNV RNA and 33 were positive for USUV including: a common Buzzard (Buteo buteo) from Lancashire; Blackbirds from Nottinghamshire, Lincolnshire, West Yorkshire; and a Greenfinch (Chloris chloris) from Leicestershire (see Figure 8 below).

The VB-RADAR project sampled >900 birds as part of the active surveillance effort to screen Passeriformes for USUV and WNV, with evidence of orthoflavivirus seroconversion and USUV RNA detected at multiple sites across the south of England (Turdus merula) (see Figure 8 below). An additional 231 Passeriformes (to-date) have been submitted from rescue centres across England in collaboration with ZSL. From this research project, WNV specific antibodies were detected in a migratory Whitethroat (Curruca communis) sampled in April 2025 from Dorset. This bird was an adult and, given the time of year, had likely just finished its migration to the UK from areas where WNV may be endemic. While this detection was not an incursion of WNV, it does illustrate that migratory birds which make landfall in the UK may have been exposed to WNV in their non-breeding regions and therefore present a risk of future WNV introduction to the UK.

WNV specific antibodies were also detected in archived serum samples taken from 2 collection birds during routine health checks. These birds were tested as part of a serosurvey on archived serum samples from ZSL London Zoo (great white pelican, *Pelecanus onocrotalus*, tested positive on samples taken during 2023) and Whipsnade Zoo (Wattled crane, Grus carunculate, tested positive on samples taken during 2023 and 2025). These were isolated detections of antibodies at 2 sites where routine WNV surveillance is undertaken, with no WNV transmission in mosquitoes or wild birds detected to date; both of these birds had been hatched outside the UK, therefore the source of virus exposure is unclear. All native-hatched birds were negative.

Figure 8. Bird surveillance across Great Britain in 2025 and USUV detections, by all birds screened for USUV and WNV, *Passeriformes* (target species) only, and birds screened through the active surveillance VBD-RADAR project



Equines

In 2025, 14 samples were submitted to the APHA Equine Test to Exclude (TTE) scheme. Orthoflavivirus-specific antibodies were detected in one horse from Dartmoor and the remaining samples were negative. Virus neutralisation assays confirmed the antibodies were specific for the TBE complex with a higher antibody titre against louping ill virus (LIV) (34).

Human surveillance

In Europe from May to October 2025, 1,112 locally acquired human WNV infection cases were reported, and 97 deaths. Italy (779 cases) and France (62 cases) reported their largest outbreaks to date. Human case numbers were above the average for the past decade, but lower than those seen in 2018, 2022, and 2024 when virus circulation was particularly intense, with over 1,300 cases reported per annum (5).

There is no equivalent European surveillance data for USUV for 2025, however blood donor screening identified locally-acquired cases of USUV in Spain for the first time in 2025 (35).

In England, there have been no locally acquired human cases of WNV or USUV reported to date.

Between 2012 and December 2025, NHSBT tested over half a million blood donations for WNV (joint NHSBT-UKHSA Epidemiology Unit data). Over this period, the number of annual WNV tests has nearly doubled with the proportion of all donations tested increasing from 1.5% to 4%. In total, 6 of these WNV-tested donations have been reactive and 4 were not confirmed (in 2014, 2016, 2022 and 2024). In 2025, 2 of 58,277 donations with a WNV test were reactive (0.003%); with help from other laboratories including RIPL, one was confirmed as WNV and one was confirmed as USUV, both in donors returned from Italy (joint NHSBT-UKHSA Epidemiology Unit data). The individuals did not report any symptoms at the time of donation and presented as healthy donors.

In addition to the travel-associated WNV case detected through blood donor screening, there was one further travel-associated WNV case from the USA, confirmed by RIPL in 2025.

Tick-borne pathogens (Group 3)

Overview

This section reports on Group 3 pathogens, *Borrelia burgdorferi* (Lyme disease), tick-borne encephalitis virus (TBEV), louping ill virus (LIV), *Babesia divergens*, *Anaplasma phagocytophilum,* and Rickettsial infections reported in 2025. Table 6 provides a short summary of activity in 2025 for these pathogens by surveillance type.

Table 6. Group 3 Surveillance summary, England 2025

Group 3 Surveillance summary, England 2025	
Vector (ticks)	• *Ixodes ricinus* remains the most common tick reported in England
Animal	Livestock • Louping ill virus (LIV) was reported in 31 sheep and 5 cattle • Tickborne fever caused by infection with *Anaplasma phagocytophilum* was reported in 104 sheep and 25 cattle • Babesiosis caused by infection with *Babesia divergens* was reported in 30 cattle
Human	• Lyme disease remains the most common locally acquired tick-borne infection • In 2025, 1,168 laboratory-confirmed acute Lyme disease cases (including acute neurological cases) were reported, this was higher than 2024 (959 cases) but similar to 2023 (1,151 cases) • Since 2019, there has been a total of 6 locally-acquired human cases of TBE complex (including confirmed and probable TBE complex). Of these cases, there were 2 locally acquired human cases of probable TBE complex in 2025 • Additionally, there were 2 travel-associated confirmed TBE complex cases (travel to Europe) in 2025 • There were 37 travel-associated cases of Rickettsial infections

Vector (tick) surveillance

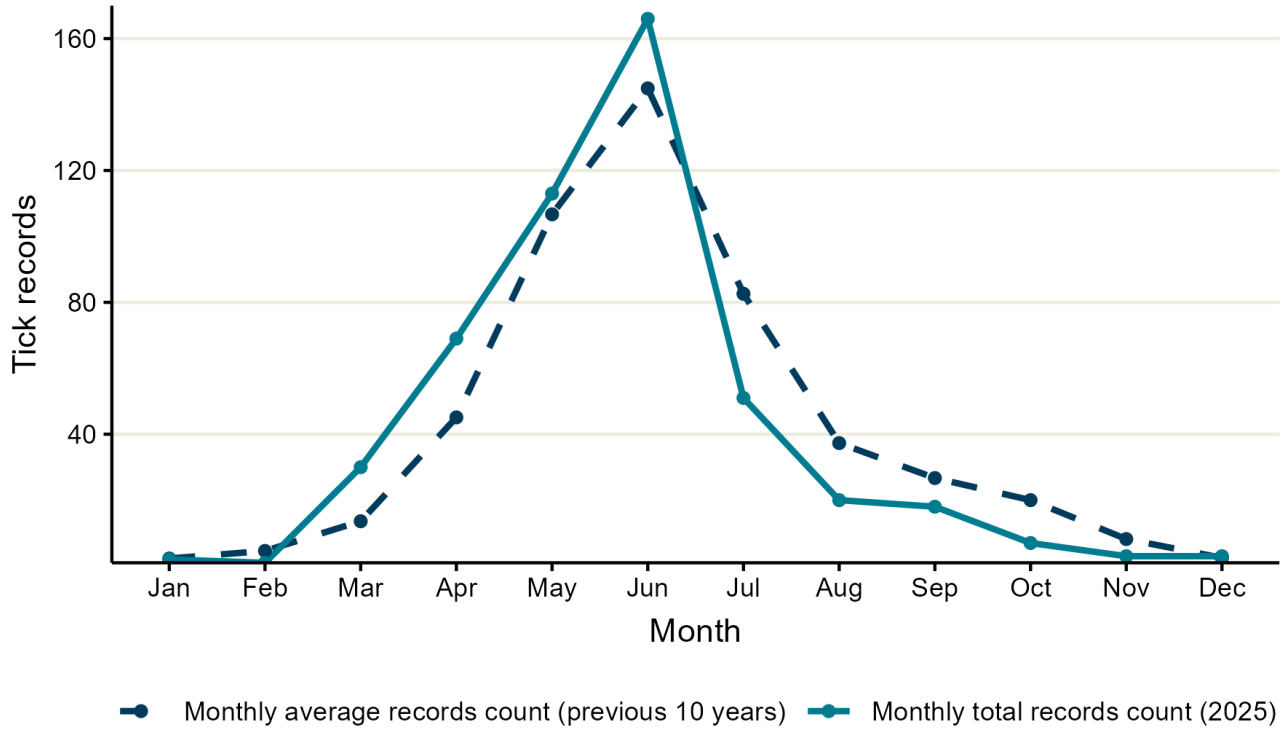
Ixodes ricinus is the most common tick in the UK. It is the primary vector for *Borrelia burgdorferi* (Lyme disease), TBEV, LIV, *Anaplasma phagocytophilum, Babesia divergens* and Rickettsia. There have been detections of non-native tick species in previous years, including *Hyalomma excavatum*, *Hyalomma marginatum* and *Rhipicephalus pulchellus*, although the risk of establishment is currently considered low.

Tick distribution

Tick Surveillance Scheme (TSS) findings during the period 2021 to 2024 were reported in a recent publication (36). This includes species distribution maps for native tick species, and a new tick-bite incidence metric with heat map of potential tick exposure for England and Wales. The highest number of tick bites were reported in the South West and the South East of England, as well as isolated districts in the East Midlands, the North West and also Wales.

In 2025, 776 ticks were submitted to the TSS (11 imported), with 483 being *Ixodes ricinus,* similar to the 2020-to-2024 5-year average of 493. Submissions followed a typical seasonal pattern, increasing in late spring to a peak in June, consistent with prior years (see Figure 9 below).

Figure 9. Total monthly records of *Ixodes ricinus* ticks submitted to the TSS for the current period in comparison to the mean monthly average from the previous 10 years



Data is shown by the month the tick was collected (UKHSA data dashboard).

Tick pathogen surveillance

In 2025, the results of a study which surveyed 84 sites within 36 recreational areas during 2021 to 2023 across England and Wales was published. *Ixodes ricinus* density was higher in woodlands and where deer were present. A total of 3,914 *Ixodes ricinus* nymphs were tested for *Borrelia burgdorferi* s.l. and the overall prevalence was 5.8% (n=228/3914; 95 %CI: 5.1-6.6). The density of infected nymphs was highest in the north and south of England, compared to central England. Prevalence rates varied between sites, ranging from 0% in Cannock Chase (West Midlands) and Eryri (Wales) to 30.4% in the Yorkshire Dales (Yorkshire and the Humber) (37).

The APHA TickTools project tested 1,674 ticks collected from UK-wide locations in 2025, all of which were *Ixodes ricinus*. Sites with the highest density of deer appeared to be associated with the highest density of ticks. Specimens were pooled for pathogen screening; of the 53 pools tested, 34% were positive for *Anaplasma phagocytophilum*, and 3.8% were positive for *Babesia* (2 different *Babesia* species); all tests for *orthoflavivirus* and Alongshan virus were negative (manuscript in preparation).

Borrelia burgdorferi (Lyme Disease)

Lyme disease, or Lyme borreliosis, is a bacterial infection that can be transmitted to humans when they are bitten by a tick infected with bacteria in the *Borrelia burgdorferi* sensu lato genospecies complex. In the UK, it is transmitted by the bite of infected *Ixodes ricinus* ticks. Ticks become infected by feeding on animals that carry the bacteria in their blood.

The most commonly reported symptom is a ‘bullseye rash’ at the site of the tick bite, which may occur within 3 to 30 days of being bitten (38). People may also experience fever, chills, headache, muscle and joint aches and swollen lymph nodes, and this may occur in the absence of the rash. Neurological complications may occur days to months after being bitten by an infected tick and include facial palsy or drooping, shooting pains in the arms or legs and very rarely meningitis. Other complications that may occur include involvement of the joints, heart or skin.

Vector surveillance

Refer to Vector (Tick) surveillance section above.

Human surveillance

Data for Lyme disease was obtained from RIPL, UKHSA. Case definitions are included in Appendix D (Overview of human surveillance). Previously, Lyme disease was reported in the annual Common animal-associated infections reports. From 2025, Lyme disease data will be included in this One Health VBD annual surveillance report.

In addition to the case definition described in Appendix D (Overview of human surveillance), for surveillance purposes, a one-year episode window has been applied from 2025 onwards. The episode window means that only one positive laboratory test will be counted per individual within a 12-month period. This change in methodology may affect case numbers and should be considered when interpreting trends in diagnoses prior to, and after, 2025.

