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SCIENTIFIC REPORT

Identification and mapping of potential and highly likely vectors for selected vector-borne diseases in the EU and neighbouring countries

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The declarations of interest of all scientific experts active in EFSA's work are available at https://open.efsa.europa.eu/experts.

Abstract

This report addresses Term of Reference 1.2 by providing a comprehensive knowledge-mapping of arthropod vector species competent to transmit selected vector-borne diseases (VBDs) including VBDs listed under Regulation (EU) 2016/429 and Regulation (EU) 2020/687, as well as additional non-listed pathogens with potential epidemiological relevance. The objective was to update and consolidate evidence on biological vector competence, mechanical transmission and vector geographic distribution for 25 selected VBDs in support of subsequent EU-level risk-assessment activities. Biological vector competence was assessed through two systematic literature reviews (SLRs), one focusing on pathogen detection in field-collected arthropods and the other on laboratory infection and transmission studies, while mechanical transmission was evaluated through a narrative literature review using predefined hierarchical criteria to classify vector likelihood. Geographic distribution data were updated via a third dedicated living SLR feeding into the VectorNet mapping workflow. Evidence from all reviews was synthesised, and expert judgement was applied where necessary to address data gaps. Literature reviews were conducted at global level, whereas geographic distribution maps were provided for vector species occurring in the EU and neighbouring countries, where available. The SLRs identified arthropod species with a highly likely biological vector competence for eight pathogens, supported by convergent field and laboratory evidence, and potential biological vectors for a further 16 pathogens based on evidence from either field or laboratory studies; for all these pathogens, at least one relevant vector species occurs in the EU or neighbouring regions and EU-level distribution maps are available. For a limited number of pathogens (5), no eligible biological vectors occurring in the EU were identified and expert judgement was therefore applied to identify plausible vectors. For mechanical transmission, the narrative review identified three pathogens associated with highly likely and four pathogens with potential mechanical vectors occurring in the EU or neighbouring countries, while expert judgement was required for two pathogens. Although EU-level distribution maps are not available for mechanically transmitted vectors, their widespread occurrence means geographic distribution is not considered a limiting factor for risk assessment. Evidence gaps remain for several pathogen–vector associations and will be further considered in subsequent assessments.

KEYWORDS

arthropods, biological transmission, geographic distribution, mechanical transmission, risk assessment, systematic literature review, vector competence, vector-borne diseases

CONTENTS

SUMMARY

Objective

This report addresses Term of Reference (TOR) 1.2 by providing a comprehensive knowledge-mapping of vector species competent to transmit vector-borne diseases (VBDs) listed under Regulation (EU) 2016/429 and Regulation (EU) 2020/687 as well as additional non-listed VBDs with potential epidemiological relevance. The aim was to update and consolidate evidence on biological vector competence, mechanical pathogen transmission, and vector geographic distribution for 25 selected VBDs, supporting subsequent risk-assessment activities.

Methodology

To achieve this objective, three complementary review approaches were applied. Two systematic literature reviews (SLRs) assessed biological vector competence, one focusing on pathogen detection in field-collected specimens and the other on laboratory infection and transmission studies. A narrative literature review evaluated mechanical transmission, categorising evidence into hierarchical levels and assigning vector likelihood accordingly. Additionally, geographic distribution data were updated via a dedicated living SLR feeding into the VectorNet mapping workflow. Evidence from all reviews was synthesised, and expert judgement applied where necessary to fill gaps and identify vector species relevant for risk assessment. Whereas the literature reviews were carried out on a worldwide level, maps displaying the geographic distribution were provided for species present in the EU and neighbouring countries only, when available.

Classification of vector likelihood

Vector species were classified according to the strength and type of evidence supporting their role in pathogen transmission. For biological transmission, species were considered highly likely biological vectors when both pathogen detection in field-collected specimens (in particular in non-blood-engorged specimens) and successful laboratory infection or transmission were demonstrated, whereas species meeting only one of these criteria were classified as potential biological vectors. A highly likely mechanical vector was defined as a species for which experimental transmission to a susceptible host has been demonstrated under laboratory conditions and for which pathogen detection has been reported in field-collected individuals. A potential mechanical vector was defined as a species lacking experimental confirmation of transmission but supported by at least one line of evidence, including pathogen detection in field-collected individuals, epidemiological associations with disease occurrence, or circumstantial evidence only.

Results

Biological vector transmission

The SLR identified arthropod species with a highly likely vector competence for eight pathogens, based on worldwide evidence from both field observations and laboratory studies. For all these pathogens, at least one competent vector species occurs in the EU or neighbouring countries, and EU-level vector distribution maps are available for use in the risk assessment. These pathogens are bluetongue virus (BTV), *Borrelia burgdorferi* sensu lato, Japanese encephalitis virus (JEV), *Leishmania infantum*, Rift Valley fever virus (RVFV), Schmallenberg virus (SBV), tick-borne encephalitis virus (TBEV) and West Nile virus (WNV).

The SLR also identified arthropod species with a potential vector competence for 16 pathogens, based on worldwide evidence from either field or laboratory studies. For all of these pathogens, vector species occur in the EU or neighbouring countries, and EU-level vector distribution maps are available for use in the risk assessment. These pathogens are: African horse sickness virus (AHSV), Akabane virus, BTV, *Borrelia burgdorferi* sensu lato, Cache Valley virus, Crimean–Congo haemorrhagic fever virus (CCHFV), epizootic haemorrhagic disease virus (EHDV), JEV, *Leishmania infantum*, RVFV, SBV, St. Louis encephalitis virus (SLEV), TBEV, Venezuelan equine encephalitis virus (VEEV), WNV and Western equine encephalitis virus (WEEV).

The SLR did not identify any highly likely or potential biological vector species for bovine ephemeral fever virus, *Coxiella burnetii*, Eastern equine encephalitis virus (EEEV), Shuni virus and vesicular stomatitis virus occurring in the EU or neighbouring countries. For these pathogens, expert judgement was used to identify potential vector species that could plausibly occur in the EU and support the subsequent risk assessment.

Mechanical vector transmission

The narrative literature review identified mechanical vector species occurring in the EU or neighbouring countries that were classified as having a highly likely competence status for *Besnoitia besnoiti (B. besnoiti)*, lumpy skin disease virus (LSDV) and *Trypanosoma vivax* (*T. vivax*). In addition, vector species with a potential competence status and occurring in the EU or neighbouring countries were identified for *B. besnoiti*, equine infectious anaemia virus (EIAV), LSDV and *T. vivax*. For

Trypanosoma evansi (*T. evansi*), the narrative review did not identify any highly likely or potential mechanical vector species occurring in the EU or neighbouring countries; therefore, expert judgement was used to identify vector species that could potentially occur in the EU for this pathogen. For mechanically transmitted pathogens, vector distribution maps are not available for the EU or neighbouring countries; however, geographical distribution was not considered a limiting factor for the risk assessment, as the relevant mechanical vectors are widely distributed across the EU.

Limitations and uncertainty

As the risk assessment following this report is to be conducted at EU level, the geographical distribution of competent vectors within the EU and neighbouring regions is a key outcome of this work. Geographical distribution maps are available for most highly likely and potential vectors considered. However, substantial evidence gaps remain in relation to pathogen–vector associations, particularly for pathogens that have never been detected in the EU – where only extra-EU vector species have been implicated – or for vector species lacking supporting evidence from field or laboratory studies. In these cases, expert judgement was required to inform the selection of potential vectors capable of transmitting the pathogens within the EU.

The scarcity of eligible experimental data is primarily due to stringent biosafety requirements for experimentation with virulent zoonotic pathogens, such as CCHFV pathogens, limited understanding of vector involvement under natural field conditions for certain pathogens (e.g. *C. burnetii*, Shuni virus), which reduces motivation for conducting transmission studies, and insufficient methodological detail in some studies. In particular, omission of explicit confirmation that female vector specimens were unfed prior to diagnostic procedures led to exclusion under the SLR eligibility criteria, reducing evidence in vector-competence assessments.

1 | INTRODUCTION

1.1 | Background as provided by the Requestor

In the last two decades, the EU has been significantly affected by various diseases of animals transmitted by arthropod vectors ('vector-borne diseases'), such as mosquitoes (e.g. West Nile fever), flies (e.g. lumpy skin disease), ticks (e.g. Crimean-Congo haemorrhagic fever) or biting midges/*Culicoides* (e.g. bluetongue, epizootic haemorrhagic disease). The EU is also at risk of a wide range of serious vector-borne diseases such as Rift Valley fever or African horse sickness.

Recent data and epidemiological events show the increase of such vector-borne diseases (VBDs), either in the vicinity of the EU, in EU trading partners, or within the EU, concomitant with the progressive widening of the geographical extent of competent vectors, such as *Culicoides* and mosquitoes, some of them being able to transmit zoonotic pathogenic agents (e.g. *Aedes* and sandflies).

In April 2017, at the request of DG SANTE, EFSA published a Scientific Opinion on 36 VBDs, assessing their risk of introduction into the EU through movement of livestock or pets. This was considered a first screening, and it was already at that time recommended in the assessment that it should be updated.

In January 2020, also at the request of DG SANTE, and following reports of occurrence of the disease in North Africa, EFSA published a Scientific Opinion on epidemiological update and risk of introduction of Rift Valley fever (RVF) into Europe.

Since 2018, twelve VBDs have been listed under the Animal Health Law and categorised by Commission Implementing Regulation (EU) 2018/1882[1] under various categories of listed diseases, depending on the level of intervention and the measures taken at EU level, and with reference to their vector species.

Those diseases largely differ one from another, in terms of pathogenic agents, host species, vector species, as well as in terms of impact and zoonotic potential. However, it is relevant to consider them together as regards their specificity of being vector-borne and what this entails in terms of risk assessment and risk management, in view of the relative rapid evolution of the geographic distribution of vectors concerned.

It is relevant to ask support from EFSA and the relevant EU Reference Laboratories, to analyse the situation and get scientific advice assessing animal health risks linked with VBDs. The scientific advice should address in particular the likelihood of introduction of new VBDs in the EU and of spread of VBDs currently affecting the EU, the role of climate evolution in this introduction or spread, and the potential evolution of the virulence or transmissibility of those VBDs. Considering the zoonotic nature of some of these VBDs, work in cooperation with ECDC appears relevant too.

This piece of scientific advice should explore and propose options to mitigate the risks of introduction and to address the suitable surveillance, prevention and control of VBDs in the EU, including through vaccination.

1.2 | Terms of Reference as provided by the requestor

In the light of the above:

1 In accordance with Article 31 of Regulation (EC) No 178/2002, the Commission requests EFSA to provide scientific and technical assistance on the epidemiology of VBDs; the following aspects are of particular relevance for the scientific reports

1.1 provide a mapping / horizon scanning / compilation / description of the VBDs that are currently listed in the EU AHL (hereafter 'listed VBDs'), as well as other VBDs not listed but formerly assessed and deemed to have a potential impact and therefore deserving attention (hereafter 'non-listed VBDs'), including their geographic distribution in the EU, neighbouring regions or other regions presenting a particular risk due to epidemiological considerations

1.2 provide a mapping / horizon scanning / compilation / description in the EU and neighbouring countries of the currently known, as well as potential new vectors competent for 'listed VBDs' and 'non-listed VBDs

1.3 provide a mapping / horizon scanning / compilation / description of the currently available surveillance, prevention and control measures for listed and non-listed VBDs in the EU; this includes the collection of data on the efficacy of these measures (e.g. vaccination efficacy, efficacy of biocidal treatments or repellents, animal treatments or insect nets or other husbandry practices)

1.4 describe the potential pathways for listed and non-listed VBDs currently present in the EU to spread, and those not currently present in the EU to be introduced, including via intra EU movements or entry into the EU of animals, products animal origin, plant material or means of transport, equipment, packaging materials, transport water and feed and fodder and other material, carrying viruses and/or vectors; and

1.5 monitor the geographic spread and potential impact of listed and non-listed VBDs already circulating in the EU, considering among others their transmissibility (per se or linked to vector activity), virulence and zoonotic potential. The monitoring will include:

1.5.1 Yearly update of the mapping requested in 1.1, 1.2 and 1.3;

[1]Commission Implementing Regulation (EU) 2018/1882 on the application of certain disease prevention and control rules to categories of listed diseases and establishing a list of species and groups of species posing a considerable risk for the spread of those listed diseases. OJ L 308, 4.12.2018, p. 21.

1.5.2 Six-monthly newsletter with important highlights about possible changes in distribution, transmissibility, virulence, or zoonotic potential of listed and non-listed VBDs inside or outside the EU;
1.5.3 Contribution to monthly automated West Nile Fever monitoring reports in collaboration with ECDC.

2 In accordance with Article 29 of Regulation (EC) No 178/2002, the Commission requests EFSA to provide a scientific opinion on the risk posed by VBDs for the EU; the following aspects are of particular relevance for the scientific opinion:
2.1 Assess the probability of introduction (i.e., the probability of entry of the pathogen from extra or intra EU origin, exposure and establishment) of listed and non-listed VBDs identified in 1.1, into previously free EU Member States, considering the relevant pathways identified in 1.4; describe possible options to prevent such introduction.
2.2 Assess the extent of spread of listed and non-listed VBDs in the previously free EU Member States, after local transmission has taken place, with a potential expected timespan for this spread.
2.3 Assess the impact of the introduction and potential further spread of listed and non-listed VBDs during 1 year after the introduction.
2.4 Critically assess the currently available risk mitigation measures for VBDs in the EU, in particular different biosecurity and surveillance systems, regionalisation, and vaccination tools; and
2.5 Assess the need for the development of these and further measures within the EU, notably to enable safe intra-EU movements of animals from affected or non-affected areas.

Consider and describe the uncertainty related to any of the above.