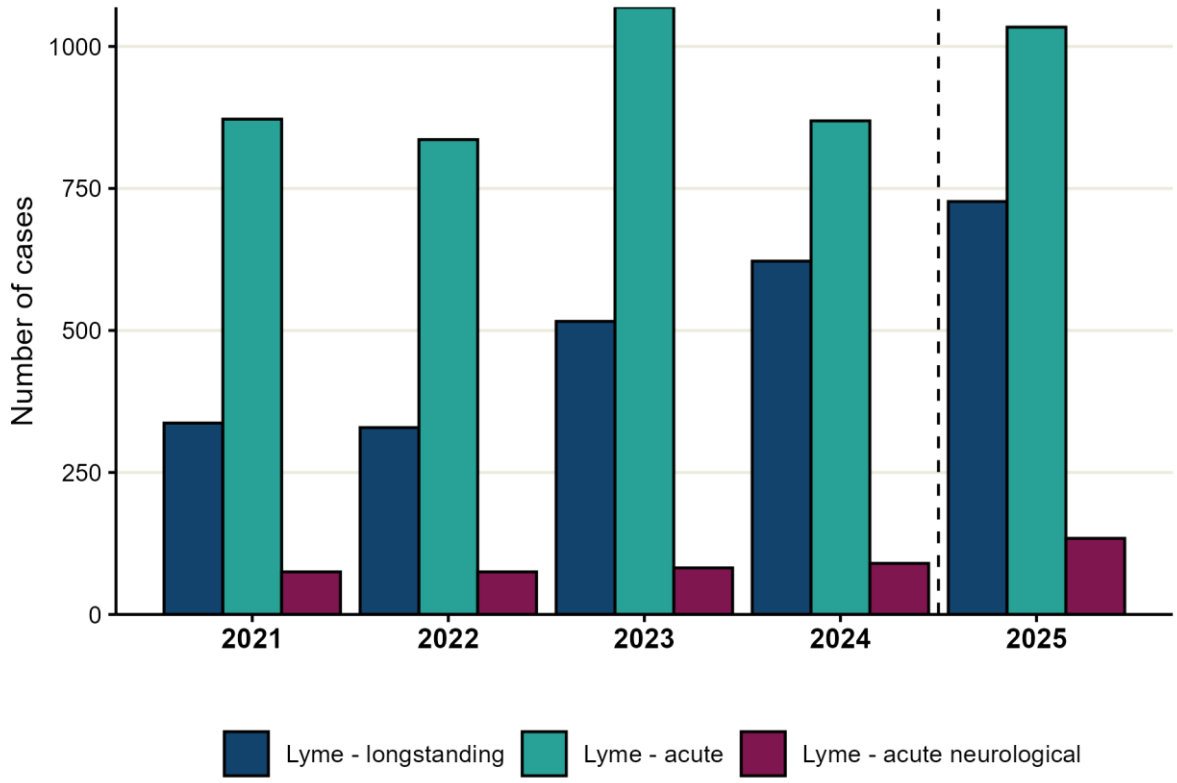
In 2025, overall, 1,168 acute Lyme disease cases were reported, including 134 acute neurological cases. This was an increase compared to 2024, when 959 acute Lyme disease cases (including acute neurological cases) were reported, but was similar to 2023, when 1,151 cases were reported (see Figure 10 below).

For validation purposes, the updated surveillance definition for 2025 was applied to previous years which showed consistent trends.

Acute Lyme disease presenting with a ‘bullseye rash’ is diagnosed clinically and testing is not recommended, per NICE guidelines. Therefore, the number of laboratory-confirmed cases presented in this report will be an underestimate of the true burden of acute Lyme disease in England. Based on previous work using data between 1998 and 2016, there could be approximately an additional 1,400 clinically diagnosed acute Lyme disease cases. This estimate is currently being recalculated using recent epidemiological information (48).

Additionally, there were 727 cases of ‘longstanding’ Lyme disease reported in 2025. ‘Longstanding’ Lyme disease may reflect past exposure to, or infection with, the bacteria that cause Lyme disease, or a late presentation of Lyme disease, and does not imply chronic infection or ‘chronic Lyme disease’.

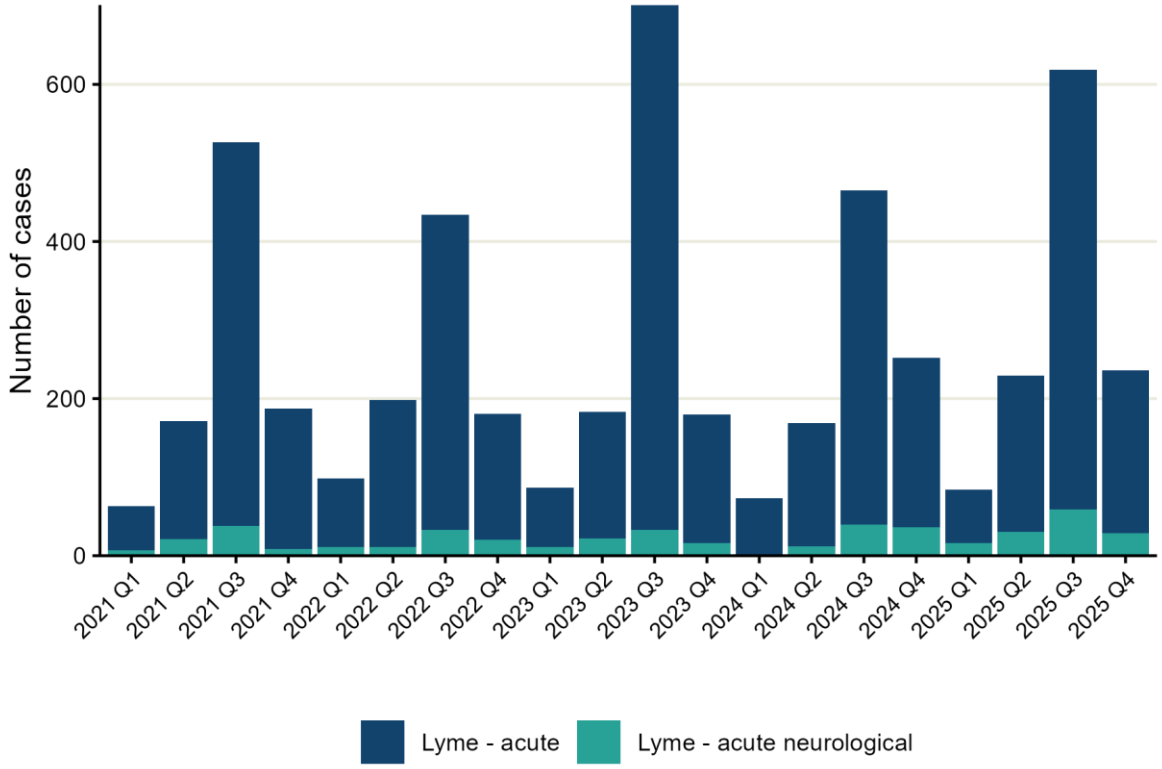
Figure 10. Laboratory confirmed cases of Lyme disease in England by year, 2021 to 2025



Note: The dashed line indicates the change in surveillance definition from 2025 onwards.

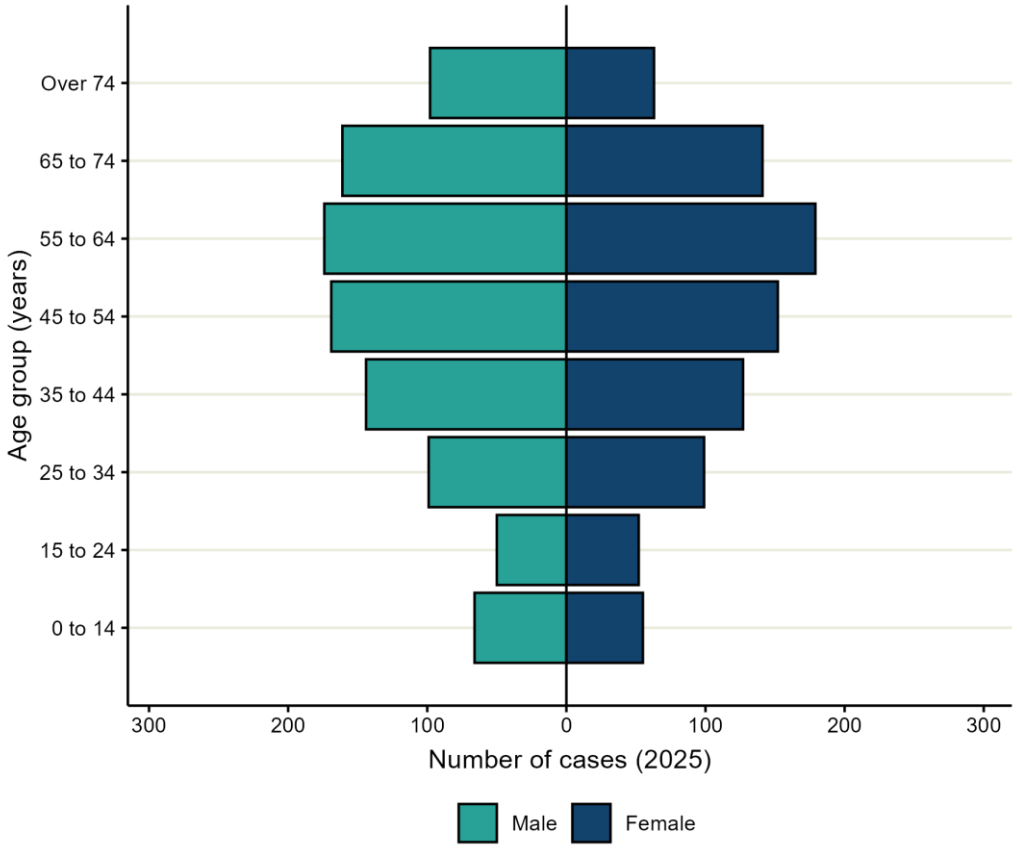
Figure 11 (below) highlights that the number of acute and acute neurological Lyme disease cases continues to peak during the summer months (Q3 2025), which corresponds to the peak period of exposure to ticks in the UK in the spring and summer months.

Figure 11. Laboratory confirmed cases of acute and acute neurological Lyme disease in England by quarter, Q1 2021 to Q4 2025



Of the acute and acute neurological Lyme disease cases in 2025, 563 (48.2%) were male (age range 2 to 87 years, median 48 years), and 562 (48.1%) were female (age range 1 to 86, median 50 years) (see **Figure** 12 below). The age sex distribution was similar to the previous 4-year period, where 50.1% of cases were female and the overall median age was 48 years (age range 1 to 91). Of the 134 acute neurological cases reported in 2025, 81 (60.4%) were male and the median age was 47 (age range 1 to 86 years).

Figure 12. Laboratory confirmed acute Lyme disease cases (including acute neurological cases) in England by age group and gender, 2025



Note: Age and/or gender was missing for n=46 cases

The regions that reported the most acute and acute neurological Lyme disease cases in 2025 (including acute neurological cases) were the South East (323 cases), the South West (281 cases) and London (244 cases) (see Figure 13 below). Over the past 5 years, these regions have consistently reported the highest annual cases of acute Lyme disease. Region is allocated using residential postcode if available, or the location of the referring hospital or laboratory.

Of the 1,168 acute and acute neurological cases in 2025, only a minority (52, 4.5%) reported overseas travel, of which 46 had travelled to areas where Lyme disease has previously been found, including Europe (41 cases) and the Americas (5 cases). The location of travel was not available for 4 cases. Travel history is not always available for laboratory diagnosed

cases. For both region and travel history, the location reported does not necessarily reflect where the infection was acquired.

Figure 13. Laboratory confirmed acute Lyme disease cases (including acute neurological cases) in England by UKHSA region, 2021 to 2025

Seroprevalence study in English blood donors

In 2025, the results of a large seroprevalence study of Lyme disease in England were published, conducted using an archive of 10,000 geographically representative residual NHSBT blood donor samples collected in 2021 to 2022. The seroprevalence of *Borrelia burgdorfe*ri was estimated to be 0.49% (95 % CI 0.36 - 0.65), which is lower than estimates in Scotland and other Northern European countries (40).

Tick-borne encephalitis virus (TBEV)

Tick-borne encephalitis virus (TBEV) is a member of the genus orthoflavivirus and is transmitted by the bite of an infected tick. It can cause TBE in humans. In the UK, the *Ixodes ricinus* tick is the primary vector for TBEV. Competent reservoir hosts of TBEV are mainly small rodents (voles, mice) and insectivores (shrews). Other animals support virus circulation indirectly by enabling tick multiplication. These include wild and domestic mammals, especially hares, deer, wild boar, sheep, cattle and goats. Humans are considered dead-end hosts for TBEV.

The mean incubation period of TBEV is 7 days but may be up to 28 days. Infection causes minimal or no symptoms in the majority of infected people (41). However, in rare cases the virus can disseminate to the central nervous system, resulting in neurological disease which may lead to long-term neurological symptoms or (very rarely) death. There is a TBEV vaccine available, and it is recommended for those who will be going to reside in an area where TBEV is endemic or epidemic, and particularly for those working in forestry, woodcutting, farming and the military (41). Current UK vaccine recommendations are under review following the identification of domestically acquired cases.

TBEV is endemic in rural and forested areas of central, eastern and northern Europe and incidence rates are considerably varied (42,43). Ticks carrying the virus can be found in many parts of Europe and Asia, but its presence is highly focal, even within the distribution of its competent tick vectors.

Since 2018, UKHSA has conducted large-scale monitoring of tick-borne orthoflaviviruses in 4 deer species and ticks from varying habitats to capture a wide range of conditions that favour transmission (44). This scheme indicated that exposure of deer to TBEV is highly focal and limited to few areas in Great Britain. The first locally acquired human case of TBE was reported in 2019 following a tick bite in the New Forest (7).

Vector surveillance

Please refer to Vector (Tick) surveillance section.

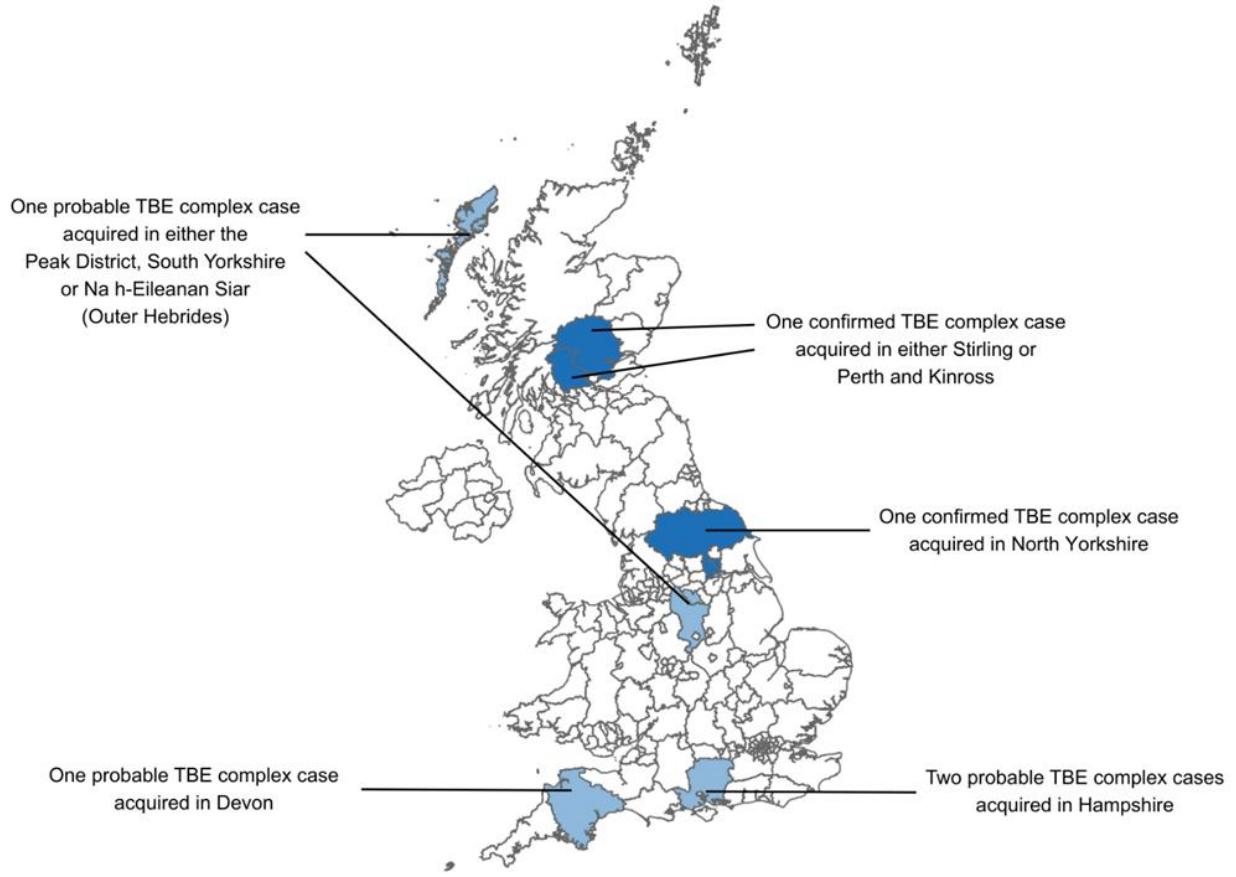
Animal surveillance

Until 2019, TBE was considered to be only an imported disease to the UK. Evidence of TBEV circulation was reported in the UK for the first time in 2019 through positive deer serology and through molecular detection in a small number of ticks from Thetford Forest and the New Forest and bordering areas (45). Subsequently, TBEV positive ticks have been found in North York Moors.

Human surveillance

During 2025, there were 2 unrelated cases of probable TBE complex with no international travel history reported to UKHSA. Diagnostic tests were unable to distinguish between TBE virus and louping ill virus (LIV). The response to both incidents is summarised in the Summary of VBD Incidents in 2025 section. A map of the likely location of acquisition for human cases is shown in Figure 14 (below). Overall, surveillance in ticks, deer and humans suggests TBEV distribution remains very focal and limited to a few areas in Great Britain including Thetford Forest, New Forest, Devon, North Yorkshire, Dartmoor and parts of Scotland.

Figure 14. Map of likely location of acquisition for probable and confirmed TBE complex cases between 2019 and 2025



In addition, 2 cases of confirmed TBE complex were reported in England in 2025, associated with travel to Europe.

Louping ill virus (LIV)

Louping ill, also referred to as ovine meningoencephalitis, is a disease of cattle and sheep which manifests as a brief febrile illness followed by sudden onset of neurological signs that can be fatal.

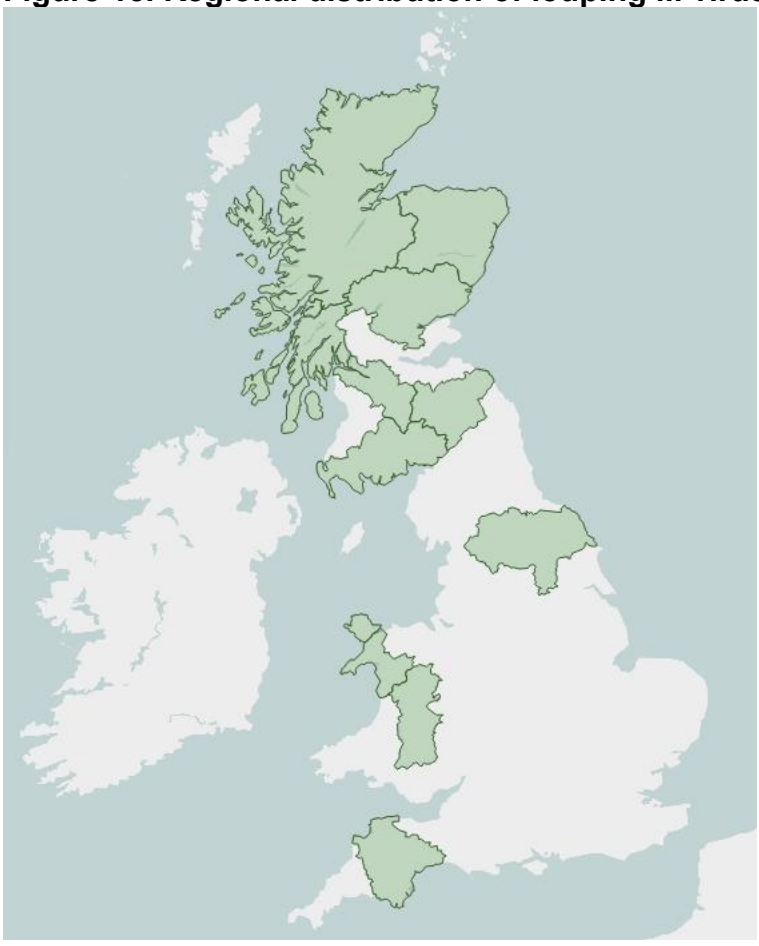
Vector surveillance

Refer to Vector (Tick) surveillance section.

Animal surveillance

In 2025 APHA detected 31 cases reported in sheep, 5 cases in cattle, and one in a horse. The disease has a distinct geographical distribution in the UK (see Figure 15 below).

Figure 15. Regional distribution of louping ill virus infections in sheep, 2025



In 2025, APHA also detected antibodies against LIV in a sample from a horse in Devon. Although the horse had no history of travel abroad, the sample had been submitted for Testing to Exclude (TTE) to rule out WNV infection, as clinical signs were suggestive of neurological disease. However, LIV infection was confirmed, and the horse subsequently recovered (46).

Human surveillance

LIV human cases are extremely rare in England with only a small number of cases recorded historically (47). As described above, serological diagnostic tests may be unable to distinguish between LIV and TBEV due to orthoflavivirus cross-neutralisation. This is because the very small number of confirmed human cases limits the development of validated human tests. Two locally acquired cases of probable TBE complex were reported in 2025 (see the Group 3 TBEV section) but could not be assigned to TBEV or LIV for the final diagnosis.

Anaplasma phagocytophilum (Tickborne fever)

Tickborne fever is a disease primarily reported in sheep caused by infection with the bacteria *Anaplasma phagocytophilum*. In sheep, initial infection can result in a febrile illness that in rare cases leads to disease and death. Severe disease is often reported in association with infection with another agent. It can also cause human granulocytic anaplasmosis, and a single human case was reported in Scotland in 2013 (48).

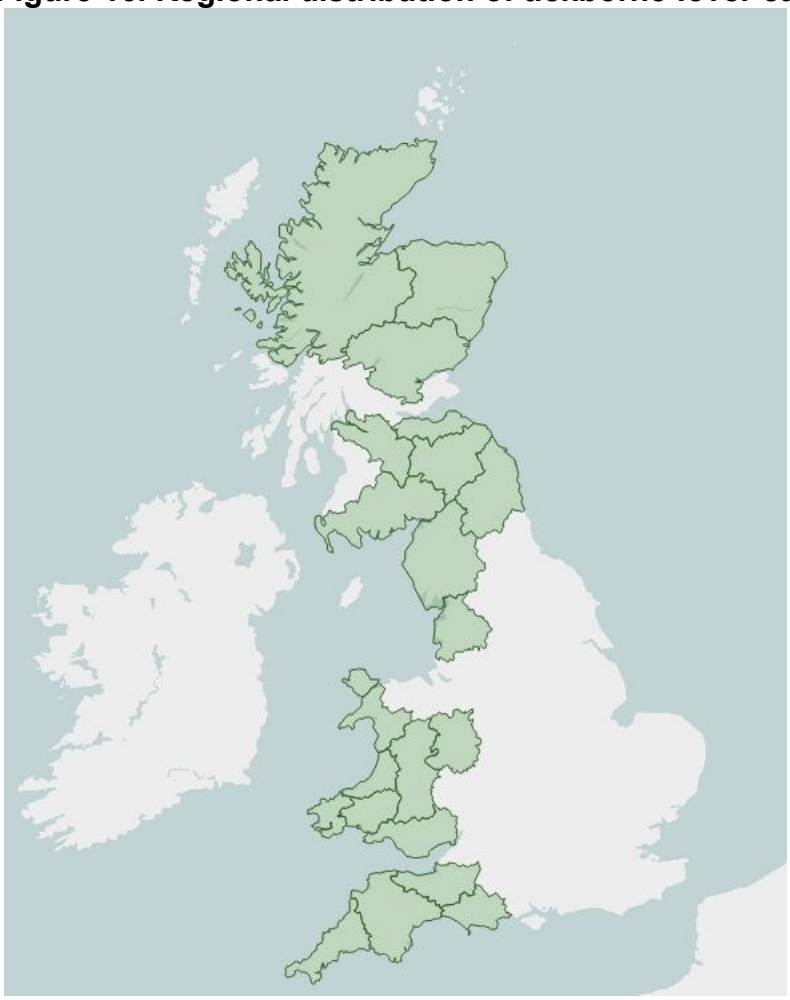
Vector surveillance

Please refer to Vector (Tick) surveillance section.