1.3 | Interpretation of the Terms of Reference

This report addresses Term of Reference (TOR) 1.2 by providing a **knowledge-mapping** of **vectors competent to transmit vector-borne diseases (VBDs) currently listed** by Regulation (EU) 2016/429 and Regulation (EU) 2020/687 (collectively referred to as the Animal Health Law, AHL) and **not listed VBDs** identified as having potential relevance due to their potential epidemiological impact ('non-listed VBDs'). Non-listed diseases were included if they met *all* the following conditions:

- The pathogen is **absent** or of **unknown status** in more than 50% of EU Member States.
- A **competent vector** is present in the EU.
- The pathogen has been **proven to infect** domestic animal species present in the EU.
- Clinical signs are present in animals *or*, if animals are asymptomatic, the disease causes **severe disease in humans**.
- **Sufficient data are available**, i.e. primary data on pathogen distribution, pathogenesis in animals, epidemiology, and competent vectors.

The resulting 25 VBDs that fulfilled the criteria provided above (12 listed by Regulation (EU) 2016/429 and Regulation (EU) 2020/687; 13 not listed) are summarised in Table 1. Information used to address these criteria was gathered through an initial scoping review of the scientific literature and complemented by expert judgement provided by the EFSA Working Group on Vector-Borne Diseases. The results were subsequently updated during report drafting based on findings from the systematic literature reviews conducted for TOR 1, including the classification of data availability (Appendix C). To address TOR 1.2 for each of the 25 VBDs, evidence is provided on the potential or highly likely **vector competence** of arthropod vectors. For those arthropod species that are judged to be potential or highly likely competent vectors, a map with their **geographic distribution** in the EU and neighbouring countries is provided. The maps will provide geographical information on presence, absence, or unknown status, summarised for relatively large subnational units so that the maps can be easily visualised according to Braks et al. (2022) and Wint et al. (2023). Underlying data can be retrieved from the VectorNet Data portal on the Global Biodiversity Facility.

This report provides a static summary of the competence and distribution details as a basis for the annual update that is requested in TOR 1.5.2. In the updates, new evidence found since the previous reports will be highlighted and detailed information about the sources and up-to-date interactive map of the geographic distributions are provided on VectorNet GBIF data portal, EFSA's and ECDCs dedicated webpages on VBDs and VectorNet and the online disease profiles. Further, a six-monthly newsletter with highlights on the 25 VBDs (TOR 1.5.2) as well as monthly monitoring reports on West Nile virus (WNV) (TOR 1.5.3) will be provided as part of the monitoring activities requisition in TOR 1.5.

To address TORs 1.1, 1.3, and 1.4, three other dedicated Scientific Reports (SR) have been prepared. These reports summarise the current knowledge on:

- Structured overview of the main characteristics of the 25 selected VBDs (TOR 1.1) (EFSA, 2026c),
- Surveillance, prevention and control measures of the 25 VBDs (TOR 1.3) (EFSA, 2026a), and
- Risk pathways for their introduction into VBD-free countries in the EU (TOR 1.4) (EFSA, 2026b)

These three SRs (EFSA, 2026a, 2026b, 2026c), together with the present report on vector species that could have a highly likely or potential role in transmission of the 25 VBDs, serve as the evidence base (dossier) for two Scientific Opinions (SO) (see Figure 1). In the first SO, the risk of introduction, spread and impact of the selected 25 VBDs will be assessed, thereby addressing TOR 2.1, 2.2 and 2.3 of the mandate. In addition, an **Expert Knowledge Elicitation** will be carried out to:

- Review and digest the compiled evidence,
- Critically assess the current risk mitigation strategies in the EU,
- Identify the most appropriate mitigation measures for the 25 selected VBDs under various epidemiological scenarios, and
- Evaluate the need for further development or adaptation of these and other mitigation measures, especially to support safe intra-EU movements of animals from affected or unaffected areas.

The **outcomes of the workshop** will be summarised and form the basis of the second Scientific Opinion that will address **TORs 2.4 and 2.5** of the mandate (Figure 1).

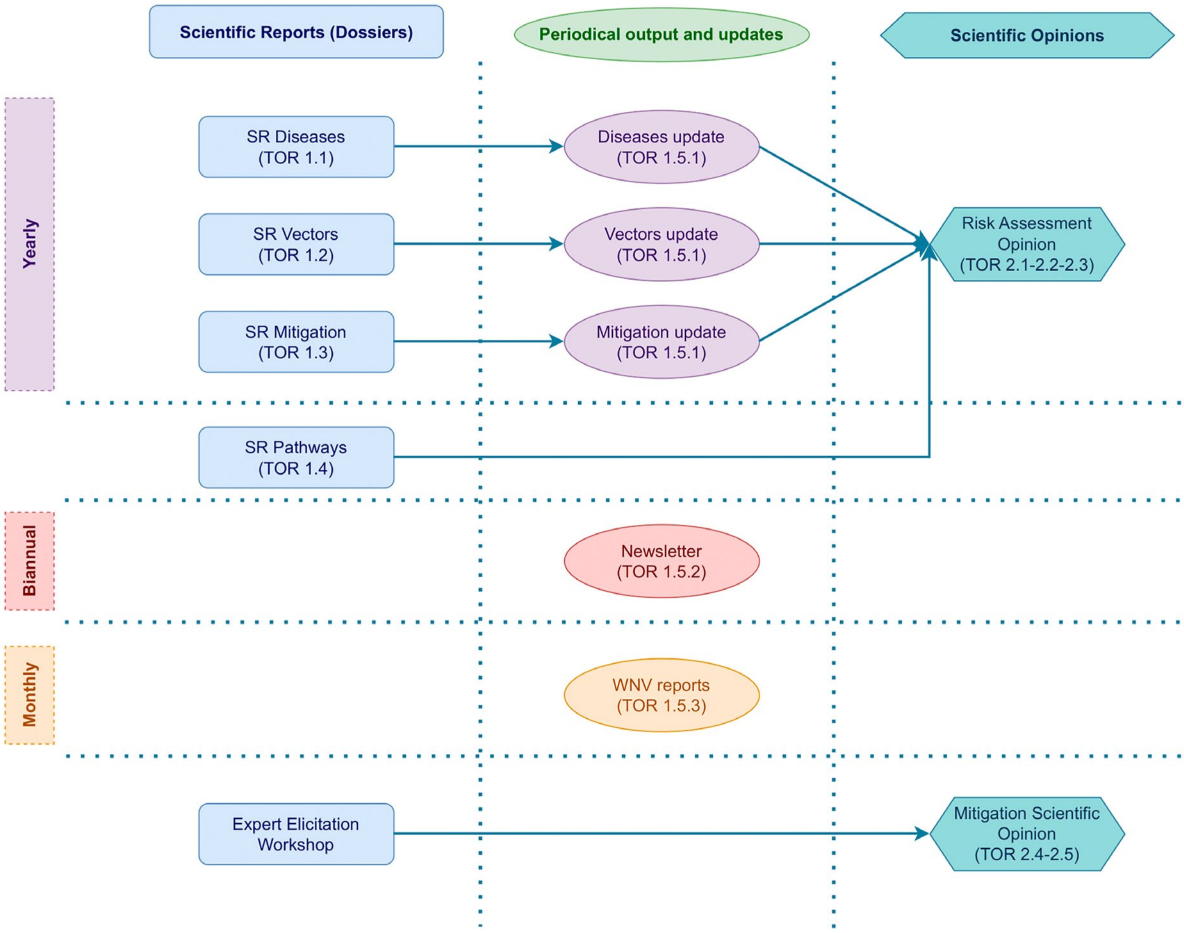

FIGURE 1 VBDs mandate workflow and outputs periodical update.

TABLE 1 Vector-borne diseases that met the eligibility criteria to be included in TOR 1.

Disease -agent	Listed disease in AHL*	Data availability**	Vector group	Pathogen present in EU	Vector(s) present in EU	Listed in WOAH	Zoonotic potential	Main amplifying hosts	Dead-end hosts	Clinical signs in animals
African horse sickness virus (AHSV)	A, D, E	++	Culicoides	✗	✓	YES		Equids		✓
Akabane virus (AKAV)		++	Culicoides	✗	✓	NO		Domestic ruminants		✓
Besnoitia besnoiti (*B. besnoiti*)		++	*Stomoxys*, Tabanidae	✓	✓	NO		Cattle		✓
Bluetongue virus (BTV)	C, D, E	+++	Culicoides	✓	✓	YES		Ruminants, camelids	Dogs	✓
Borrelia burgdorferi s.l. (*B. burgdorferi*)		+++	Ixodidae	✓	✓	NO		Wide host range, rodents, birds	Dogs horses, humans	✓
Bovine ephemeral fever virus (BEFV)		++	Culicoides	✗	✓	NO		Cattle		✓
Cache Valley virus (CVV)		+	Culicidae	✗	✓	NO		Deer	Ruminants, horses, humans	✓

(Continues)

TABLE 1 (Continued)

Coxiella burnetii (*C. burnetii*)	E	+++	Ixodidae	✓	✓	YES		Wide host range, ruminants	Humans	✗
Crimean-Congo haemorrhagic fever virus (CCHFV)		++	Ixodidae	✓	✓	YES		Wide host range, ruminants	Equids	✗
Eastern equine encephalitis virus (EEEV) **** and Western equine encephalitis virus (WEEV)****	E	+	Culicidae	✗	✓	YES		Birds	Equids, humans	✓
Epizootic haemorrhagic disease virus (EHDV)	D, E	++	Culicoides	✓	✓	YES		Cattle, cervids		✓
Equine infectious anaemia virus (EIAV)	D, E	++	Stomoxys, Tabanidae	✓	✓	YES		Equids		✓
Japanese encephalitis virus (JEV)	E	++	Culicidae	✗	✓	YES		Swine, birds	Equids, humans	✓
Leishmania infantum (*L. infantum*)		+++	Phlebotominae	✓	✓	YES		Canids, cats, lagomorphae ,	Equids	✓

TABLE 1 (Continued)

Lumpy skin disease virus (LSDV)	A, D, E	++	*Stomoxys*, Tabanidae, Culicidae, Culicoides, Ixodidae	✓	✓	YES		Cattle		✓
Rift Valley fever virus (RVFV)	A, D, E	+++	Culicidae	✗	✓	YES		Ruminants, camelids	Humans	✓
Schmallenberg virus (SBV)		++	Culicoides	✓	✓	NO		Ruminants		✓
Shuni virus (SHUV)		+	Culicoides Culicidae	✗	✓	NO		Domestic ruminants, horses	Humans	✓
St. Louis encephalitis virus (SLEV)		+++	Culicidae	✗	✓	NO		Birds	Horses, humans	✓
Tick-borne encephalitis virus (TBEV)		++	Ixodidae	✓	✓	NO		Wide host range, wild rodents	Humans	✓
Trypanosoma evansi (*T. evansi*)	D, E	++	Stomoxys	✓	✓	YES	Unclear	Ruminants, camelids, equids	Humans, Pigs	✓

(Continues)

TABLE 1 (Continued)

Trypanosoma vivax (T. vivax)		+++	Glossinidae, Tabanidae, *Stomoxys*	✗	✓	YES		Ruminants, camelids, equids		✓
Venezuelan equine encephalitis virus (VEEV)	D, E	+	Culicidae	✗	✓	YES		Horses, wild rodents	Humans	✓
Vesicular stomatitis virus (VSV)		+	Culicoides	✗	✓	NO		Cattle, equids, pigs	Humans	✓
West Nile virus (WNV)	E	+++	Culicidae	✓	✓	YES		Birds	Horses, humans	✓

*Listed disease categories and definition as described in Regulation (EU) 2016/429. **Data availability based on the systematic literature reviews available on the Disease Profiles (https://animal-diseases.efsa.europa.eu/) and VectorNet for vector competence: +++ well documented (> 100 publications), ++ some papers available (51–100 publications), + only few papers available (0–50 publications). ***Mechanical transmission. ****EEEV and WEEV will be summarised together in this report, in line with the AHL and the WOAH terrestrial code. However, their risk will be assessed separately in the Scientific Opinion addressing TOR 2.1–2.3.

Table legend		
Pathogen type	Zoonotic potential	EU distribution
Virus Bacteria Parasite	Zoonotic Non-zoonotic	✓ Present in the EU ✗ Absent in the EU

2 | DATA AND METHODOLOGIES

2.1 | Data

Data generated through the systematic literature review (SLR) on the geographic distribution of key vector species (Section 2.2.1.3) are published on the **VectorNet Data Portal**. The occurrence datasets were generated separately for each vector group and are publicly available through the **GBIF** platform. The mosquito dataset was generated by De Marco and Schaffner (2026), the sand fly dataset by Alten et al. (2026), the tick dataset by Hansford et al. (2026) and the *Culicoides* dataset by Cvetkovikj et al. (2026).

2.2 | Methodologies

2.2.1 | Literature reviews

Two literature reviews have previously been carried out by Massoels et al. (2023) and Braks et al. (2017) to identify potentially competent biological or mechanical vectors of 36 pathogens and determine their geographic distribution. More details of each are explained in the sections below. Mechanical transmission refers to the passive transfer of a pathogen by a vector in which the organism does not undergo replication or development, typically occurring when pathogens are carried on contaminated body surfaces or mouthparts and transferred between hosts through incidental contact. In contrast, biological transmission requires that the pathogen infects the vector and undergoes multiplication and/or developmental changes before being transmitted to a new host, usually via blood feeding. This process involves an extrinsic incubation period, during which the pathogen becomes infective within the vector (Eldridge & Edman, 2004). These distinctions guided our interpretation of vector–pathogen interactions throughout the experimental procedures. The below sections explain how the reviews have been updated for the selected 25 VBDs. All literature reviews were updated to include papers published up to March 2026.

2.2.1.1 | *Biological vector competence systematic literature review*

The SLR conducted by Massoels et al. (2023) aimed at identifying the available knowledge in the areas of biological vector competence of 36 VBDs. The protocol for that review can be applied periodically to update knowledge when needed. Massoels et al. (2023) reviewed publications published between 2017 and 2023. The review of Massoels et al. was already an update of an earlier SLR, handling a similar research question, by Braks et al. (2017), who reviewed papers published between 1950 and 2016.