Animal surveillance

In 2025, APHA reported 104 cases reported in sheep and 25 cases in cattle (see Figure 16 below). The distribution of tickborne fever is similar to that of louping ill.

Figure 16. Regional distribution of tickborne fever cases in sheep, 2025



Human surveillance

No human cases of *Anaplasma phagocytophilum* were reported in 2025.

Babesiosis

Infection with the protozoan parasite *Babesia divergens* is the most common cause of zoonotic babesiosis in Europe (49) . Babesiosis in livestock primarily affects cattle and in severe cases can result in haemolytic anaemia. Infection in humans can lead to severe haemolytic anaemia, fever, jaundice and renal failure, often in splenectomised patients. There have been 2 human cases reported in the UK: one in Devon in 2020 and one in Scotland in 1979 (50 to 52).

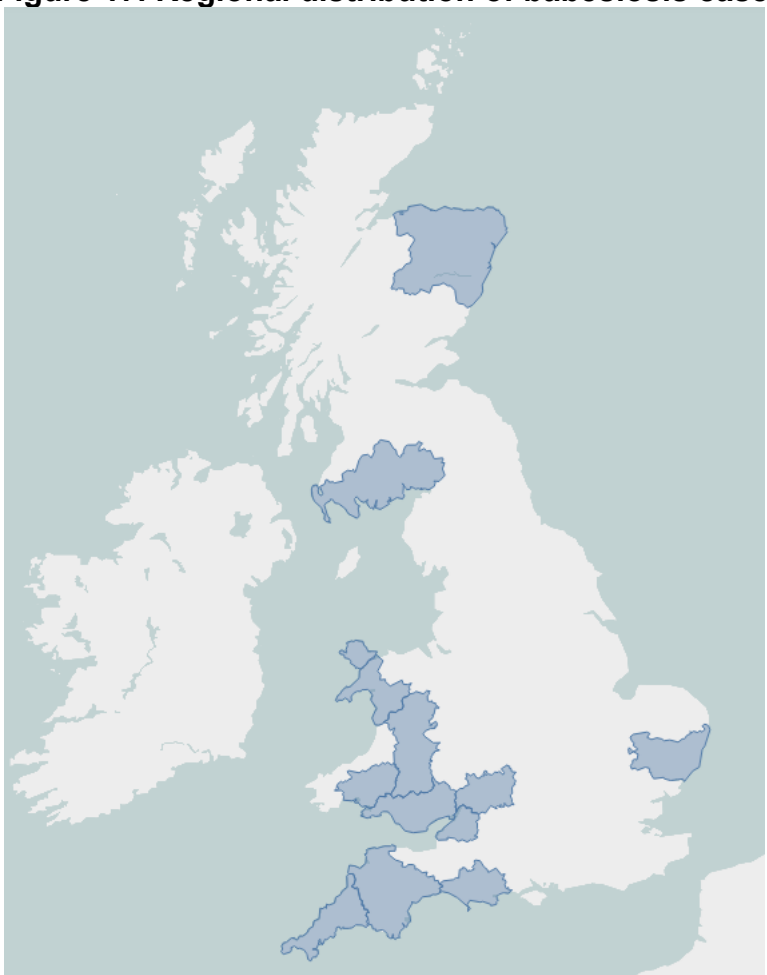
Vector surveillance

Refer to Vector (Tick) surveillance section.

Animal surveillance

In 2025, APHA reported 30 cases of bovine babesiosis in Great Britain (see Figure 17 below). The distribution of bovine babesiosis cases is shown below.

Figure 17. Regional distribution of babesiosis cases in cattle, 2025



Human surveillance

Babesiosis is not a notifiable disease or organism and there is currently no routine surveillance in humans. Limited awareness and the lack of a reliable test could lead to under-ascertainment of human cases.

Rickettsial infections

Rickettsial infections are a group of bacterial infections which are transmitted by different arthropod vectors, including ticks, mites, lice and fleas, to animals such as humans, dogs, cats and cattle.

Vector surveillance

Previous surveillance has identified *Rickettsia helvetica* in *Ixodes. ricinus*, *Rickettsia raoultii* in *Dermacentor reticulatus* and *Rickettsia massiliae* in *Haemaphysalis punctata*. It is also possible that imported *Rhipicephalus sanguineus* could be infected with *Rickettsia conorii*, although none has been confirmed in the UK. Recently, locally-acquired *Hyalomma marginatum* have been found infected with *Rickettsia aeschlimannii*, but neither the tick nor the pathogen is endemic to the UK (53–55).

Human surveillance

UKHSA carries out passive surveillance for rickettsial infections in humans caused by the *Orientia* and *Rickettsia* genera in the Rickettsiaceae family. These are classified into 3 main groups: spotted fever group, typhus group and scrub typhus group. In general, the incubation period is between 6 to 14 days post infection and symptoms vary but may include fever, myalgia, headache, dry cough and rash (4) .

In 2025, 37 travel-associated rickettsial infections were reported in England, a 12% decrease compared to 42 cases reported in 2024 (4).

Other vectors (Group 4)

Overview

This section reports on cases of disease caused by Group 4 pathogens (transmitted by arthropod vectors other than mosquitoes and ticks) reported in 2025. Table 7 provides a short summary of activity in 2025 for these pathogens by surveillance type.

Table 7. Group 4 Surveillance summary, England 2025

Group 4 Surveillance summary, England 2025	
Vector	• To date, there is no evidence of primary vectors of Oropouche virus
Animal	• No key animal reservoirs present
Human	• In 2025, there were 3 travel-associated cases of Oropouche virus were reported in England for the first time

Oropouche virus

Oropouche virus disease, caused by a virus from the *Peribunyaviridae* family, is an infection primarily transmitted by the bite of the midge *Culicoides paraensis*. The main animal reservoirs of Oropouche virus are sloths and non-human primates, such as Howler monkeys. Most cases recover within 7 days of onset of symptoms, which include fever, headache, joint pain, muscle pain, chills, nausea, vomiting and rash (56).

Local transmission continues to be reported in multiple countries in South America, Central America and the Caribbean. In 2024, there was a steep increase in case numbers in the Americas and additional countries reporting cases, with over 16,000 confirmed cases recorded in the Americas, the majority of which occurred in Brazil. In 2025, 12,786 cases were reported between epidemiological weeks 1 and 30, with Brazil accounting for 11,888 cases during this period. Geographical expansion continued as the virus spread to new areas in the Americas. Additionally, Oropouche virus disease cases continued to be reported in North America and Europe in 2025 among travellers returning from countries with local transmission (57).

Vector surveillance

There is no evidence of *Culicoides paraensis,* the primary vector of Oropouche virus, in the UK (58). The Pirbright Institute is conducting research to assess if native UK biting midges and mosquitoes are capable of transmitting Oropouche virus.

Human surveillance

In 2025, 3 travel-associated cases of Oropouche virus were reported in England with recent travel to Brazil, representing the first cases diagnosed in the UK (4).

Research and special studies

This section highlights recent mosquito-, tick-borne and other VBD research and special studies of interest conducted in collaboration with Defra, APHA or UKHSA that were either published or ongoing during 2025, and where they have not been described in the report already. Defra and UKRI funded a number of VBD research projects from 2023 to 2026 including VB-RADAR, OpTick, TickTools. Table 8 provides a brief overview of these studies, and links to further reading or publications.

Table 8. Research and special studies, up to end 2025

Type of research	Research/Special study title	Description	Relevant links/further reading
Tick-borne disease	Modelling the distribution of the tick *Ixodes ricinus* in England and Wales using passive surveillance data from citizen science reports, 2025	Risk map showing *Ixodes ricinus* tick predicted areas in England and Wales based on data from the TSS and information on temperatures, environment, deer presence and woodland. The main predicted area was in southern England, while the Midlands and much of Wales were less likely to have ticks. Areas with deer and more woodland as more likely to have ticks.	Modelling the distribution of the tick Ixodes ricinus in England and Wales using passive surveillance data from citizen science reports | PLOS Neglected Tropical Diseases
Tick-borne disease	Identifying hotspots and risk factors for TBEV emergence at its range margins to guide interventions, Great Britain, 2025	Risk factors for TBEV and suitable areas for TBEV transmission were identified and mapped and overlaid with recreational demand to identify where people may be at higher risk of contracting TBEV. TBEV was more likely to be detected in areas with more coniferous woodland, more deer species, higher winter temperatures and more rapid temperature increases in spring. Areas of highest risk included the heavily forested areas of Hampshire, Dorset and East Anglia that have high deer numbers.	Eurosurveillance | Identifying hotspots and risk factors for tick-borne encephalitis virus emergence at its range margins to guide interventions, Great Britain

Type of research	Research/Special study title	Description	Relevant links/further reading
Tick-borne disease	Tick-Solve, 2021-2025	Tick-Solve investigated the ecological conditions that enable tick-borne infections to spread, and focused on environmental solutions to reduce the risk.	TickSolve | TickSolve
Tick-borne disease	TickTools, 2023-2026	TickTools aims to develop tools to monitor and control tick-borne diseases, including metagenomics to investigate pathogen diversity within the tick. Alongshan virus (ALSV) was detected in *Ixodes hexagonus* from hedgehogs, using a metagenomics approach.	Investigating British ticks for viral threats – APHA Science Blog Alongshan virus in the virome of Ixodes hexagonus ticks in the United Kingdom by Ben Paul Jones, Elena De Candia, Hannah Davies, Akbar DASTJERDI, Daniel L. Horton, Nicholas Johnson :: SSRN
Tick-borne disease	Optick, 2023-2026	Project focused on understanding and mitigating the changing burdens and impacts of tick-borne diseases in UK farmland.	OPTICK | Optik

Type of research	Research/Special study title	Description	Relevant links/further reading
Tick-borne disease	Lyme and TBEV serosurveillance studies, 2020-ongoing	UKHSA led serosurveillance studies to monitor past exposure to *B. burgdorferi* and TBEV in groups at high-risk of tick bites due to their occupation or recreational activities, such as farmers, deer stalkers and orienteers in areas where there is evidence of TBEV in ticks and evidence of TBE exposure in biosentinel animals, namely the North York Moors, Thetford and the New Forest, and is due to be published in 2026.	

Type of research	Research/Special study title	Description	Relevant links/further reading
Tick and mosquito-borne disease	CODONET, 2024-2027	The CODONET study, led by the NIHR Blood and Transplant Research Unit in Genomics in collaboration with UKHSA and NHSBT), is creating a donation bioarchive to be used for surveillance of pathogens emerging in England, including TBEV, WNV and USUV. Around 5,000 samples have been collected from consenting blood donors in geographic areas at risk from new vector-borne diseases. Samples are accompanied by demographic information, details of donors' travel history, vaccinations and animal and vector exposures. Testing is underway for molecular evidence of WNV and USUV infections and for serological evidence of TBEV exposure.	New blood donation monitoring for viruses which could be driven to the UK by climate change Design and implementation of blood donor sample bioarchives to enhance preparedness for emerging and pandemic pathogens in England

Type of research	Research/Special study title	Description	Relevant links/further reading
Tick-borne disease	LYME-UK	Prospective observational cohort study of early Lyme disease recruiting patients at participating GP sites in England and Scotland with a first-time clinical diagnosis of Lyme disease with antibiotic treatment. Samples are collected within 3 days of starting their antibiotic treatment and at 3- and 6-month follow-up visits. The study samples are archived for future use in the evaluation of new diagnostic tests and Lyme disease research. Participants also complete health questionnaires to enable analysis of outcomes up to 12 months after diagnosis and treatment. The study opened to recruitment in July 2023, and to date 29 patients have taken part.	LYME-UK – Health Research Authority
Mosquito-borne disease	AI-enabled mosquito traps, 2025-2026	UKHSA are piloting AI-enabled mosquito traps that use computer vision to automatically identify mosquitoes and generate real-time alerts. This may support invasive mosquito surveillance at key high-risk sites.	

Type of research	Research/Special study title	Description	Relevant links/further reading
Mosquito-borne disease	Modelling the extrinsic incubation period (EIP) of West Nile virus using Bayesian time delay models	This research is the first use of time delay models to characterise the temperature dependent EIP of WNV. Findings highlights the sensitivity of the WNV EIP to temperature and characterises the importance role of the variation in EIP across individual mosquitoes, particularly at low temperatures. Work is underway to apply this to UK temperatures.	Modelling the temperature dependent extrinsic incubation period of West Nile Virus using Bayesian time delay models – PubMed
Mosquito-borne disease	ARBO-UK	This study aims to gather samples and clinical data from individuals who have recently travelled from outside of the UK who have been infected by an arbovirus. Participants' clinical data will be collected on admission, including blood pressure and tests. Samples will be collected at admission and on days 30 and 180 post-infection. Participants will also complete a quality of life questionnaire at these time points.	ARBO-UK, ISRCTN – ISRCTN98882766: A study of arbovirus-infected individuals that have travelled from outside of the UK

Type of research	Research/Special study title	Description	Relevant links/further reading
Other	metagenomics Surveillance Collaboration and Analysis Programme (mSCAPE), 2025-ongoing	UKHSA with NHS and academic partners launched a pilot of the use of metagenomics for public health surveillance and pathogen analysis in 2025.	UKHSA launches new metagenomic surveillance for health security
Other	Oropouche rapid evidence gap map, 2025	A rapid evidence gap map on Oropouche virus was conducted by UKHSA on behalf of WHO. The 269 studies identified (search date: 5 June 2025) were mapped onto an interactive evidence gap map by area of research, study design and geographic region.	Oropouche virus: a rapid evidence gap map

List of acronyms

APHA – Animal Plant Health Agency
BTO – British Trust for Ornithology
CI – Confidence interval
GB – Great Britain
HTD – Hospital for Tropical Diseases
MEZE – Medical Entomology and Zoonoses Ecology
MOLIS – Modular Laboratory Information System
NHSBT – NHS Blood and Transplant
RIPL – Rare and Imported Pathogens Laboratory, UKHSA
RSPB – Royal Society for Protection of Birds
SGSS – Second Generation Surveillance System (UKHSA laboratory reporting system)
TBE – Tick-borne Encephalitis
TBEV – Tick-borne Encephalitis virus
TTE – Testing to Exclude
UKHSA – UK Health Security Agency
UKRI – UK Research and Innovation
VBD – Vector-borne diseases
WNV – West Nile virus
WWT – World Wildlife Trust
USUV – Usutu virus

Appendix A

Summary of evidence underpinning VBD risk monitoring matrix

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
Group 1		
Dengue virus	Imported human cases diagnosed in UK (1). Autochthonous cases diagnosed in multiple European countries (2).	(1A) Isolated incursions of *Aedes albopictus* and *Aedes aegypti* recorded in southern England, but no evidence of establishment (3)
Chikungunya virus	Imported human cases diagnosed in UK (1). Autochthonous cases diagnosed in multiple European countries (4).	
Zika virus	Imported human cases diagnosed in UK (1). Autochthonous cases diagnosed in France in 2019 (5).	
Yellow fever Virus	Imported human cases diagnosed in UK and Europe (1,6).	
Mayaro virus	Imported cases diagnosed in Europe (7,8) .	
Plasmodium spp (malaria)	Imported human cases diagnosed in UK and cryptic cases of malaria in UK (9). No evidence of autochthonous transmission in UK. Autochthonous cases diagnosed in multiple European countries (10).	(1B) *Anopheles* species, such as *Anopheles plumbeus,* that are capable of transmitting malaria are present and established in the UK

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
Group 2		
Equine encephalitis viruses	Imported case diagnosed in UK (11).	(0) *Culiseta melanura* mosquitoes not detected in the UK
Ross River Virus	Imported cases diagnosed in UK (RIPL). Imported cases diagnosed in Europe (12).	(0) Principal vectors (*Aedes camptorhychus, Ae. vigilax, Ae. notoscriptus, Culex annulirostris*) not present in UK.
Japanese encephalitis virus	Imported human cases diagnosed in UK and Europe (1,13)	(1A) Key *Culex (Cx. tritaenorhychus)* vectors not detected in UK
Inkoo virus	No UK cases diagnosed. Autochthonous cases diagnosed in multiple European countries (14,15)	(1A) Primary vector (*Aedes communis*) rare in UK, secondary vectors (for example *Aedes punctor*) established
Rift Valley fever virus	Imported human cases diagnosed in UK and Europe (12,16)	(1B) Key vectors such as Aedes vexans established in a few locations in England
Ťahyňa virus	No UK cases diagnosed. Autochthonous cases diagnosed in multiple European countries (12,17,18) .	(1B) *Aedes vexans* (principal vector) established in a few locations of England
Dirofilaria spp	Imported human cases only diagnosed in UK (RIPL). Autochthonous cases diagnosed in multiple European countries.	(1B) Isolated incursions of *Aedes albopictus* recorded in southern England, but no evidence of establishment. Other potential mosquito vectors (for example several native Aedes, Ochlerotatus, Anopheles, Culex, Coquillettidia species) established in UK
Sindbis virus	Imported case diagnosed in UK (RIPL). Autochthonous cases diagnosed in multiple European countries (19).	(1B) Vectors (a range of native *Aedes* species, including *Aedes cinereus*) established in UK

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
West Nile virus	Imported human cases only diagnosed in UK (RIPL). Autochthonous cases diagnosed in multiple European countries (20).	(2A) Main vectors *Culex pipiens* and *Culex modestus* established in UK. Single detection of WNV in mosquitoes in 2023 (21).
Usutu virus	Single imported UK case (RIPL/NHSBT internal data). Autochthonous cases diagnosed in multiple European countries (22)	(2A and B) Usutu virus detected in mosquitoes and birds in England (23)
Group 3		
Other spotted fever group rickettsioses (includes *R.rickettsii, R.conorii conorii, R.conorii indica* and *R.africae*) [Note 1]	Imported human cases diagnosed in UK (1,24). Autochthonous cases diagnosed in multiple European countries (25,26).	(1A) *Rhipicephalus sanguineus* vector of *R. conorii* imported on travelled and adopted dogs in UK (27,28) . Not currently established. American *Dermacentor* and African *Ambylomma* (vectors of *R. rickettsii, R. africae*) not present in UK
Crimean-Congo Haemorrhagic Fever (CCHF) virus	Imported human cases diagnosed in UK (29) . Autochthonous cases diagnosed in multiple European countries (30).	(1A) *Hyalomma marginatum* detected but not established in UK, frequently imported on birds as immature ticks, occasional reports of adults currently rare. Pathogen not detected in vector
Rickettsia raoultii	Single confirmed UK case – likely imported (RIPL). Autochthonous cases diagnosed in multiple European countries (25,31)	(2A) Pathogen has been detected in *D. reticulatus,* which has a limited UK distribution in Wales, Devon and Essex (32)
Rickettsia massiliae	Limited cases in Europe (25,31).	(2A) Pathogen has been detected in *Haemaphysalis punctata*, which had a limited UK distribution in Sussex, Kent and Hampshire (33).
Rickettsia helvetica	Seroepidemiological studies in humans suggests infection in Europe (25,31)	(2A) *Ixodes ricinus* established in UK, and pathogen present in vector. *Rickettsia helvetica* has widespread

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
		distribution in vector within the UK, including parts of South West England and northern Scotland. Also detected in *D. reticulatus*, which has a limited UK distribution (Wales, Devon, Essex) (34)
Borrelia miyamotoi (Tick-borne relapsing fever)	No UK cases diagnosed. Autochthonous cases diagnosed in multiple European countries (35–38).	*(*2A*) Ixodes ricinus* established in UK and pathogen present in vector
Spiroplasma ixodetis	Autochthonous cases diagnosed in multiple European countries (39,40)	(2A) *Ixodes ricinus* established in UK and pathogen present in vector
Neoehrlichoa milkurensis	Autochthonous cases diagnosed in a number of European countries (41–44)	*(1B) Ixodes ricinus* established in UK
Babesia divergens	Two autochthonous cases diagnosed in UK (45). Autochthonous cases diagnosed in multiple European countries (46)	(3) *Ixodes ricinus* established in UK and pathogen present in vector
Francisella tularensis (tularaemia)	Imported human cases diagnosed in UK. Probable UK acquired case in north-west England in 2023 (47). Autochthonous cases diagnosed in multiple European countries (48).	Francisella tularensis can be transmitted in a number of ways, including ticks, mosquito, animal contact, ingestion, airborne. Some competent vector species present in UK, but pathogen not detected in vectors to date.
Anaplasma phagocytophilum	UK acquired cases diagnosed (49). Human cases detected in multiple European countries (50,51)	(3) *Ixodes ricinus* established in UK. *Anaplasma phagocytophilum* has widespread distribution in vector in UK
Louping ill virus	Probable UK cases diagnosed (52,53)	(3) *Ixodes ricinus* established. Pathogen endemic in vector.
Tick-borne encephalitis virus	Six probable or confirmed autochthonous cases (European subtype) since	(3) *Ixodes ricinus* established in UK and pathogen detected in vector and deer in several regions of UK

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
	2019 in UK (54,55) . Autochthonous cases diagnosed in multiple European countries (56).	
Borrelia burgdorferi (Lyme disease)	Endemic across UK and Europe (57).	(4) *Ixodes ricinus* established in UK and pathogen present in vector
Group 4		
Oropouche virus	3 imported cases diagnosed in UK (58).	(0) Main vector species not present in UK
Leishmania spp (leishmaniasis)	Imported cases diagnosed in UK (59). Autochthonous cases of cutaneous and visceral leishmaniasis diagnosed in multiple European countries (60).	(0) Vector not present in UK (although expanding range in northern Europe)
Trypanosoma spp	Imported cases in UK and Europe (61–63).	(0) Vector not present in UK
Onchocerca volvulus	Imported cases in UK (64) and Europe (65)	(0) Vector not present in UK
Wuchereria bancrofti	Imported cases in UK (66)	(0) Vector not present in UK
Brugia spp	Imported cases in UK (HDT)	(0) Vector not present in UK
Loa loa	Imported cases in UK (67) and Europe (68)	(0) Vector not present in UK
Mansonella spp	Imported cases in UK and Europe (69,70)	(0) Vector not present in UK
Sand fly fever viruses	Imported cases diagnosed in UK (71). Autochthonous cases diagnosed in multiple European countries (72)	(0) Vector not present in UK
Orientia tsutsugamushi	Imported cases diagnosed in UK (73). Imported cases diagnosed in Europe (74).	Vector (*Leptotrombidium spp*) not present in UK
Rickettsia typhi (Murine typhus)	Imported cases diagnosed in UK (24). Autochthonous	(1B) *Ctenocephalides felis* fleas established in UK

Pathogen	Evidence for inclusion in VBD risk monitoring matrix	Evidence for position on VBD risk monitoring matrix (brackets indicate assigned level)
	cases diagnosed in multiple European countries (31)	
Borrelia recurrentis (Louse-borne relapsing fever)	Imported cases diagnosed in UK. Autochthonous cases diagnosed in European countries (75).	(1B) Body lice (*Pediculus humanus corporis)* established in UK
Rickettsia prowazekii (Epidemic typhus)	Not reported in UK in 21st century (24)	(1B) Body lice (*Pediculus humanus corporis)* established in UK
Thelazia callipaeda	Autochthonous cases diagnosed in Europe (76,77)	(1B) Phortica variegata established in the UK
Babesia venatorum	Autochthonous cases diagnosed in Europe (46)	(1B) *Ixodes ricinus* established in UK and pathogen present in vector
Rickettsia felis (Flea-borne spotted fever)	Autochthonous cases diagnosed in Europe (31,78)	(2A) *Rickettsia felis* identified in vector (for example*Ctenocephalides felis*) in multiple studies

Note 1: Not *R. massiliae*, *R. raoultii*, *R. helvetica* or *R. felis*

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Appendix B. Overview of vector surveillance

Vector surveillance involves the monitoring of ticks, mosquitoes and other vectors to map species distribution and seasonality, detect non-native species in England, and monitor nuisance biting. Vectors can also be screened for presence and prevalence of pathogens.

Vectors can be categorised as native species, non-native or invasive species. There are 36 recorded species of mosquitoes in the UK and 20 species of native ticks. Non-native species refer to those that have been introduced outside their native range, and invasive non-native species are those that have the ability to spread causing damage to the environment, economy, health or the way we live.

UKHSA coordinates a number of vector surveillance schemes, including citizen science and active vector surveillance schemes as summarised in Table 9. Vector surveillance is delivered in collaboration with Local Authorities, nature reserve wardens, the Royal Society for the Protection of Birds (RSPB), the British Trust for Ornithology (BTO), the Wildfowl and Wetlands Trust (WWT), the Wildlife Trust, other volunteers and the public.

Maps of mosquito surveillance sites and locations of samples submitted by citizens for selected schemes are presented in (Figure 17 to Figure 20 below).