For this specific mandate, focusing on a selection of 25 VBDs, a third SLR with the same objectives has been carried out, for which the search strings were updated to add four additional diseases not already included in 36 VBDs already reviewed by Massoels et al. (2023) and Braks et al. (2017) and update the review for the 21 VBDs that were already included in the previous 2 reviews. The remaining VBDs covered in the two previous SLRs were not selected for this report. The new review was divided into two SLRs addressing different review questions both aimed at collecting evidence to assess vector competence. The first SLR focused on the detection of the selected pathogens in field-collected vectors. The second SLR focused on vector-pathogen infection studies under laboratory conditions.

Both literature reviews include a title and abstract screening performed independently by two reviewers, a full-text screening performed by one reviewer, and a manual process of data collection. The list of eligibility criteria is described in the updated review protocol, published by Dagostin et al. (2025b).

The data extracted from both SLRs was combined to evaluate the biological transmission vector competence status for the 25 VBDs. For each disease agent, and according to the risk of transmission, vector species were classified as having either a 'potential' or 'highly likely' role in biological transmission. A species is classified as having a '**potential' role**, if it meets only one of the following conditions:

a. Pathogen detected under field conditions.
b. Pathogen transmitted under laboratory conditions.

If both conditions are fulfilled, the species was classified as having a '**highly likely**' role in biological transmission. Potential and highly likely vector competence definitions are adopted in this report for the purpose of assessing the risk of transmission of pathogens and do not necessarily follow the "proven vector" definition.

2.2.1.2 | *Mechanical vector competence narrative review*

The arthropods involved in mechanical transmission were reviewed through a narrative literature review, aiming to identify the vector species of six pathogens that are either proven or strongly suspected to be mechanically transmitted, and to assess the type and quality of supporting evidence.

The six investigated pathogens were *Coxiella burnetii* (*C. burnetii*), equine infectious anaemia virus (EIAV), lumpy skin disease virus (LSDV), *Trypanosoma evansi* (*T. evansi*), *Trypanosoma vivax* (*T. vivax*), and *Besnoitia besnoiti* (*B. besnoiti*) associated with biting hematophagous insects: Tabanidae, *Stomoxys* spp., *Haematobia* spp., *Haematobosca* spp., *Simulium* spp., Hippoboscidae and *Culicoides* spp.

Also the detailed protocol for the mechanical vectors and the list of eligibility criteria are described by Dagostin et al. (2025b).

Evidence supporting the role of arthropods in mechanical pathogen transmission was classified into four hierarchical categories according to the strength and nature of the available data, with each study assigned to the highest applicable level of evidence.

- **Confirmed transmission in laboratory settings** refers to experimental demonstrations in which an arthropod successfully transmitted a pathogen to a susceptible host under controlled conditions.
- **Pathogen field detection** comprises the identification of a pathogen, or its genetic material or antigens, in or on field-collected arthropods using laboratory detection methods (e.g. molecular, microscopic, culture-based or immunological), without evidence of successful transmission to a new host.
- **Epidemiological evidence** includes temporal and/or spatial associations between animal disease occurrence and arthropod presence, activity or abundance, derived from field observations or outbreak investigations, without requiring pathogen detection in vectors or confirmed transmission.
- **Circumstantial evidence** encompasses indirect indications of possible arthropod involvement in pathogen spread, based on anecdotal observations, historical reports or inference by exclusion, in the absence of direct or epidemiological support.

Based on these evidence categories, arthropod species were further classified according to their likelihood of acting as mechanical vectors. A **highly likely mechanical vector** was defined as a species for which experimental transmission to a susceptible host has been demonstrated under laboratory conditions and for which pathogen detection has been reported in field-collected individuals. A **potential mechanical vector** was defined as a species lacking experimental confirmation of transmission but supported by at least one line of evidence, including pathogen detection in field-collected individuals, epidemiological associations with disease occurrence, or circumstantial evidence only.

2.2.1.3 | *Geographic distribution systematic literature review*

Underlying data on geographic distribution are updated annually through a living systematic literature review for which the protocol has been described by Dagostin et al. (2025a). Data are published on the VectorNet Data portal and updated on an annual basis.

2.2.2 | Selection of vector species to be included in the EU risk assessment of 25 pathogens

For the purpose of the risk assessment, all vector species classified as highly likely or potential vectors with EU vector maps were retained. In a limited number of cases, however, the SLR did not identify any highly likely or potential vector species for a given pathogen in Europe. To enable the risk assessment as requested in TORs 2.1–2.3, expert opinion was therefore applied to identify EU vector species that could plausibly contribute to pathogen transmission and to address these specific evidence gaps.

Therefore, the experts of the WG identified additional sources of evidence (i.e. scientific publications not included in the SLRs) to assess the potential role of plausible vector species present in the EU in transmitting pathogens that are currently absent from the EU. In forming their expert judgement, they also considered past disease episodes that occurred within the EU (e.g. African horse sickness virus), as well as the possibility that species or groups of species present in the EU may play epidemiological roles similar to those documented for non-EU species.

Finally, inclusion was restricted to vector species for which geographical distribution data at EU level (i.e. Vector Distribution Status maps) were available, as this information is essential for the subsequent EU-level risk assessment. Complexes and groups of species were considered for the EU list of highly likely/ potential vectors, however biotypes of vector species were not taken into account for the selection of species for the risk assessment.

Figure 2 summarises the evidence collection and decision process underpinning the selection of vector species presented in Section 3.1. Vector species were first categorised through the SLR as highly likely vectors or potential vectors, based on the definitions provided in Section 2.2.2.

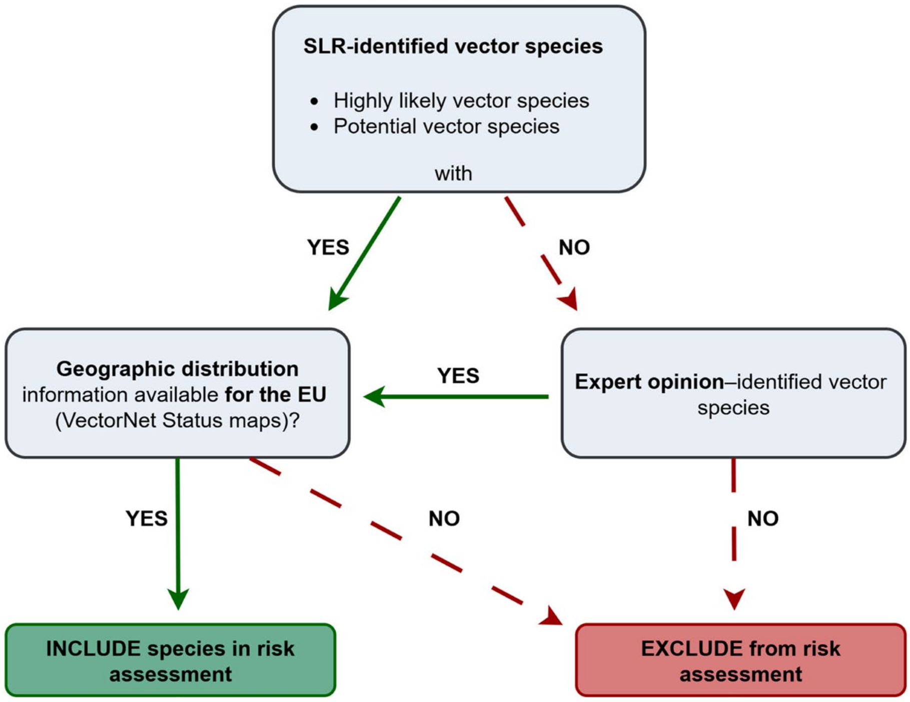

FIGURE 2 Evidence collection process to identify EU vector species to be included for risk assessment on 25 selected VBDs.

2.2.3 | Mapping of geographic distribution of vector species in vector distribution status maps

For those species that were identified to be highly likely or potential vector species, maps displaying their geographic distribution status are provided in Section 3.2, if the maps are available for the EU and neighbouring countries.

In short, the vector distribution status was assigned in the maps at NUTS3 polygon level or, where unavailable, at GAUL 2 polygon level. Colours in the maps represent the distribution category attributed to each spatial unit. 'Established (present)' indicates confirmed or expert-assessed self-sustaining populations. 'Introduced' denotes recorded presence without evidence of establishment. 'Absent' indicates confirmed absence based on observations, while 'anticipated absent' refers to inferred absence due to expert judgement or environmental constraints. The category 'no data' is applied when no information is available, while 'unknown' is used when information existed but was insufficient or unreliable. Classifications were based on expert assessment within the VectorNet network and reflect presence at the spatial-unit level, acknowledging that vectors may not occupy all areas within a polygon. Further description of the methodology for the production of the VectorNet Status maps is available in Wint et al. (2023).

3 | ASSESSMENT

3.1 | Literature review outcomes

3.1.1 | Biological vector transmission

The following sections present the results of the SLR grouped by vector competence status summarising the worldwide evidence available for each vector species. To support interpretation, species names were highlighted in **bold** to indicate whether they are present in the EU. 'Present' refers solely to confirmed occurrence within the EU and does not imply that distribution maps are available. All taxa including groups, complexes and hybrids were included. Biotypes were not included since they are not considered a taxon. For taxonomic groups and complexes, vector competence was attributed at the group or complex level when demonstrated for at least one its constituent species.

3.1.1.1 | *Biting midges*

Because *Culicoides* taxonomy remains partly unresolved, several studies classified specimens into species complexes or groups in the absence of molecular confirmation. We therefore present results according to the taxonomic classifications reported in the studies identified through the SLR. The results of the SLR are displayed in Table 2.

TABLE 2 Systematic literature review (SLR) summary matrix of worldwide evidence on vector competence status of *Culicoides* species. Species present in the EU are shown in bold. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies).

Arthropod species	AHSV	BTV	EHDV	AKAV	BEFV	SBV	VSV
Culicoides chiopterus						*	
Culicoides fulvus		*					
Culicoides imicola		*		*		*	
Culicoides insignis			*				
Culicoides nubeculosus						*	
Culicoides obsoletus						*	
***Culicoides obsoletus* complex**[1]	*	**	*			**	
***Culicoides obsoletus* group**[2]	*	**	*			***	
Culicoides obsoletus s.l.	*	*	*				
Culicoides obsoletus/scoticus	*	*	*				
Culicoides orientalis		*					
Culicoides oxystoma		*		*			
Culicoides pulicaris		*				*	
Culicoides sonorensis		**	*		*	*	**
Culicoides tainanus		*		*			

Potential vector | Highly likely vector | No data or did not meet SLR criteria

[1]*Culicoides obsoletus* complex includes *C. obsoletus* and *C. scoticus. In some papers, this is expressed as Culicoides obsoletus /scoticus.*

[2]*Culicoides obsoletus* group includes *C. obsoletus, C. scoticus, C. montanus, C. chiopterus* and *C. dewulfi*.

3.1.1.2 | *Ticks*

The classification of the vector competence status of tick species based on the SLR results is shown in Table 3. Results are presented following the taxonomic classifications reported in the studies identified through the SLR.

TABLE 3 Systematic literature review (SLR) summary matrix for worldwide evidence on vector competence of tick species. For *B. burgdorferi* s.l. and TBEV, assessment was limited to tick species occurring within the VectorNet area. Species present in the EU are shown in bold. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies).

Arthropod species	*C. burnetii*	*B. burgdorferi* s.l.	CCHFV	TBEV
Amblyomma testudinarium		*		
Dermacentor marginatus		***		
Dermacentor nuttallii				*
Dermacentor reticulatus		***		***
Dermacentor silvarum		*		*
Haemaphysalis concinna		*		*
Haemaphysalis inermis		*		
Haemaphysalis japonica douglasi		*		*
Haemaphysalis punctata		**		
Haemaphysalis spp.		**		
Hyalomma aegyptium		*	*	
Hyalomma anatolicum		*	*	
Hyalomma asiaticum			*	
Hyalomma dromedarii		**		
Hyalomma lusitanicum		*		
Hyalomma marginatum		**	*	
Hyalomma rufipes		*		
Ixodes persulcatus × Ixodes pavlovskyi		*		*
Ixodes ricinus × Ixodes persulcatus				*
Ixodes arboricola		*		
Ixodes ariadnae		*		

TABLE 3 (Continued)

Arthropod species	*C. burnetii*	*B. burgdorferi s.l.*	CCHFV	TBEV
Ixodes canisuga		*		
Ixodes cf. kaiseri		*		
Ixodes frontalis		**		
Ixodes hexagonus		***		
Ixodes inopinatus		**		
Ixodes kaiseri		*		
Ixodes pavlovskyi		*		**
Ixodes persulcatus		***		***
Ixodes ricinus		***		***
Ixodes simplex		*		
Ixodes spp.		*		*
Ixodes uriae		*		
Ixodes vespertilionis		*		
Rhipicephalus annulatus		**		
Rhipicephalus bursa		*		
Rhipicephalus rutilus		*		
Rhipicephalus sanguineus		***		
Rhipicephalus turanicus		*		

Potential vector | Highly likely vector | No data or did not meet SLR criteria

3.1.1.3 | *Mosquitos*

The classification of the vector competence status of mosquito species based on the SLR results is shown in Table 4. Results are presented following the taxonomic classifications reported in the studies identified through the SLR.

TABLE 4 Systematic literature review (SLR) summary matrix for worldwide evidence on vector competence of mosquito species. Species present in the EU are shown in bold. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies).