APHA also undertakes vector surveillance activities, through several collaborative research programmes including Vector-borne RADAR (VB-RADAR) (mosquitoes) and TickTools (ticks).

UKHSA and APHA vector surveillance activities are summarised in Table 9 (below).

Table 9. Overview of vector surveillance in UK, 2025

Scheme	Established	Aims	Sites	Coverage	Survey period	Further reading
Tick surveillance schemes						
Tick Surveillance Scheme	2005	To map and monitor the distribution of native tick species, tick numbers, seasonal activity, and host associations across the UK To detect, identify and monitor frequency of imported tick species In 2004, a new tick bite indicator was developed to identify areas of high human tick exposure. This is calculated using TSS records of *Ixodes ricinus* on humans only per 100,000 human population per local authority district over a 5-year period.	UK wide tick submissions from public, GPs, veterinary surgeons, wildlife charities	Most submissions are from South-West and South-East England. 600-1,150 submissions per annum since 2013.	Continuous. Most submissions received in late Spring and early Summer	Tick Surveillance Scheme; Tick Surveillance in Great Britain Mapping ticks (Acari: Argasidae, Ixodidae) and informing local public action: Insights from the United Kingdom Tick Surveillance Scheme (2021-2024) – PubMed
National Tick Survey	2014	To provide a snapshot of current tick activity and pathogen circulation in the UK tick population	England and Wales	40 locations	May or June	Tick surveys

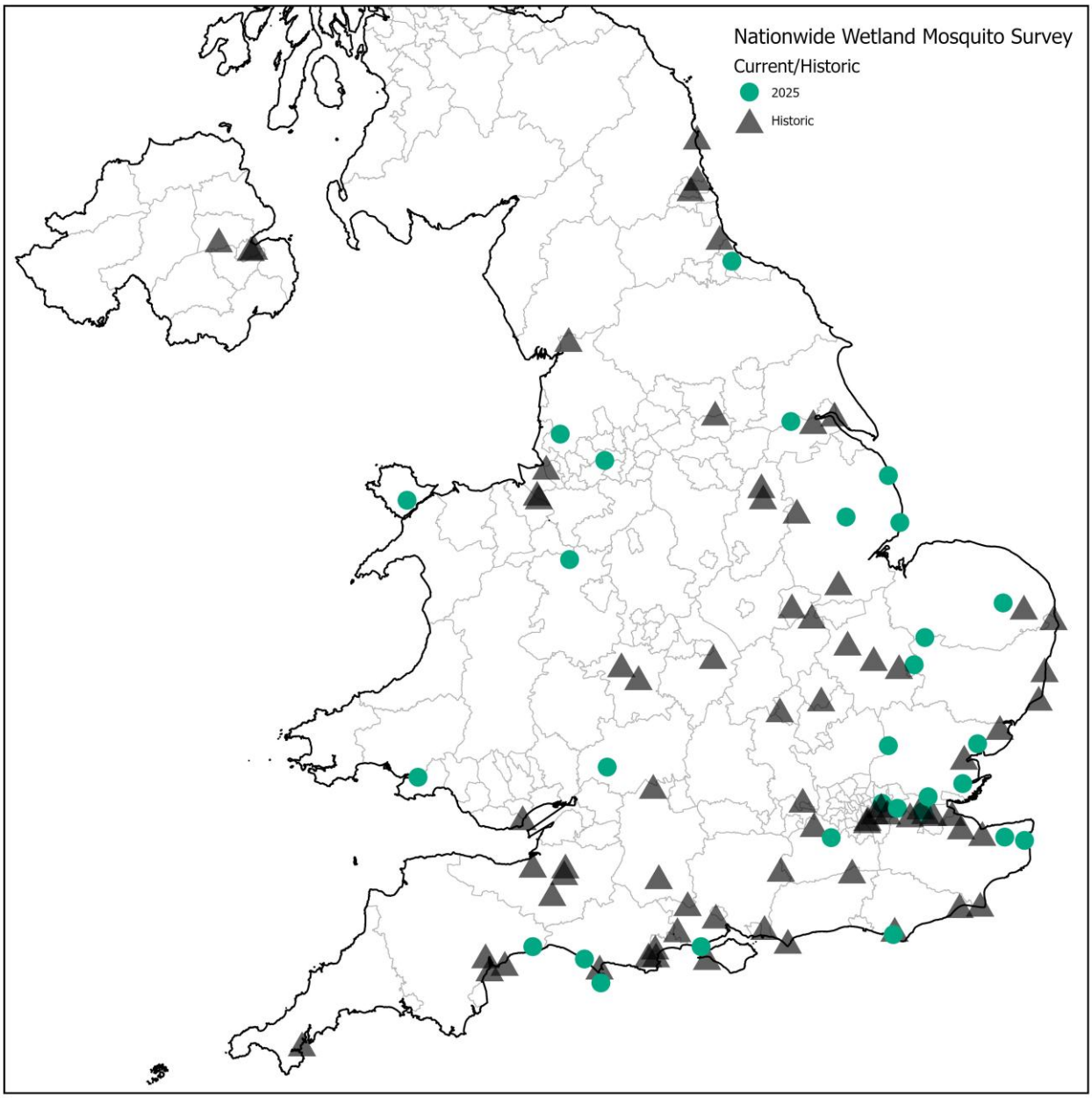
Scheme	Established	Aims	Sites	Coverage	Survey period	Further reading
Red sheep tick (*Haemaphysalis punctata*) surveillance	2010	To monitor species distribution and estimate prevalence of pathogens	Known endemic regions of England	Mainly South East England	May	Red sheep tick surveillance Has the red sheep tick, *Haemaphysalis punctata*, recently expanded its range in England? – Medlock – 2018 – Medical and Veterinary Entomology – Wiley Online Library

Scheme	Established	Aims	Sites	Coverage	Survey period	Further reading
Ornate cow tick (*Dermacentor reticulatus*) surveillance	2010	To monitor activity of the ornate cow tick and estimate prevalence of pathogens	Known endemic regions of England and Wales	Devon, Essex and Wales	February or March	Ornate cow tick surveillance Distribution of the tick *Dermacentor reticulatus* in the United Kingdom – MEDLOCK – 2017 – Medical and Veterinary Entomology - Wiley Online Library
Mosquito surveillance schemes						
Nationwide Wetland Mosquito Survey	2010	To map and monitor presence and abundance of native mosquito species, to detect novel species. Samples screened for arboviruses from 2023	Wetlands, parks and nature reserves in England	30 localities in 2025, with a total of 98 sites involved since 2010	1 June to 31 October, fortnightly	Nationwide mosquito survey

Scheme	Established	Aims	Sites	Coverage	Survey period	Further reading
Invasive mosquito surveillance	2010	To detect invasive mosquitoes that is *Aedes albopictus* and *Aedes aegypti*	Seaports, airports, highway transport hubs, international railway stations, service stations, and high-risk urban centres	Network of over 1,500 traps in 110 localities in 2025	May to October, ovitraps checked fortnightly	Invasive mosquito surveillance from 2020 to 2024
Mosquito recording scheme	2013	A forum for environmental health officers, pest controllers and the public to report nuisance and invasive mosquito species	UK wide	UK wide	Continuous	Mosquito recording scheme
Snapshot Wetland Mosquito Survey	2024	To extend mosquito surveillance and strengthen public engagement. Samples screened for WNV and Usutu virus	Wetlands in England	Within every 50km^2 grid square in England	01 July to 30 September, traps run 2-3 times	Mosquito Map | Vector-Borne Radar

Scheme	Established	Aims	Sites	Coverage	Survey period	Further reading
Vector-Borne RADAR (VB-RADAR) research project	2023-March 2026	To understand the emergence, transmission and establishment of mosquito-borne flaviviruses in the UK, where wild birds are a primary host.	Arrival routes of WNV infected birds in Southeast and parts of South-West England		May to October, 2023-2025	Vector-Borne RADAR | Mosquito-borne viral diseases of wild birds See also page 30
TickTools	April 2023-December 2026	To development tools to monitor and control tick-borne diseases of humans and livestock, including metagenomics to investigate pathogen diversity within the tick.	UK wide: including sites in England, Wales and Scotland.		March to October	Investigating-british-ticks-for-viral-threat (APHA blog)

Figure 17. Map showing Nationwide Wetland Mosquito Survey sites



Grey triangles represent sites run between 2010 and 2024, teal circles represent sites run in 2025

Figure 18. Locations of submissions to the Mosquito Recording Scheme in the UK, with each point representing at least one report, 2013 to 2025

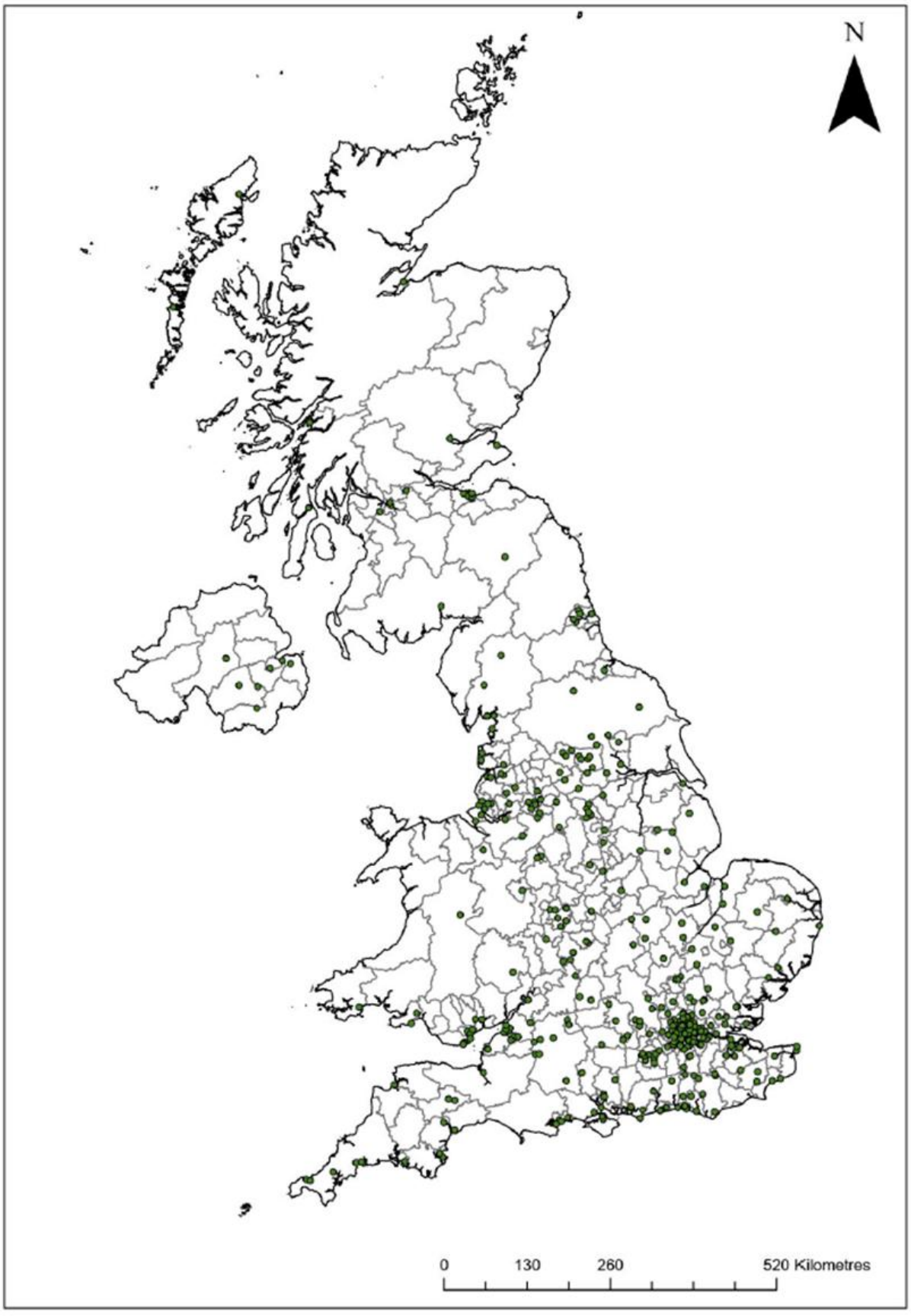


Figure 19. All locations of invasive mosquito traps and invasive mosquito detections since the first detection of *Aedes albopictus* in 2016

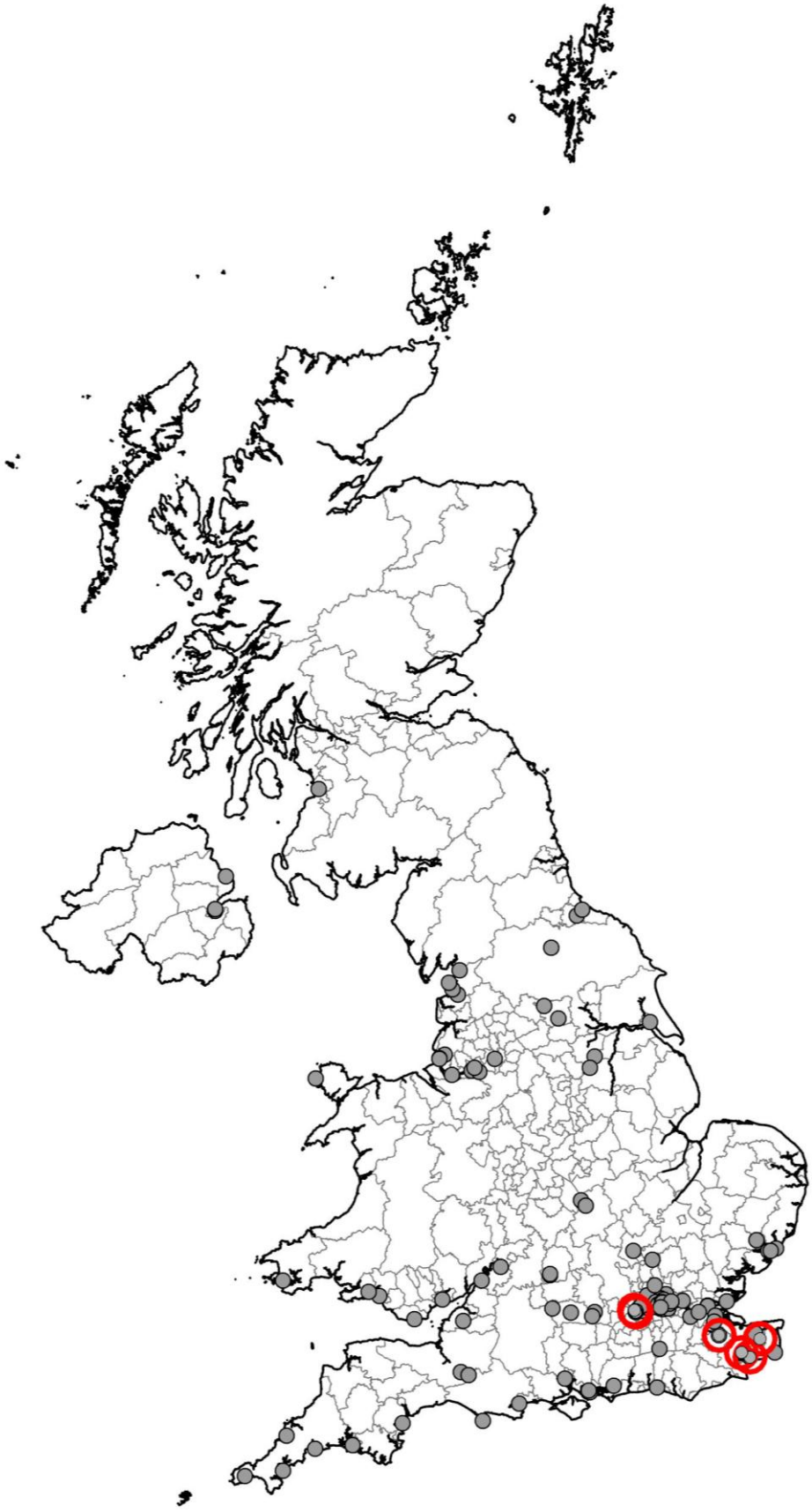
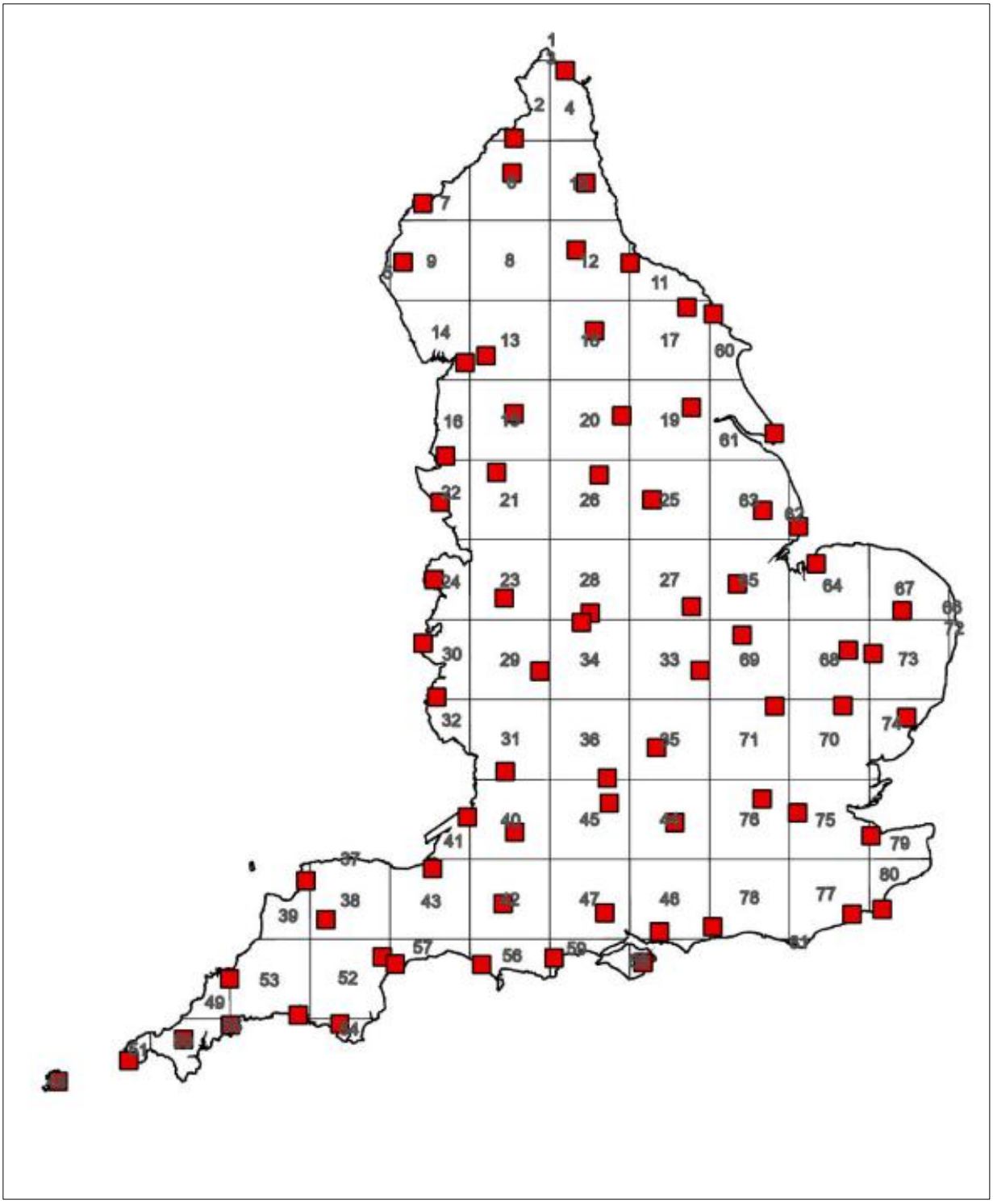


Figure 20. Map showing location of all Snapshot traps (combined 2024 and 2025)



Appendix C. Overview of animal surveillance

Animal surveillance of VBDs in England and Wales focuses on the detection of pathogens circulating in domestic animals, wildlife and sentinel species which can signal the presence or emergence of vector-borne pathogens in the environment.

It includes routine case-based surveillance to monitor laboratory confirmed infection numbers, active surveillance studies, and event-based surveillance. A summary of the current surveillance activities for each type of animal surveillance is presented in this section.

Case-based surveillance

APHA carries out disease surveillance to identify new and re-emerging threats to animal and public health in England, Scotland and Wales through:

- statutory surveillance, by monitoring and collecting notifiable and reportable disease information (notifiable VBDs in animals include West Nile virus, Rift Valley fever virus, Bluetongue virus, African horse sickness, and Lumpy skin disease virus)
- scanning surveillance, through voluntary submission and collection of information by practicing veterinary surgeons

APHA coordinates several animal surveillance schemes including equine, livestock (including farm animals) and wildlife surveillance (59). APHA's Surveillance Intelligence Unit analyses and publishes surveillance data from these schemes as part of monthly animal surveillance reports and on disease dashboards.

APHA holds the animal health UK National Reference Laboratory (NRL) for mosquito-borne viruses such as WNV and Rift Valley Fever virus (RVFV). APHA undertake diagnostics and monitoring of endemic livestock diseases and screening for new and emerging vector-borne disease in livestock, companion animals (pets) and wildlife.

As APHA report data for Great Britain, data presented in this report cover Scotland and Wales in addition to England.

Active surveillance studies

APHA, UKHSA and collaborating organisations conduct active surveillance studies to further understand the epidemiology of certain diseases, including Lyme disease, TBEV, WNV and USUV.

APHA led on the Vector-Borne RADAR research project (2023 to March 2026) with UKHSA, the Institute of Zoology, and British Ornithology Trust (BTO) to enhance surveillance of zoonotic mosquito-borne viruses of wild birds in the United Kingdom (6).

Since 2018, UKHSA has conducted large-scale monitoring of tick-borne orthoflaviviruses in 4 deer species and ticks. This scheme provided the first evidence of TBEV in the UK in 2019, and indicated that exposure of deer to TBEV is highly focal and limited to few areas in Great Britain (45). Subsequent tick surveillance and testing in the same areas identified TBEV in local tick populations and was used to map the distribution of the virus and monitor changes over time. This sampling methodology can provide a sensitive and cost-effective means of conducting large-scale surveillance for pathogens that may be difficult to detect through human or vector-only monitoring. The resulting biobank supports ongoing research projects and permits rapid mobilisation when new threats emerge. For example, during the COVID-19 pandemic there were reports of widespread infection in white-tailed deer in North America and UKHSA rapidly tested archived deer samples to demonstrate no evidence of SARS-CoV-2 exposure in European deer species (60).

Event based surveillance

APHA conduct horizon scanning for diseases of animals, including VBDs and will raise signals of note to the HAIRS group and VBD horizon scanning group for consideration.

Table 10 (below) summarises animal surveillance schemes related to vector-borne diseases.

Table 10. Animal surveillance schemes for vector-borne diseases

Type of animal surveillance	Description	Relevant links/further reading
Equine surveillance	Private Veterinary Surgeons (PVS) can submit samples for West Nile fever (WNF) testing directly to Weybridge without an APHA investigation through the Test To Exclude (TTE) West Nile Virus in horses. The TTE scheme can only be used when disease is very low on the differential list and not suspected, but the practising veterinary surgeon wants to exclude disease as a differential diagnosis. If WNF is considered a probable diagnosis or if another notifiable disease is suspected, this must be reported to APHA immediately.	Test to exclude West Nile Virus in horses Equine Quarterly Disease Surveillance Report (EIDS)
Livestock surveillance	APHA collects data from carrying out diagnostic tests and post-mortem examinations on farm animals including cattle, pigs, sheep and goats, poultry and gamebirds, and other farmed mammals. Submissions to the GB veterinary diagnostic network are tested for a range of infections, including a number of tick-borne diseases in livestock that is louping ill virus (LIV), tick-borne fever, tick pyaemia and babesiosis.	Sheep Dashboard | Tableau Public Great Britain disease surveillance and emerging threats reports

Type of animal surveillance	Description	Relevant links/further reading
Wildlife surveillance	Dead wild bird surveillance Passive surveillance of dead wild birds for WNV and USUV is undertaken by the Arbovirus National Reference Laboratory (NRL) at APHA, involving molecular testing of brain and kidney samples from target bird species. Diseases of Wildlife Scheme - surveillance for mosquito-borne viruses in birds This focuses on orthoflaviviruses where wild birds are a primary host. Brain and kidney tissues from wild birds collected by APHA regional laboratories or Scotland's Rural College are combined with submissions through the Garden Wildlife Health project (coordinated by the Institute of Zoology [IoZ]) for molecular screening undertaken by APHA.	Wildlife: GB disease surveillance and emerging threats reports Great Britain Wildlife Health Partnership Annual Report for 2024
Vector-Borne RADAR	A UKRI and Defra funded research project from 2023-2026 to understand the emergence, transmission and establishment of mosquito-borne flaviviruses in the UK, where wild birds are a primary host. The project was a collaboration between APHA, BTO, IoZ and UKHSA and undertook active surveillance in mosquitoes and birds combined with passive surveillance of passerines through engagement with wildlife rescue centres and national general wildlife health surveillance programmes integrated with population monitoring schemes. VB-RADAR identified an increasing known range of Usutu virus in mosquitoes and birds in southern England, and the first detection of WNV RNA in UK mosquitoes.	Vector-Borne RADAR | Mosquito-borne viral diseases of wild birds

Appendix D. Overview of human surveillance

Human surveillance of VBDs in England includes routine case-based surveillance to monitor laboratory confirmed infection numbers, active serological surveillance studies, and event-based surveillance. Additional data sources include UK blood service testing. A summary of the current surveillance activities for each type of human surveillance is presented in this section.