Arthropod species	EEEV	WEEV	JEV	RVFV	VEEV	WNV	CVV	SLEV
Aedes aegypti		*	*	**			*	
Aedes albopictus		*	*	*		*	**	
Aedes australis						*		
Aedes canadensis						*		
Aedes caspius				*				
Aedes detritus				*	*	*		
Aedes dorsalis						*		
Aedes durbanensis				*				
Aedes japonicus			*			*	*	
Aedes kochi						*		
Aedes melanimon				*		*		
Aedes notoscriptus			*			*		
Aedes procax						*		
Aedes purpureus			*					
Aedes sierrensis						*		
Aedes taeniorhynchus						*		
Aedes riseriatus						*	*	
Aedes vexans				***		**		
Aedes vigilax			*			*		
Anopheles coustani				*				
Anopheles gambiae							*	

(Continues)

TABLE 4 (Continued)

Arthropod species	EEEV	WEEV	JEV	RVFV	VEEV	WNV	CVV	SLEV
Anopheles quadrimaculatus							*	
Anopheles sinensis			*					
Coquillettidia linealis						*		
Coquillettidia perturbans						*		
Culex annulirostris			*			*		
Culex annulus			*					
Culex antennatus				*				
Culex bitaeniorhynchus						*		
Culex erraticus				*				
Culex erythrothorax				*		*		
Culex gelidus			*			*		
Culex gnomatos					*			
Culex gnomatos/vomerifer					*			
Culex incidens						*		
Culex interfor								*
Culex modestus						*		
Culex neavei group						*		
Culex nigripalpus				*		*		*
Culex pervigilans						*		
Culex perexiguus						*		
Culex pipiens			*	**		***		*
Culex pipiens molestus				*		***		
Culex pipiens molestus × *Culex quinquefasciatus*						*		
Culex pipiens			*	*		**		
Culex pipiens* × *molestus				*		*		
Culex pipiens × *Culex quinquefasciatus*						*		
Culex pipiens pallens		*						
Culex pipiens s.l.				*		*		
Culex pipiens/restuans						*		
Culex poicilipes				*				
Culex quinquefasciatus		*	**	*		***		**
Culex restuans						**		
Culex salinarius						*		
Culex saltanensis								*
Culex sitiens			*			*		
Culex sitiens group			**					
Culex stigmatosoma						**		*
Culex taeniopus					*			
Culex tarsalis		*		***		***	*	*
Culex thriambus						*		
Culex torrentium						*		
Culex tritaeniorhynchus			***	*				
Culex univittatus						*	*	
Culex vansomereni						*		
Culex vishnui			*					
Culex zombaensis				*				
Culiseta annulata			*					
Culiseta inornata				*		*		
Culiseta melanura	*					*		
Mansonia septempunctata			*					

TABLE 4 (Continued)

Arthropod species	EEEV	WEEV	JEV	RVFV	VEEV	WNV	CVV	SLEV
Mansonia uniformis			*					
Psorophora columbiae					*			
Verrallina carmenti						*		
Verrallina funerea						*		
Verrallina lineato						*		

Potential vector | Highly likely vector | No data or did not meet SLR criteria

3.1.1.4 | *Sandflies*

The classification of the vector competence status of sandfly species based on the SLR results is shown in Table 5. Results are presented following the taxonomic classifications reported in the studies identified through the SLR.

TABLE 5 Systematic literature review (SLR) summary matrix of worldwide evidence on vector competence of sandfly species. Species present in the EU are shown in bold. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies).

Arthropod species	L. infantum
Evandromyia cortelezii	* (Potential vector)
Evandromyia edwardsi	* (Potential vector)
Expapillata firmatoi	* (Potential vector)
Lutzomyia cavernicola	* (Potential vector)
Lutzomyia cortelezzii s.l.	* (Potential vector)
Lutzomyia cruzi	* (Potential vector)
Lutzomyia lloydi	* (Potential vector)
Lutzomyia longipalpis	*** (Highly likely vector)
Lutzomyia migonei	* (Potential vector)
Lutzomyia renei	* (Potential vector)
Micropygomyia quinquefer	* (Potential vector)
Nyssomyia whitmani	* (Potential vector)
Phlebotomus longicuspis	* (Potential vector)
Phlebotomus mascittii	* (Highly likely vector)
Phlebotomus neglectus	* (Potential vector)
Phlebotomus papatasi	* (Potential vector)
Phlebotomus perfiliewi	* (Potential vector)
Phlebotomus perniciosus	*** (Highly likely vector)
Phlebotomus tobbi	* (Potential vector)
Pintomyia fischeri	* (Potential vector)
Psathyromyia lutziana	* (Potential vector)
Sergentomyia minuta	** (Potential vector)

Potential vector | Highly likely vector

3.1.2 | Mechanical transmission

This section summarises the main findings of the narrative review on the mechanical transmission of six pathogens: *T. evansi*, *T. vivax*, *C. burnetii*, *B. besnoiti*, EIAV and LSDV. The review primarily addressed mechanical transmission by vector species reported in Europe. However, as no European studies met the eligibility criteria for *T. vivax* and *T. evansi*, evidence on the mechanical transmission of these pathogens was additionally retrieved from studies conducted outside Europe. These findings are presented separately and are restricted to fly species.

3.1.2.1 | *Biting midges*

Among the pathogens assessed in this report, *C. nubeculosus* was identified as a potential mechanical vector for LSDV based on circumstantial findings (Chihota et al., 2003).

3.1.2.2 | *Ticks*

While ticks are suspected to be involved in mechanical pathogen transmission, the narrative review did not identify any supporting evidence of mechanical transmission of the investigated pathogens by this vector group.

3.1.2.3 | *Mosquitoes*

Among the pathogens assessed in this report *Aedes aegypti* was found experimentally implicated in mechanical transmission of LSDV based on confirmed transmission in a laboratory experiment (Chihota et al., 2001).

3.1.2.4 | *Flies*

3.1.2.4.1 | *European fly species*

Evidence has been found on the vector status for mechanical transmission of EIAV, LSDV and *B. besnoiti* for five European fly species, and one biting midge and mosquito species. Table 6 summarises the mechanical vector status of selected European arthropod species based on the results of the literature review. Details and references can be found in Table B.2 in Appendix B.

TABLE 6 Narrative review summary matrix of evidence of mechanical transmission of selected pathogens. In this case, only species present in the EU were considered and are shown in bold. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies).

Arthropod species	EIAV	LSDV	*B. besnoiti*
Culicoides nubeculosus		*	
Aedes aegypti		*	
Haematobia irritans		*	
Haematopota spp.		*	
Stomoxys calcitrans	*	***	**
Stomoxys spp.			**
Tabanidae	*		*

Potential vector | Highly likely vector | No data or did not meet SLR criteria

3.1.2.4.2 | *Mechanical transmission of* T. evansi *and* T. vivax

Since there were no European studies investigating the mechanical transmission of *Trypanosoma* spp., the review scope was expanded to include relevant studies conducted outside Europe. In most of the cases vector species involved were not present in Europe Table 7 summarises the outcomes of the review.

TABLE 7 Summary of non-European fly species' role in *Trypanosoma* spp. mechanical transmission. Asterisks indicate the number of studies identified per pathogen–vector combination (*1–2 studies; **3–4 studies; ***≥ 5 studies). Species in bold are present in Europe, although the referenced studies were conducted on non-European populations or unspecified taxa. The cross (+) indicates that pathogen was only detected in studies that included populations or species outside Europe.

Arthropod species	*T. evansi*	*T. vivax*
Stomoxys calcitrans	*	*
Stomoxys spp. +	*	*
Tabanidae		**
Stomoxys niger+	*	
Stomoxys taeniatus+	*	
Haematobosca+		*
Atylotus agrestis+		*
Atylotus fuscipes+		*
Hippoboscidae		*

Potential vector | Highly likely vector | No data or did not meet SLR criteria

3.1.3 | Summary of evidence based on literature review, available geographic distribution data and expert opinion

3.1.3.1 | *Biological vector transmission*

Table 8 shows the summary of the evidence for arthropods that were considered highly likely or potential vectors, either based on the SLR or expert opinion, that were provided in Tables 2–5 but selecting only those arthropod species for which geographical distribution maps are available for the EU (Figures 4–32) plus neighbouring countries, which can be used for the risk assessment to be performed under TOR 2.1 to 2.3.

TABLE 8 Summary of evidence on biological vectors based on SLR or Expert Opinion with geographical distribution maps for EU and neighbouring countries. In the assessment for the EU list of highly likely/potential vectors, biotypes of vector species were not taken into account for the selection of species for the risk assessment. For vector complexes and groups, competence was attributed at the group or complex level when demonstrated for at least one constituent species. Asterisks indicate expert input: *Potential vector species; **Evidence from scientific publications that were identified after the SLR by experts.

Vector-borne pathogen	Arthropod species	Vector competence status
African horse sickness virus	*C. imicola*	Potential*
	C. obsoletus complex[a]	Potential
	C. chiopterus	Potential*
Akabane virus	*C. imicola*	Potential
Bluetongue virus	*C. imicola*	Highly likely
	C. obsoletus complex[a]	Highly likely
	C. dewulfi	Potential*
	C. pulicaris	Potential
	C. obsoletus group[b]	Highly likely
Borrelia burgdorferi s.l.	*D. reticulatus*	Potential
	H. lusitanicum	Potential
	H. marginatum	Potential
	I. persulcatus × *I. pavlovskyi*	Potential
	I. persulcatus	Highly likely
	I. ricinus	Highly likely
	Rh. bursa	Potential
	Rh. sanguineus	Potential
Bovine ephemeral fever virus	*C. imicola*	Potential*
	C. obsoletus complex[a]	Potential*
	C. dewulfi	Potential*
	C. chiopterus	Potential*
Cache Valley virus	*Ae. aegypti*	Potential
	Ae. albopictus	Potential
	Ae. japonicus	Potential
	Cx. univittatus	Potential
Coxiella burnetii	*I. ricinus*	Potential*
	D. reticulatus	Potential*
	D. marginatus	Potential*
Crimean-Congo haemorrhagic fever virus	*H. marginatum*	Potential
Eastern equine encephalitis virus	*Ae. vexans*	Potential*
	Ae. albopictus	Potential**
	Ae. japonicus	Potential**
Epizootic haemorrhagic disease virus	*C. obsoletus complex*[a]	Potential
	C. imicola	Potential*
	C. dewulfi	Potential*
	C. chiopterus	Potential*

(Continues)

TABLE 8 (Continued)

Vector-borne pathogen	Arthropod species	Vector competence status
Japanese encephalitis virus	*Cx. pipiens*	Highly likely
	Cx tritaeniorhynchus	Highly likely
	Ae. aegypti	Potential
	Ae. albopictus	Potential
	Ae. japonicus	Potential
	Cs. annulata	Potential
Leishmania infantum	*Ph. mascittii*	Potential
	Ph. neglectus	Potential
	Ph. papatasi	Potential
	Ph. perfiliewi	Potential
	Ph. perniciosus	Highly likely
	Ph. tobbi	Potential
Rift Valley Fever Virus	*Ae. aegypti*	Highly likely
	Ae. vexans	Potential
	Cx. pipiens × *Cx. molestus*	Potential
	Ae. albopictus	Potential
	Ae. caspius	Potential
	Ae. detritus	Potential
	Cx. antennatus	Potential
	Cx. tritaeniorhynchus	Potential
Schmallenberg virus	*C. chiopterus*	Potential
	C. obsoletus complex[a]	Highly likely
	C. obsoletus group[b]	Highly likely
	C. pulicaris	Potential
	C. imicola	Potential
	C. obsoletus	Potential
	C. dewulfi	Potential*
Shuni virus	*C. imicola*	Potential*
	C. obsoletus complex[a]	Potential*
	C. dewulfi	Potential*
	C. chiopterus	Potential*
St. Louis encephalitis virus	*Cx. pipiens*	Potential
	Cx. pipiens s.l.	Potential*
	Cx. univittatus	Potential*
Tick-borne encephalitis virus	*D. reticulatus*	Highly likely
	I. persulcatus × *I. pavlovskyi*	Potential
	I. ricinus × *I. persulcatus*	Highly likely
	I. persulcatus	Highly likely
	I. ricinus	Highly likely
Venezuelan equine encephalitis virus	*Ae. detritus/coluzzii*	Potential
	Ae. vexans	Potential*
	Cx. pipiens s.l.	Potential*
	Cx. univittatus	Potential*
Vesicular stomatitis virus	*C. imicola*	Potential*
	C. obsoletus complex[a]	Potential*
	C. dewulfi	Potential*
	C. chiopterus	Potential*

TABLE 8 (Continued)

Vector-borne pathogen	Arthropod species	Vector competence status
West Nile virus	*Ae. albopictus*	Potential
	Ae. aegypti	Potential
	Ae. detritus	Potential
	Ae. japonicus	Potential
	Ae. vexans	Potential
	Cx. modestus	Potential
	Cx. pipiens s.l.	Highly likely
	Cx. pipiens	Highly likely
	Cx. univittatus	Highly likely
	Cx. perexiguus	Potential
Western equine encephalitis virus	*Ae. albopictus*	Potential
	Ae. aegypti	Potential

[a]*Culicoides obsoletus* complex includes *C. obsoletus* and *C. scoticus. In some papers, this is expressed as Culicoides obsoletus /scoticus.*
[b]*Culicoides obsoletus* group includes *C. obsoletus, C. scoticus, C. montanus, C. chiopterus* and *C. dewulfi.*

3.1.3.2 | *Mechanical transmission*

In addition, Table 9 summarises mechanical vectors with potential or highly likely vector status that occur in Europe and neighbouring countries. However, because these species are ubiquitous, no distribution maps are available, as their detailed spatial distribution is of limited relevance. Their widespread occurrence means that geographic distribution should therefore not be considered a limiting factor in the risk assessment for Europe.

TABLE 9 Summary of evidence of mechanical vectors. Asterisks (*) indicate potential vector species based on expert opinion.