There are a number of routinely published reports on the human surveillance of some common VBDs including:

- Malaria in the UK: annual reports
- Imported malaria in the UK: statistics
- Travel-associated infections report including dengue, chikungunya, Japanese encephalitis, yellow fever, Zika virus, rickettsial infections and Oropouche virus
- Common animal-associated infections report which until 2024 included data on Lyme disease – from 2025, the Lyme disease data will be published in this annual report as found in the Tick-borne pathogen (Group 3) – Lyme Disease section

Case-based surveillance

Laboratory diagnostic services for VBDs are available through the Rare and Imported Pathogens Laboratory (RIPL), the Malaria Reference Laboratory (MRL) and the Hospital for Tropical Diseases (HTD) (61 to 63). Additionally, some diagnostic services are provided by NHS and private laboratories, in which case data is made available to UKHSA via the Second-Generation Surveillance System (SGSS) (64).

Fourteen of the VBD risk monitoring matrix pathogens are notifiable causative agents under the Health Protection (Notification) Regulations 2010 in England, meaning laboratories must report any confirmed case to UKHSA (65). In addition, typhus, yellow fever and acute encephalitis – a possible clinical presentation of some VBDs, are also notifiable infectious diseases under the regulations (66).

There are diagnostic tests available for all 33 pathogen or pathogen groups included in the VBD risk monitoring matrix, including: 24 with accredited tests, 6 with development assays and 3 with research use only assays (see Table 11 below). Research to support additional diagnostic approaches for VBDs is underway, including development of metagenomic approaches for testing, as described in the Research and Special Studies section.

Table 11. Summary table of notifiable status, and diagnostic test provision for pathogens in VBD risk monitoring matrix

Pathogen	Notifiable causative agent	Laboratory	Assay within current UKAS scope*	Developmental assays†	Research Use Only (RUO) assays‡
Anaplasma phagocytophilum	-	RIPL	Yes (serology)	Yes (PCR)	
Babesia divergens‡	-	MRL/HTD	Yes	Yes	
Borrelia burgdorferi (Lyme disease)	Yes	RIPL	Yes	-	
Borrelia miyamotoi	Yes	RIPL	Yes (pan Borrelia PCR)	-	Yes (species specific PCR)
Borrelia recurrentis	Yes	RIPL	Yes (pan Borrelia PCR)	-	Yes (species specific PCR)
Crimean-Congo haemorrhagic fever virus	Yes	RIPL	Yes	-	
Chikungunya virus	Yes	RIPL	Yes	-	
Dengue virus	Yes	RIPL	Yes	-	
Dirofilaria spp.‡	-	MRL/HTD	Yes	-	
Equine encephalitis viruses	-	RIPL	-	Yes	
Francisella tularensis spp. (tularaemia)	Yes	RIPL	Yes	-	
Filaria‡	-	MRL/HTD	Yes	-	
Inkoo virus	-	RIPL	-	-	Yes
Japanese encephalitis virus	-	RIPL	Yes	-	

Pathogen	Notifiable causative agent	Laboratory	Assay within current UKAS scope*	Developmental assays†	Research Use Only (RUO) assays‡
Leishmania spp. (leishmaniasis) ‡	-	MRL/HTD	Yes	-	
Louping ill virus§	-	RIPL	Yes (TBE group serology)	-	Yes (LIV specific PCR)
Mayaro virus	-	RIPL	-	Yes	
Orientia tsutsugamushi (Rickettsiaceae family)‖	Yes	RIPL	Yes	-	
Oropouche virus	-	RIPL	-	Yes (PCR)	Yes (serology)
Plasmodium spp. (malaria)	Yes	MRL/HTD	Yes	-	
Rickettsia spp. *(Rickettsiaceae* family) ‖	Yes	RIPL	Yes	-	
Rift Valley fever virus	Yes	RIPL	-	Yes	
Ross River virus	-	RIPL	-	Yes	
Sandfly fever viruses	-	RIPL	Yes	-	
Sindbis virus	-	RIPL	-	Yes	
Ťahyňa virus	-	RIPL	-	-	Yes
Thelazia callipaeda‡	-	MRL/HTD	Yes	-	
Tick-borne encephalitis virus§	Yes	RIPL	Yes	-	
Trypanosoma spp.‡	-	MRL/HTD	Yes	-	
Usutu virus	-	RIPL	-	-	Yes
West Nile virus	Yes	RIPL	Yes	-	
Yellow fever virus	Yes	RIPL	Yes	-	

Pathogen	Notifiable causative agent	Laboratory	Assay within current UKAS scope*	Developmental assays†	Research Use Only (RUO) assays‡
Zika virus	-	RIPL	Yes	-	

(MRL = Malaria Reference Laboratory; HTD=Hospital for Tropical Diseases; RIPL = Rare and Imported Pathogens Laboratory, UKHSA; UKAS=United Kingdom Accreditation Service)

*Tests within the scope of current UKAS accreditation for the testing laboratory or have otherwise undergone full internal validation
† Tests which are not included in the laboratory's UKAS scope and for which there has been limited technical validation data and/or which may not be performed regularly
‡ RUO testing may be performed by RIPL, or by other UKHSA Porton laboratories at the request of RIPL
‡ Pathogens where data was not available to report for 2025
§ Louping ill and Tick-borne encephalitis are currently differentiated using molecular methods, infections diagnosed using serological assays without molecular confirmation are reported as probable cases of Tick-borne encephalitis complex and cannot be differentiated further.
‖ Reported as a group under 'Rickettsial infections'

An overall summary of VBD cases in humans in England in 2025 is reported in the Summary of human cases section. The report focuses on reporting data for pathogens from each category of the VBD risk monitoring matrix where there were detections reported through human, vector or animal surveillance in 2025, where data is available. Cases were defined for surveillance purposes as listed in Table 12 (below). For all cases, specimen collection date was used where available, and laboratory receipt date if not, to conduct analysis.

Table 12. Case definitions for pathogen surveillance reporting*

Disease	Case definitions
Chikungunya, dengue, Oropouche virus disease, and Zika virus disease	• Confirmed: molecular detection by PCR; IgG seroconversion between acute and convalescent samples • Probable: IgM and IgG positive and compatible clinical syndrome Please note that there is no serological testing currently available for Oropouche virus and testing is by PCR only
Lyme disease	• Acute Lyme disease cases are those with significant serological IgM response and compatible clinical details (excluding neurological symptoms) or those with positive serology and erythema migrans. Cases with serology compatible with acute infection but where no clinical information is provided, are also categorised as acute Lyme disease cases

Disease	Case definitions
	• Acute neurological cases are those with positive serology and any compatible neurological symptoms • Longstanding Lyme disease cases are those with a significant IgG response A significant IgG response may reflect past exposure or past infection with *Borrelia*, or a non-acute presentation of Lyme disease, and does not imply chronic, active infection. Antibodies may persist for several years despite treatment and resolution of disease and this does not indicate ongoing infections Note that while a pan-Borrelia PCR is available, it is only used occasionally in suspected Lyme arthritis, neuroborreliosis or skin disease. PCR confirmation of Lyme disease is exceptionally rare.
Tick-borne encephalitis (TBE) complex	• Confirmed: molecular detection by PCR of TBEV RNA in blood, urine or cerebrospinal fluid (CSF); significant rise or seroconversion for TBEV IgG in paired serum samples • Probable: rise in TBEV antibody titre in paired serum samples but not meeting threshold for confirmed; positive IgM and IgG TBEV antibody in single serum sample; evidence of intrathecal antibody production of IgG to TBEV Differentiation between LIV and TBEV is based on an RUO LIV assay and/or sequencing and is often not possible
West Nile virus (WNV)†	• Confirmed case: molecular detection by PCR of WNV RNA in blood, urine or cerebrospinal fluid (CSF) • Probable case: A compatible clinical syndrome with serological evidence (seroconversion to WNV IgG over time or strongly positive IgM and IgG in late acute setting), interpreted in the context of other flavivirus serology results and without another clear explanation for seropositivity

* Note that for an individual case, additional clinical or exposure data may be used in interpreting laboratory results in order to advise on optimal patient management and definitions given here are for surveillance reporting only

† For USUV, diagnosis is currently based on RNA detection only (Table 11)

Active surveillance studies

Seroprevalence studies aim to determine the proportion of individuals in a population who have antibodies against a specific pathogen. This indicates past exposure to the pathogen, regardless of whether the exposure caused clinical symptoms. Serological surveillance can be conducted in particular groups, for example recreational or occupational groups who may be at increased risk of exposure.

UKHSA, NHSBT and collaborating organisations conduct active surveillance studies to further understanding of epidemiology of certain diseases including Lyme disease, TBE, WNV and USUV.

Event-based surveillance

UKHSA conduct event-based surveillance to detect, assess and investigate potential health risks related to emerging infections including VBDs. Event signals can include reports, media information and any other information reported about health events online. Episodes of human infection or events are reported on UKHSA's Outbreaks under monitoring webpage. These signals feed into VBD horizon scanning and the Human and Animal Infection Risk Surveillance (HAIRS) group for risk assessment as described in the One Health VBD Coordination section.

The joint NHSBT UKHSA epidemiology unit performs horizon scanning in close association with UKHSA colleagues to provide Emerging Infection Reports for risk assessment by Joint UK Blood Transfusion and Tissue Transplantation Services Professional Advisory Committee's (JPAC) JPAC standing advisory committee on Transfusion Transmitted Infections (SACTTI) to help ensure the Geographical Disease Risk Index is up to date.

Other data sources for VBD human surveillance

UK blood service testing

Blood safety risk from VBD is mitigated by appropriate deferral and testing guided by donor health and travel history and the Geographical Disease Risk Index (GDRI) maintained by the Joint United Kingdom (UK) Blood Transfusion and Tissue Transplantation Services Professional Advisory Committee (JPAC). Donors are asked to wait for 28-days after returning from chikungunya, dengue, yellow fever or Zika virus disease affected areas. Where testing is available, donors are asked to wait for at least 4-months after returning from a malaria or *Trypanosoma cruzi* (Chagas disease) affected area before donating with an additional test. Donors returning from West Nile virus (WNV)-affected areas are deferred for 28 days unless testing is available.

Since 2012, NHS Blood and Transplant (NHSBT) has performed nucleic acid testing for WNV ribonucleic acid (RNA) in apparently healthy donors returning within 28 days from WNV-affected areas between 1 May to 30 November, to allow safe release of donations. The testing is performed in pools of 6 and may also demonstrate reactivity with viruses related to WNV.

Donors at risk of malaria are screened for malarial antibodies, and reactive donations have confirmatory malarial antibody and PCR testing performed. Evaluation of new molecular methods for routine malaria donor screening is underway.

Results of a blood donor travel survey will help to inform travel patterns and blood service planning for spread of arboviruses.

Insect bite metrics

UKHSA's Real-time Syndromic Surveillance Team monitors syndromic data on episodes of insect bites collected through anonymised NHS health data. Insect bite syndromic indicators are published in routine weekly syndromic surveillance bulletins during warmer weather to coincide with the UKHSA Heat Health Watch (67).

The Royal College of General Practitioners (RCGP) publishes weekly reports including a metrics on infected insect bites (68).

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UK Health Security Agency (UKHSA) prevents, prepares for and responds to infectious diseases, and environmental hazards, to keep all our communities safe, save lives and protect livelihoods. We provide scientific and operational leadership, working with local, national and international partners to protect the public's health and build the nation's health security capability.

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