Vector-borne pathogen	Arthropod species	Vector status based on SLR or expert opinion
Besnoitia besnoiti	*Stomoxys calcitrans*	Potential
	Stomoxys spp.	Highly likely
	Tabanidae	Potential
Equine infectious anaemia virus	*Stomoxys calcitrans*	Potential
	Tabanidae	Potential
Lumpy skin disease virus	*Haematobia irritans*	Potential
	Haematopota spp.	Highly likely
	Stomoxys calcitrans	Highly likely
	C. nubeculosus	Potential
	A. aegypti	Potential
Trypanosoma evansi	*Stomoxys calcitrans*	Potential*
Trypanosoma vivax	Tabanidae	Highly likely
	Haematopota	Potential*
	Hippoboscidae	Potential

3.1.3.3 | *Limitations and uncertainty*

It is important to note that the categorisation of arthropod species as 'highly likely' or 'potential' vectors is constrained by the availability and quality of existing field and experimental evidence in scientific literature. A designation of 'highly likely' does not imply a higher intrinsic vector competence but rather reflects the presence of more complementary or robust data supporting their role in transmission. Conversely, classification as a 'potential' vector should not be interpreted as evidence of low competence or biological irrelevance; instead, it often indicates a lack of targeted field studies or insufficient experimental confirmation of transmission. Thus, the categorisation should be interpreted as evidence-based assessments of data availability rather than definitive measures of the vector competence.

In addition, Figure 3 shows a highly uneven distribution of available evidence across the 25 pathogens, with the majority of publications reporting on just a few select pathogens, notably *B. burgdorferi*, WNV and TBEV accounting for 54.2%, 12.1% and 11.5% of publications, respectively ($n=520$). For 16 pathogens, both experimental and/or field evidence is available, while for 9 VBDs expert opinion was needed to address some knowledge gaps on diseases without any field evidence, or with one or less experimental studies.

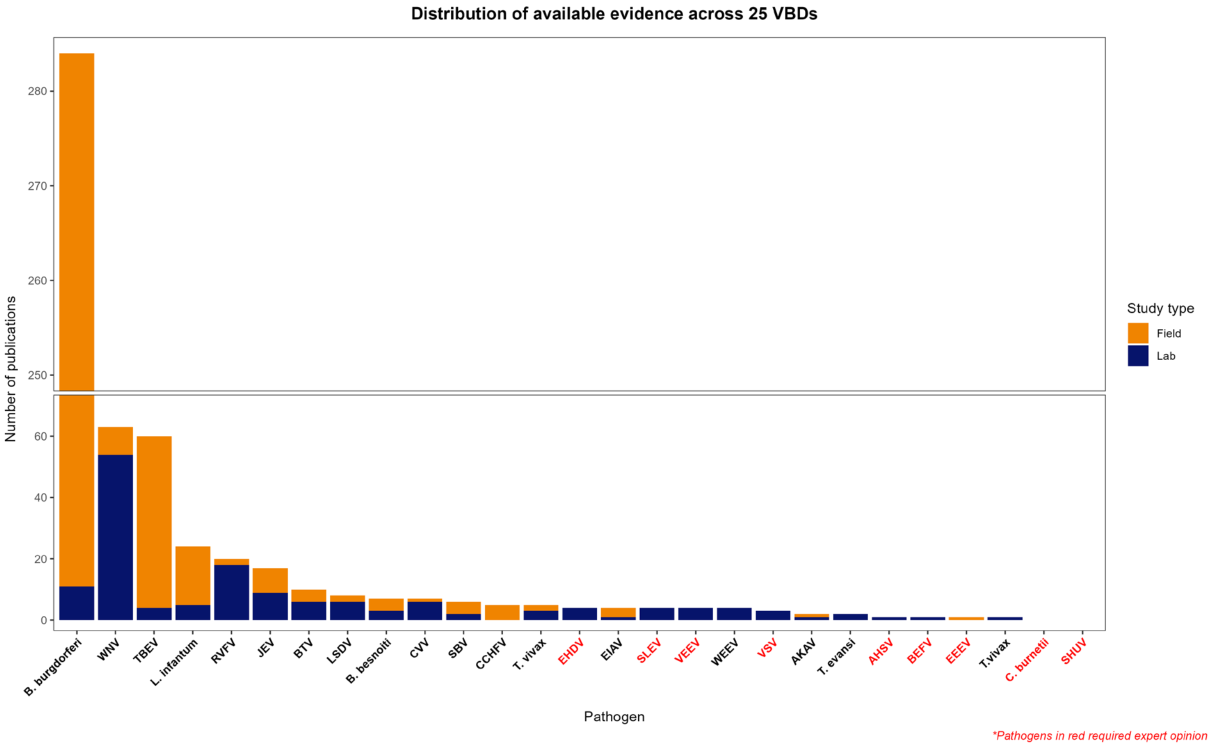

FIGURE 3 Available evidence on potential or highly likely vectors for the 25 vector-borne diseases (WEEV and EEEV are considered together). Y-axis refers to the publications that were considered eligible in the SLR. A publication providing both field and laboratory evidence for the same pathogen is counted twice.

3.2 | Geographic distribution

3.2.1 | Biting midges

3.2.1.1 | *Culicoides chiopterus*

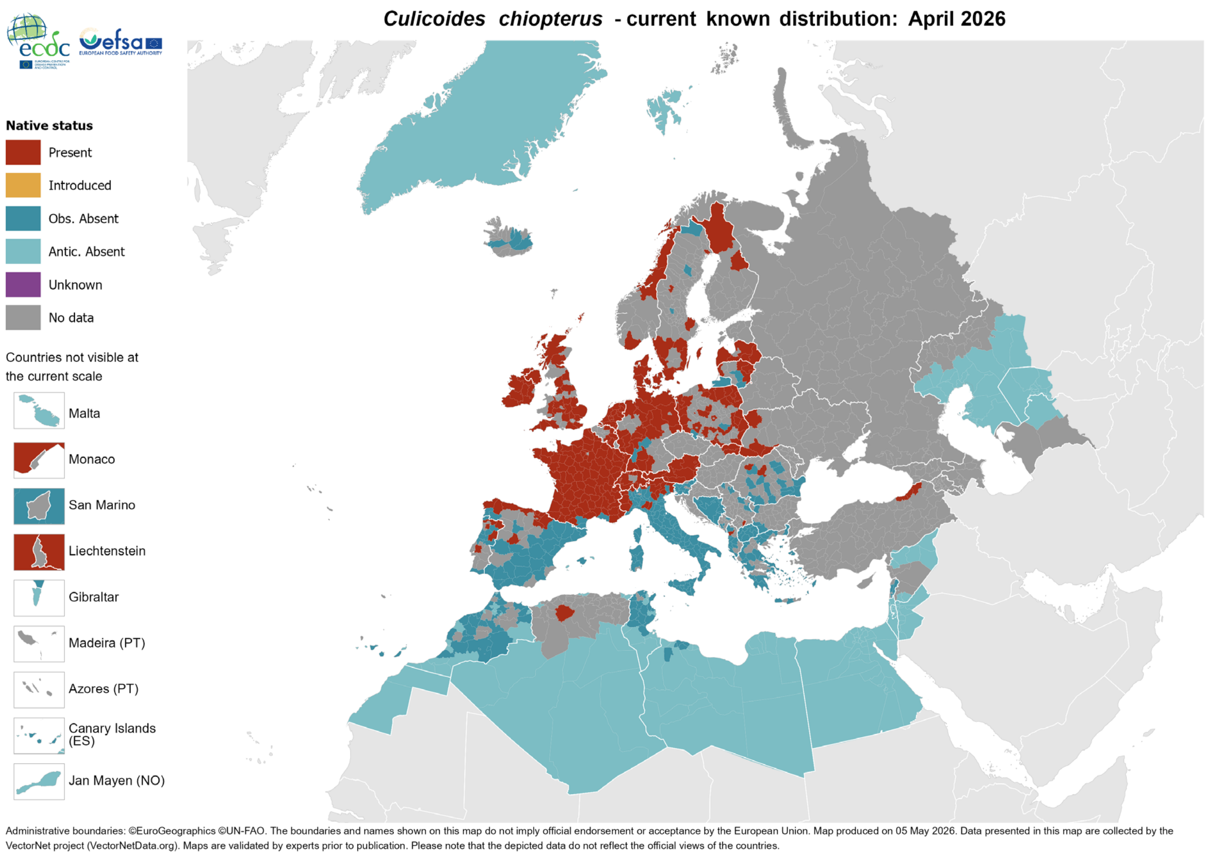

FIGURE 4 Vector status maps of *Culicoides chiopterus* provided by VectorNet (last updated in April 2026).

Figure 4 displays the geographic distribution of *C. chiopterus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *C. chiopterus* can be used to assess the risk for AHSV, BEFV, EHDV, SBV, SHUV, VSV for which it can be a potential biological vector.

3.2.1.2 | *Culicoides dewulfi*

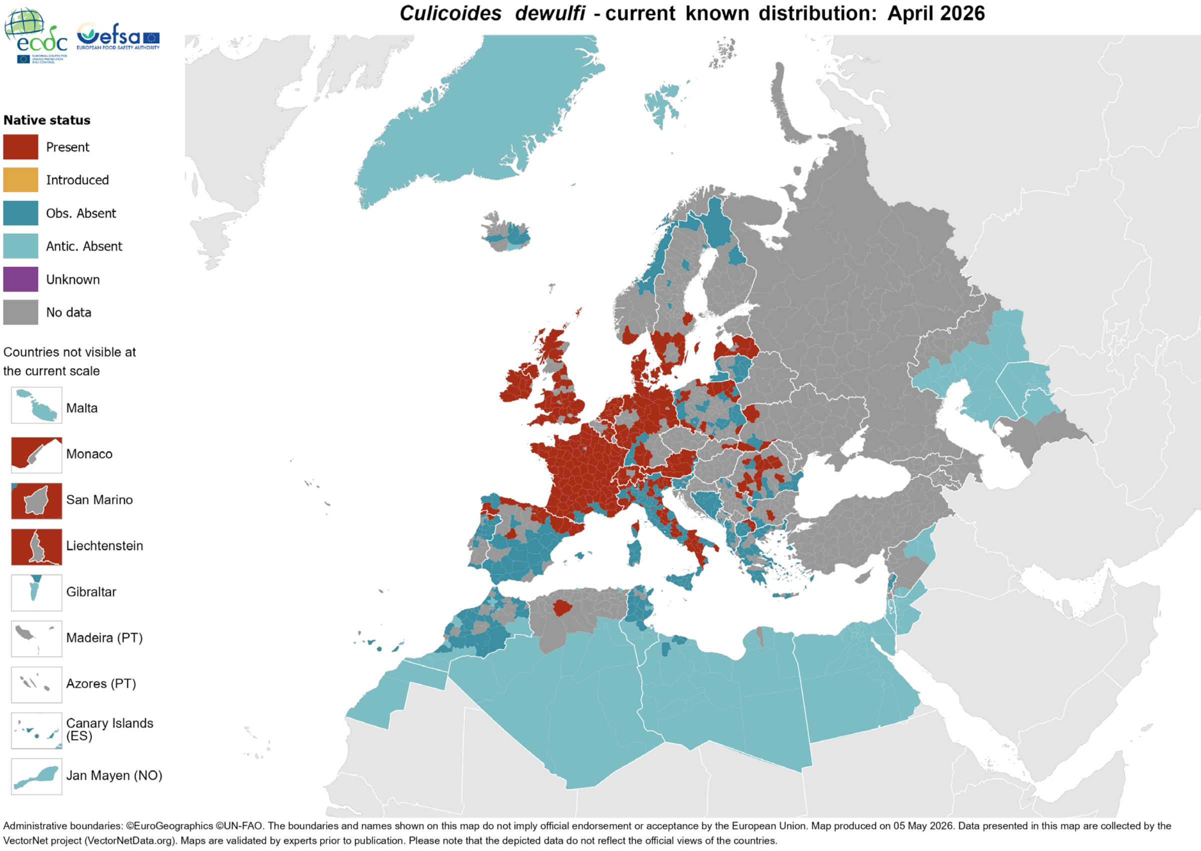

FIGURE 5 Vector status maps of *Culicoides dewulfi* provided by VectorNet (last updated in April 2026).

Figure 5 displays the geographic distribution of *C. dewulfi* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *C. dewulfi* can be used to assess the risk for BEFV, EHDV, SBV, SHUV, VSV for which it can be a potential biological vector.

3.2.1.3 | *Culicoides imicola*

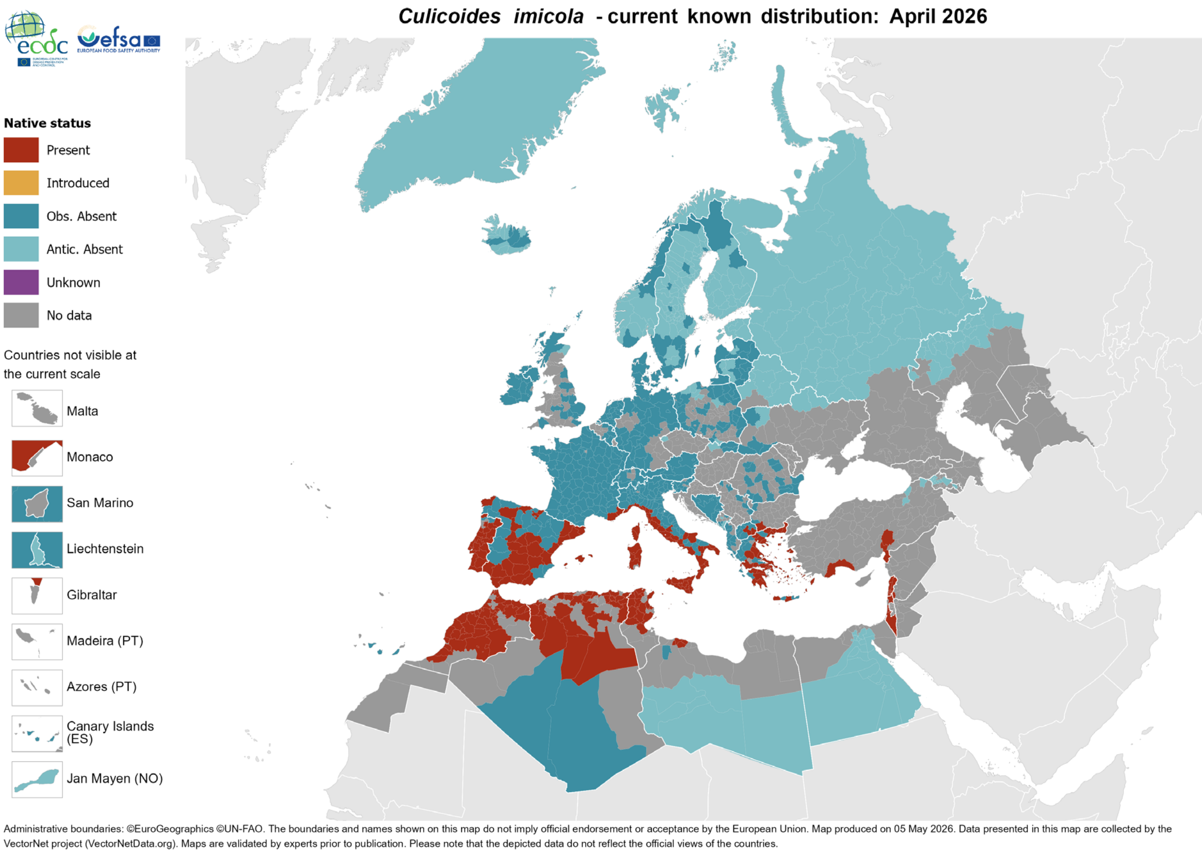

FIGURE 6 Vector status maps of *Culicoides imicola* provided by VectorNet (last updated in April 2026).

Figure 6 displays the geographic distribution of *C. imicola* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *C. imicola* can be used to assess the risk for BTV, for which it can be a highly likely biological vector, and for AHSV, AKAV, BEFV, EHDV, SBV, SHUV, VSV for which it can be a potential biological vector.

3.2.1.4 | *Culicoides obsoletus/scoticus*

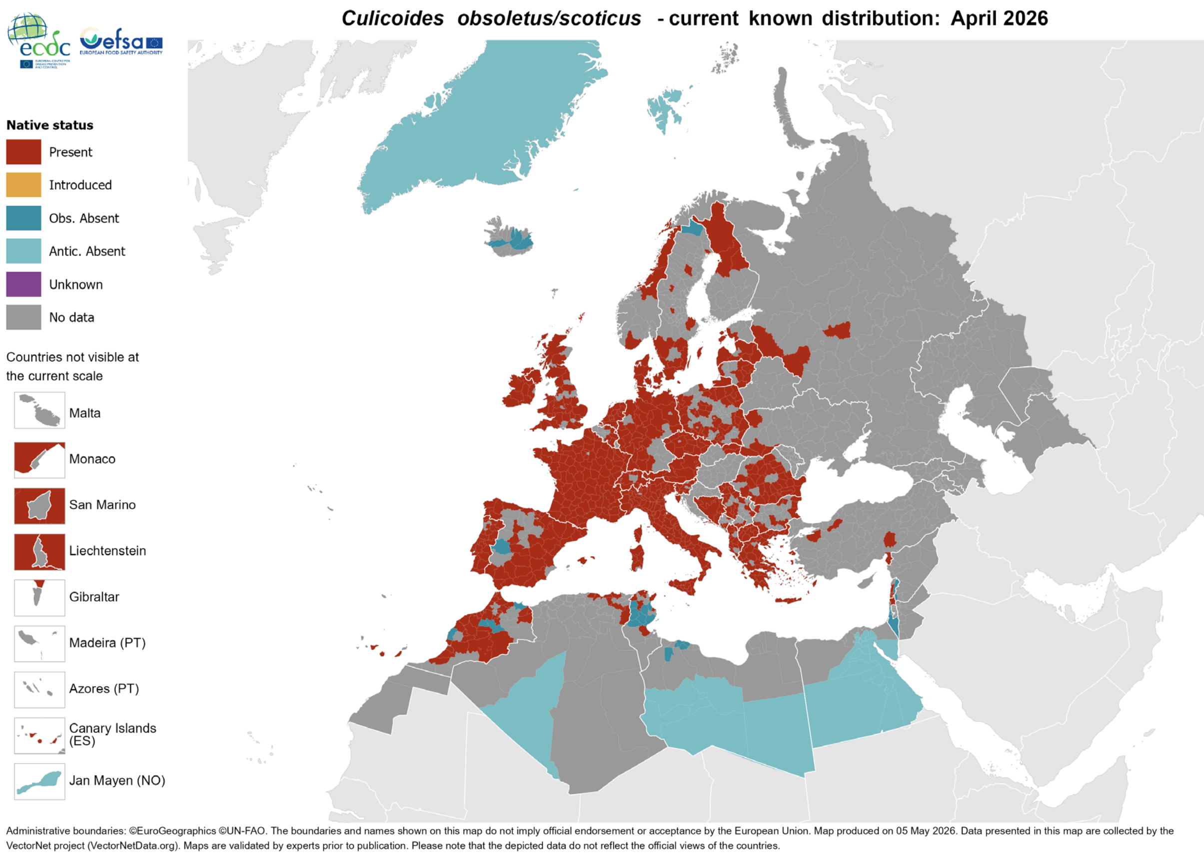

FIGURE 7 Vector status maps of *Culicoides obsoletus/scoticus* provided by VectorNet (last updated in April 2026).

Figure 7 displays the geographic distribution of *C. obsoletus complex* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *C. obsoletus complex* can be used to assess the risk for BTV and SBV for which it can be a highly likely biological vector, and for AHSV, BEFV, EHDV, SHUV, VSV for which it can be a potential biological vector.

3.2.1.5 | *Culicoides pulicaris*

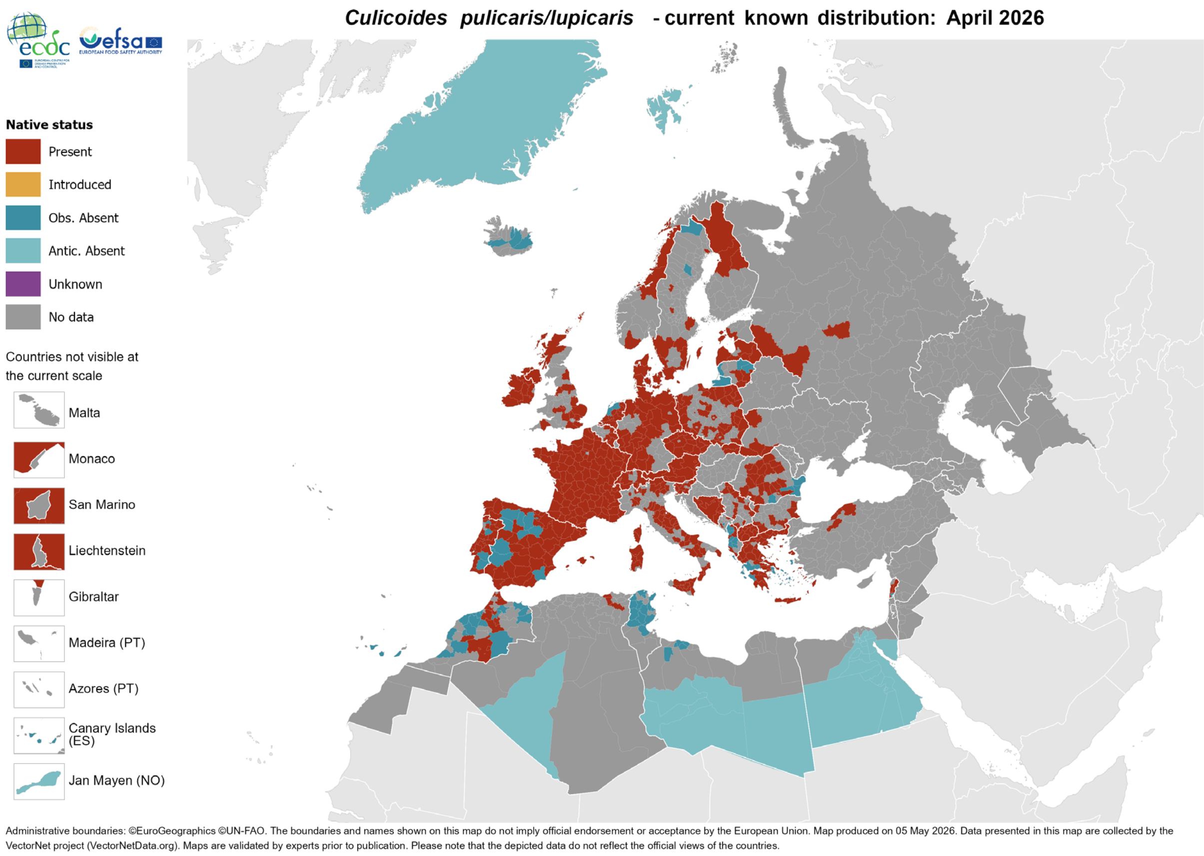

FIGURE 8 Vector status maps of *Culicoides pulicaris/lupicaris* provided by VectorNet (last updated in April 2026).

Figure 8 displays the geographic distribution of *C. pulicaris/lupicaris* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *C. pulicaris/lupicaris* can be used to assess the risk for BTV and SBV for which it can be a potential biological vector.

3.2.2 | Ticks

3.2.2.1 | *Dermacentor reticulatus*

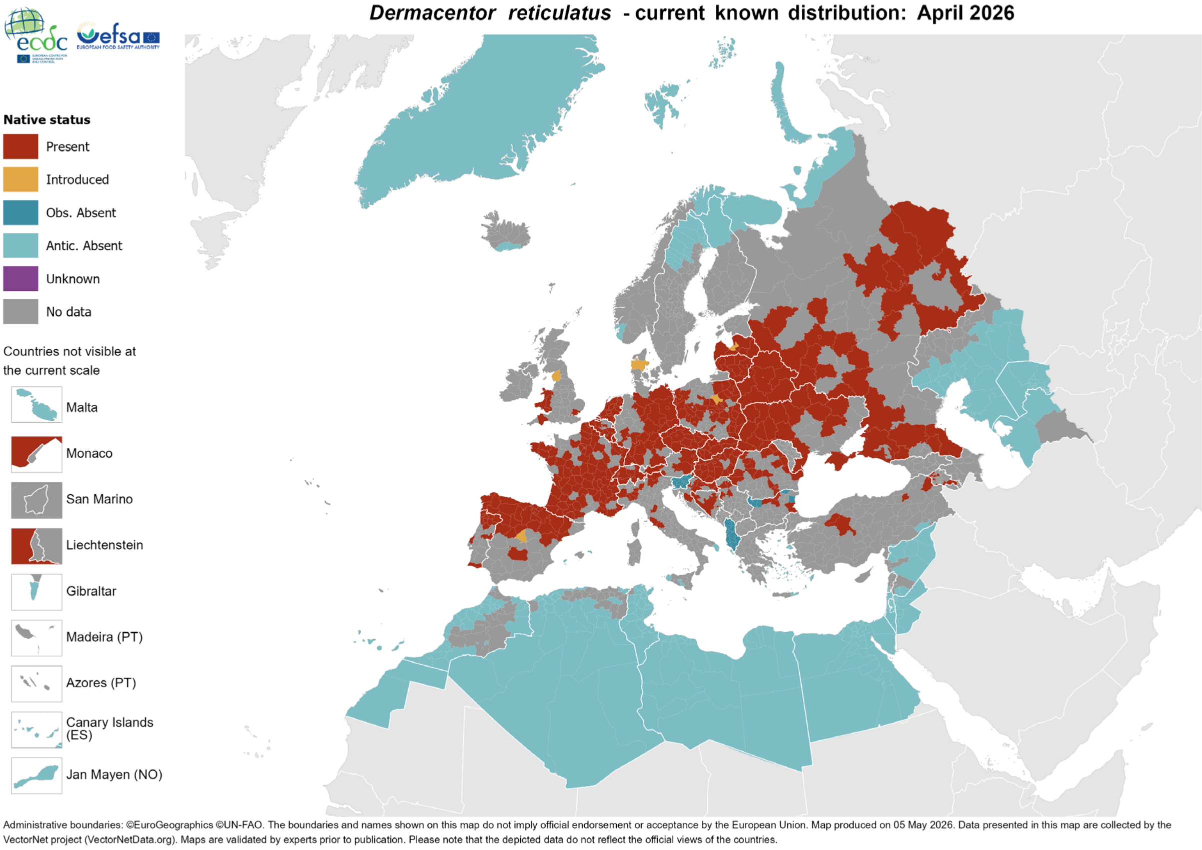

FIGURE 9 Vector status maps of *Dermacentor reticulatus* provided by VectorNet (last updated in April 2026).

Figure 9 displays the geographic distribution of *D. reticulatus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *D. reticulatus* can be used to assess the risk for TBEV, for which it can be a highly likely biological vector, and for *Borrelia burgdorferi* s.l. and *Coxiella burnetii* for which it can be a potential biological vector.

3.2.2.2 | *Hyalomma lusitanicum*

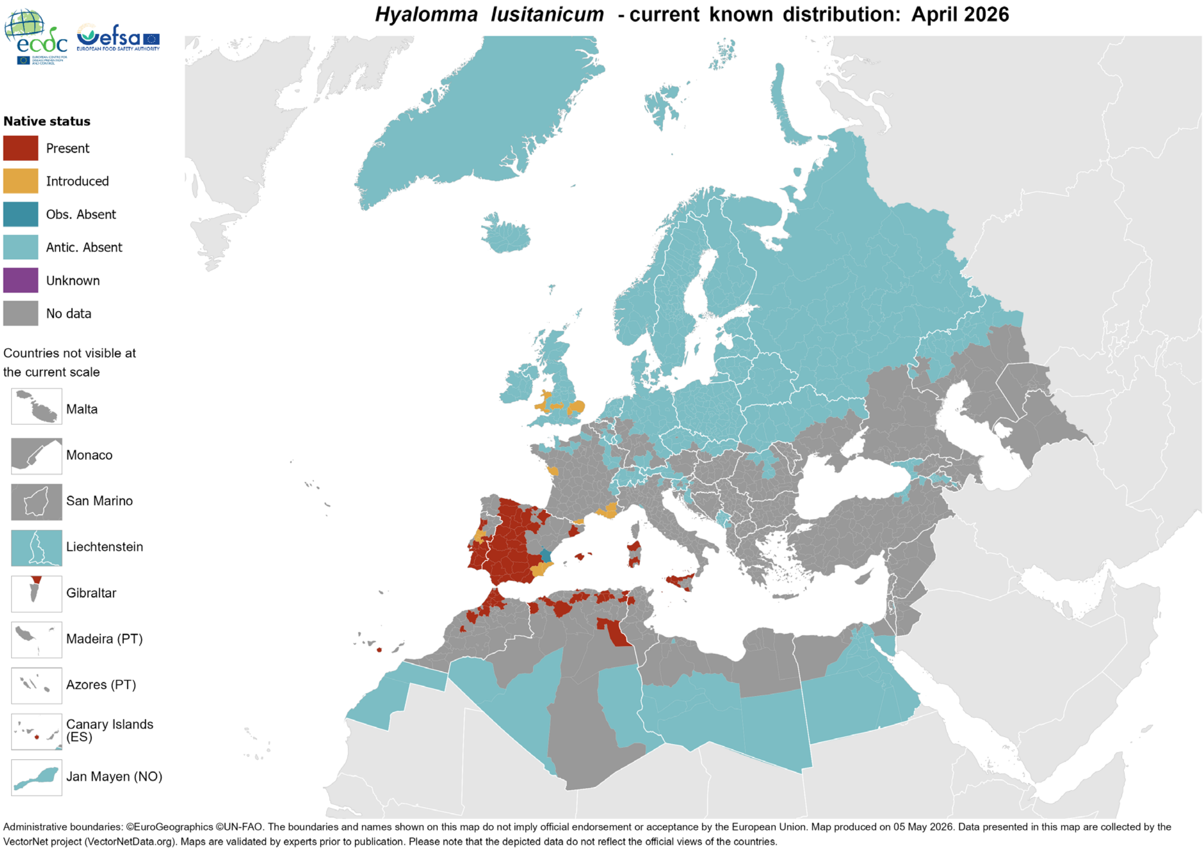

FIGURE 10 Vector status maps of *Hyalomma lusitanicum* provided by VectorNet (last updated in April 2026).

Figure 10 displays the geographic distribution of *H. lusitanicum* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *H. lusitanicum* can be used to assess the risk for *Borrelia burgdorferi* s.l. for which it can be a potential biological vector.

3.2.2.3 | *Hyalomma marginatum*

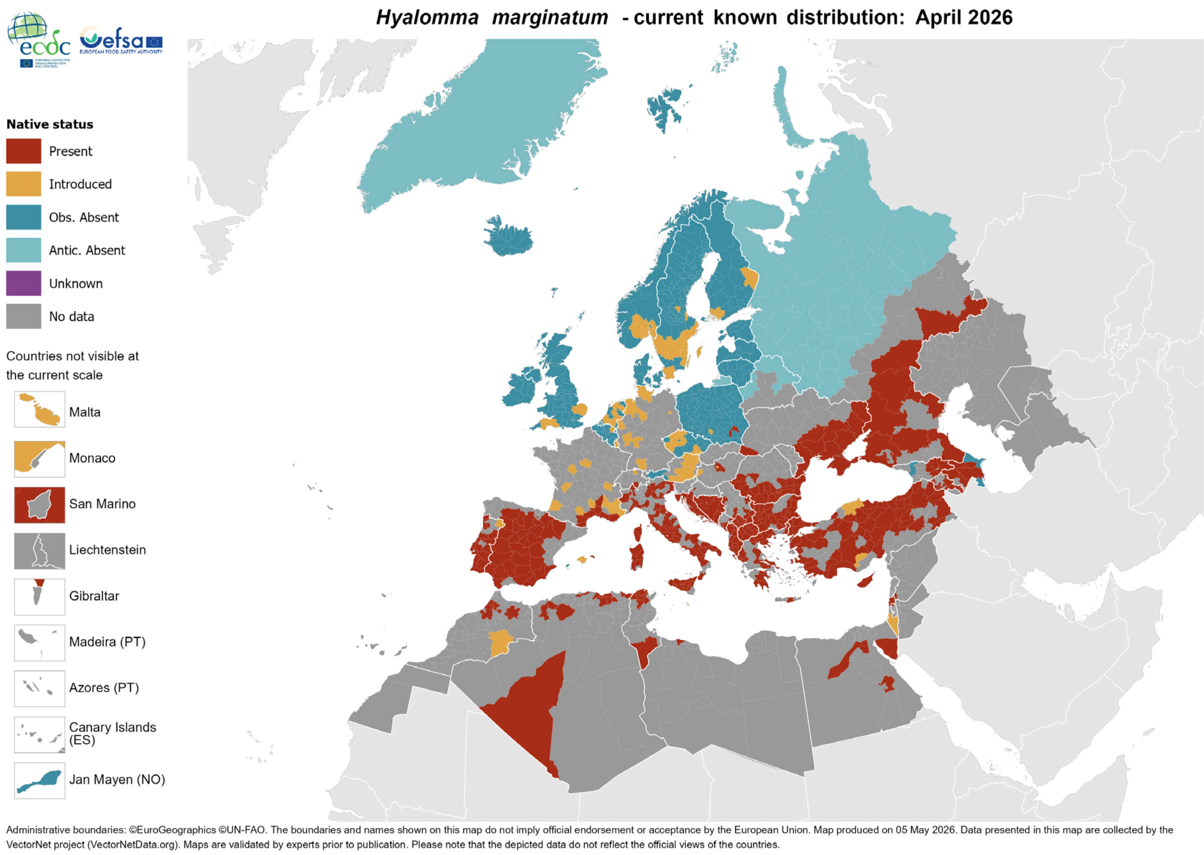

FIGURE 11 Vector status maps of *Hyalomma marginatum* provided by VectorNet (last updated in April 2026).

Figure 11 displays the geographic distribution of *H. marginatum* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *H. marginatum* can be used to assess the risk for *Borrelia burgdorferi* s.l. and CCHFV for which it can be a potential biological vector.

3.2.2.4 | *Ixodes ricinus*

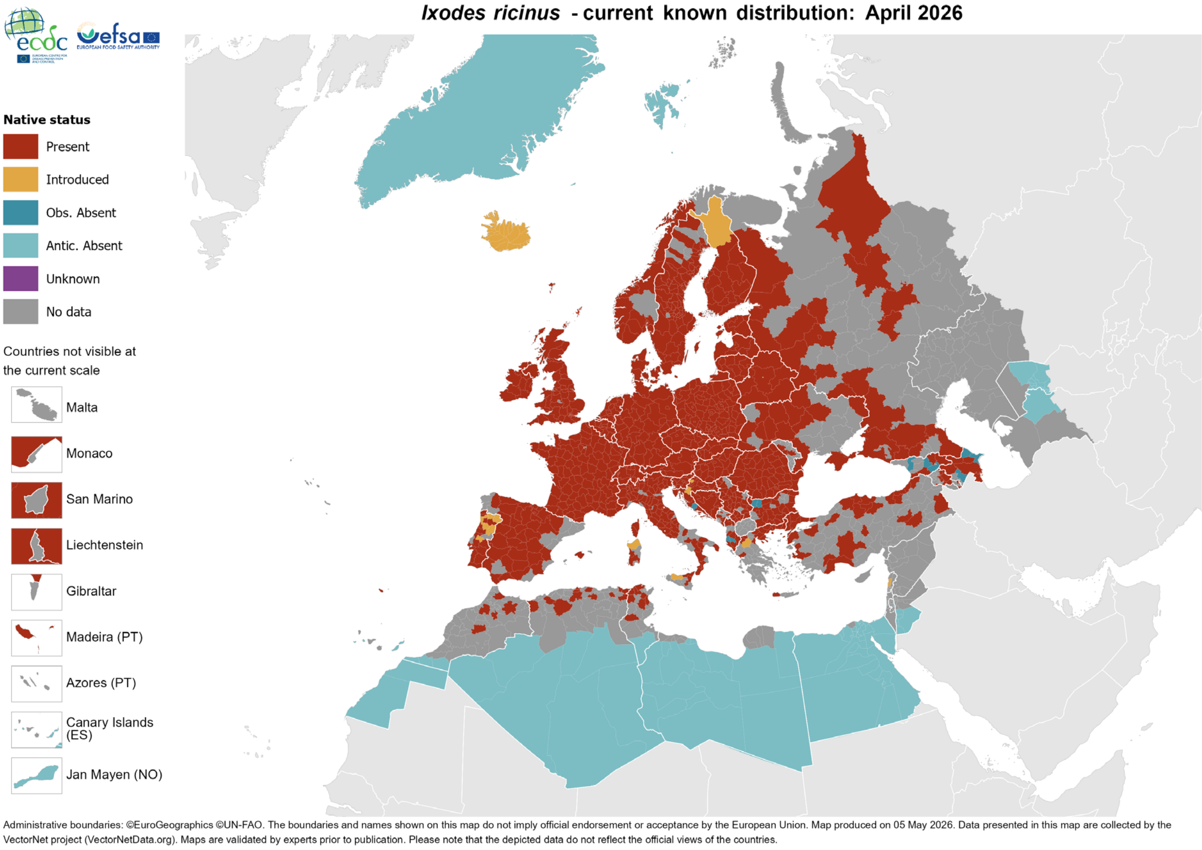

FIGURE 12 Vector status maps of *Ixodes ricinus* provided by VectorNet (last updated in April 2026).

Figure 12 displays the geographic distribution of *I. ricinus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *I. ricinus* can be used to assess the risk for TBEV and *Borrelia burgdorferi* s.l. for which it can be a highly likely biological vector, and for and *Coxiella burnetii* for which it can be a potential biological vector.

3.2.2.5 | *Ixodes persulcatus*

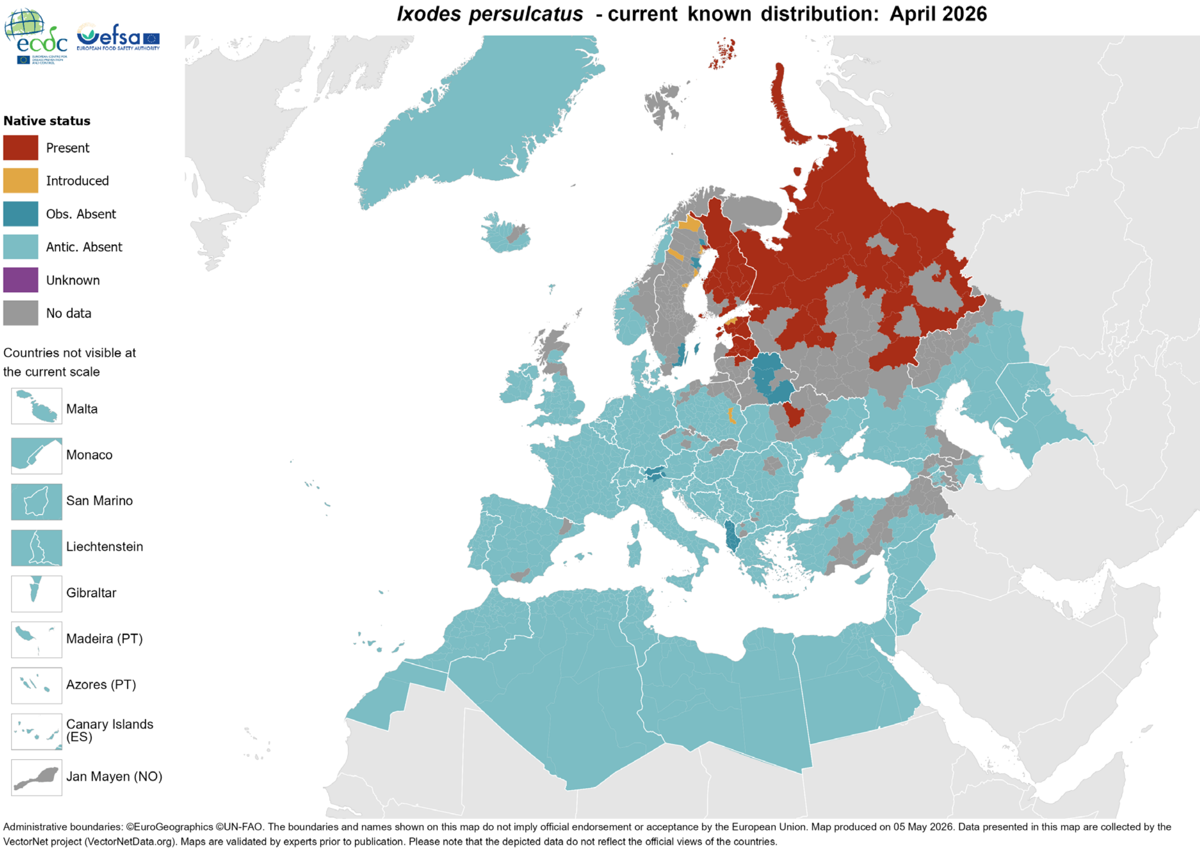

FIGURE 13 Vector Status maps of *Ixodes persulcatus* provided by Vectornet (last updated in April 2026).

Figure 13 displays the geographic distribution of *I. persulcatus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *I. persulcatus* can be used to assess the risk for TBEV and *Borrelia burgdorferi* s.l. for which it can be a highly likely biological vector.

3.2.2.6 | *Rhipicephalus bursa*

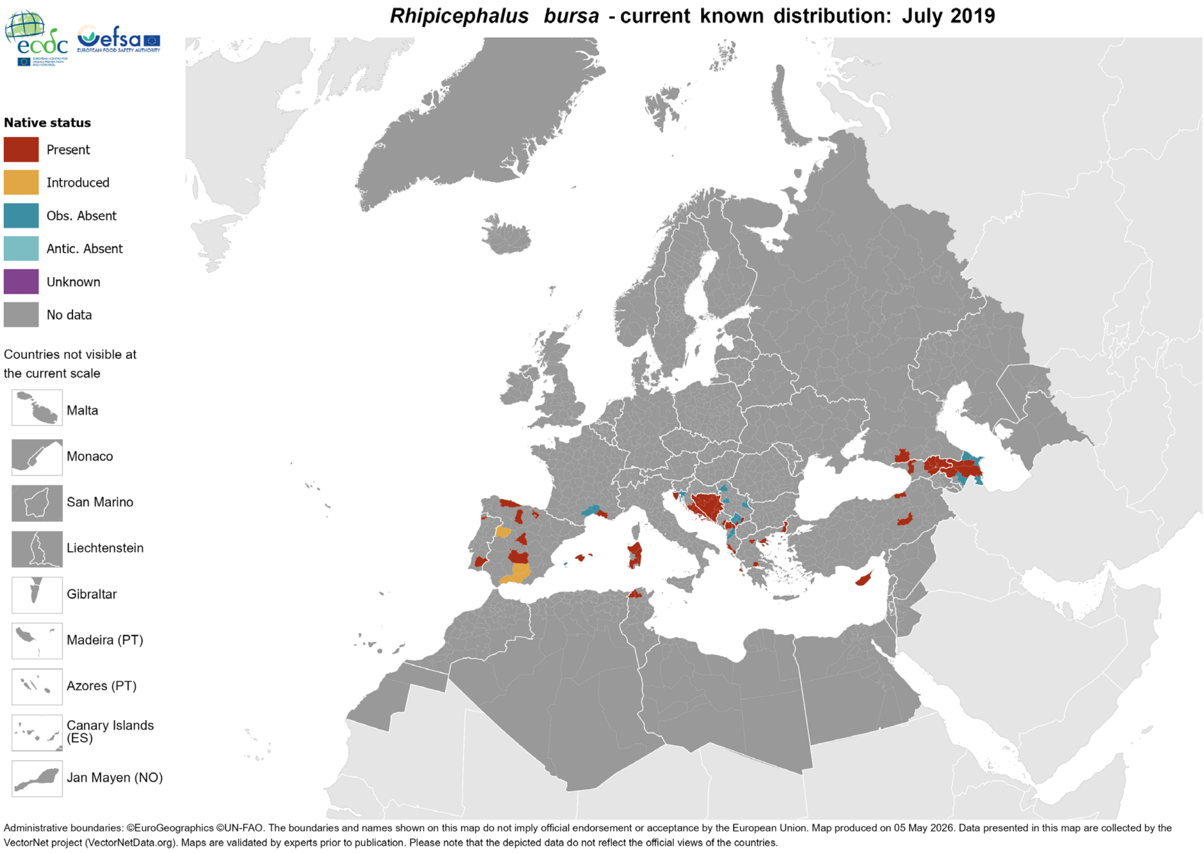

FIGURE 14 Vector Status maps of *Rhipicephalus bursa* provided by VectorNet (last updated in July 2019).

Figure 14 displays the geographic distribution of *Rh. bursa* according to the vector status maps produced by VectorNet in July 2019. The geographic distribution data of *Rh. bursa* can be used to assess the risk for *Borrelia burgdorferi* s.l. for which it can be a potential biological vector.

3.2.2.7 | *Rhipicephalus sanguineus*

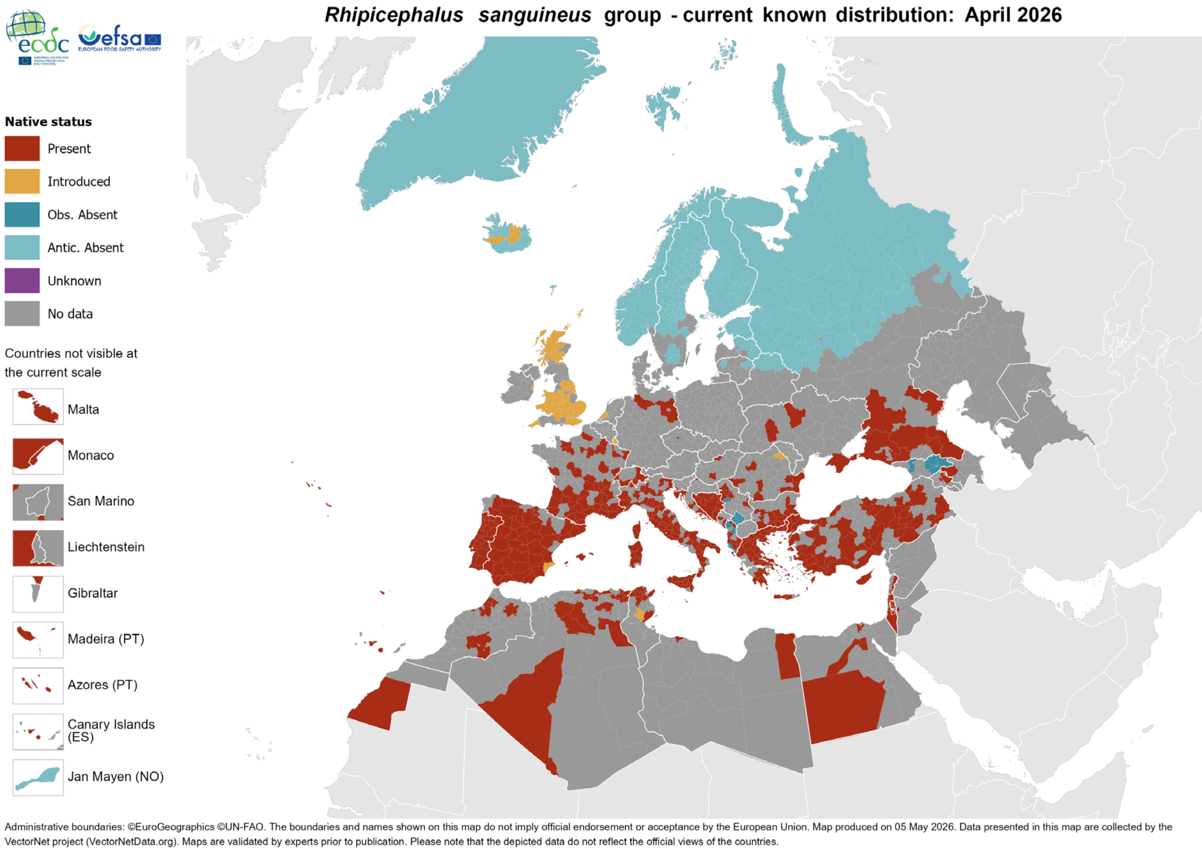

FIGURE 15 Vector Status maps of *Rhipicephalus sanguineus* provided by VectorNet (last updated in April 2026).

Figure 15 displays the geographic distribution of *Rh. sanguineus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Rh. sanguineus* can be used to assess the risk for *Borrelia burgdorferi* s.l. for which it can be a potential biological vector.

3.2.3 | Mosquitoes

3.2.3.1 | *Aedes aegypti*

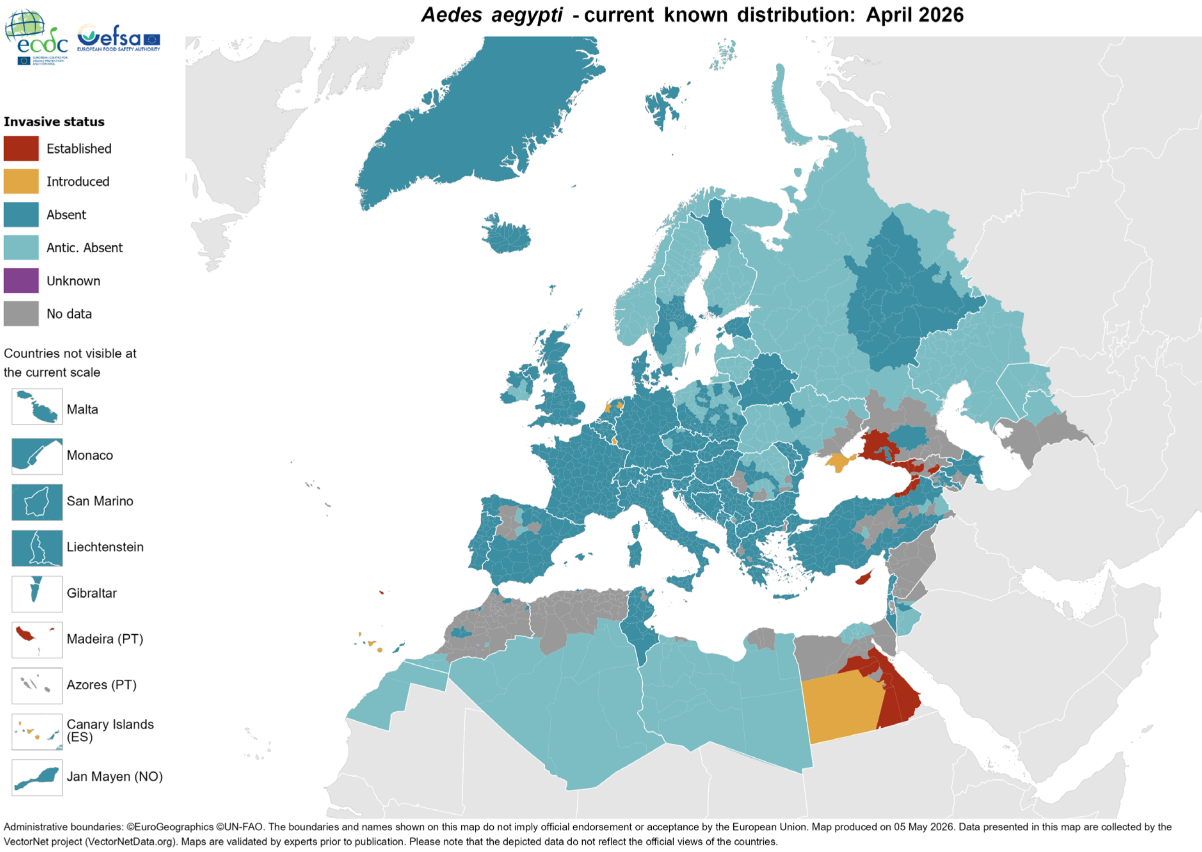

FIGURE 16 Vector Status maps of *Aedes aegypti* provided by VectorNet (last updated in April 2026).

Figure 16 displays the geographic distribution of *A. aegypti* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *A. aegypti* can be used to assess the risk for RVFV, for which it can be a highly likely biological vector, and for WEEV, JEV, CVV for which it can be a potential biological vector. In addition, it can be a potential mechanical vector for LSDV.

3.2.3.2 | *Aedes albopictus*

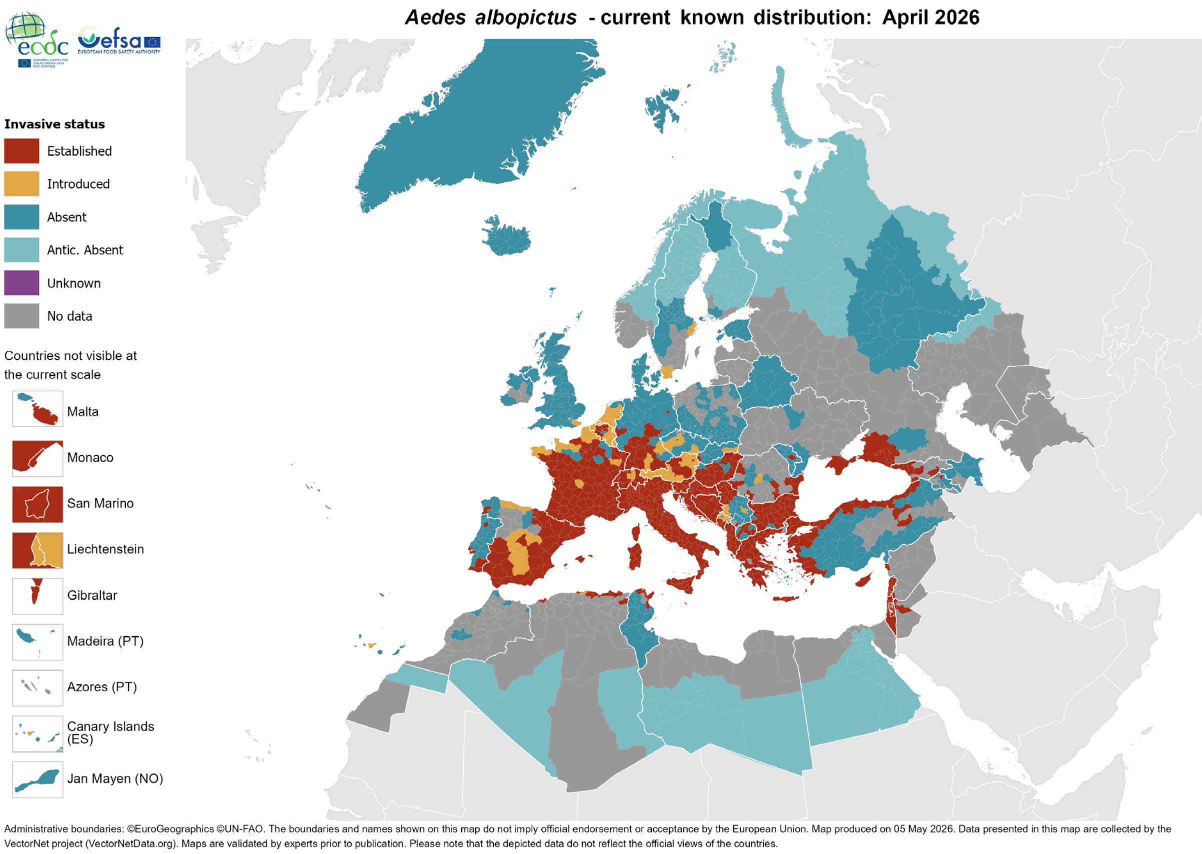

FIGURE 17 Vector Status maps of *Aedes albopictus* provided by VectorNet (last updated in April 2026).

Figure 17 displays the geographic distribution of *Aedes albopictus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ae. albopictus* can be used to assess the risk for WEEV, EEEV, JEV, CVV, RVFV, WNV for which it can be a potential biological vector.

3.2.3.3 | *Aedes caspius*

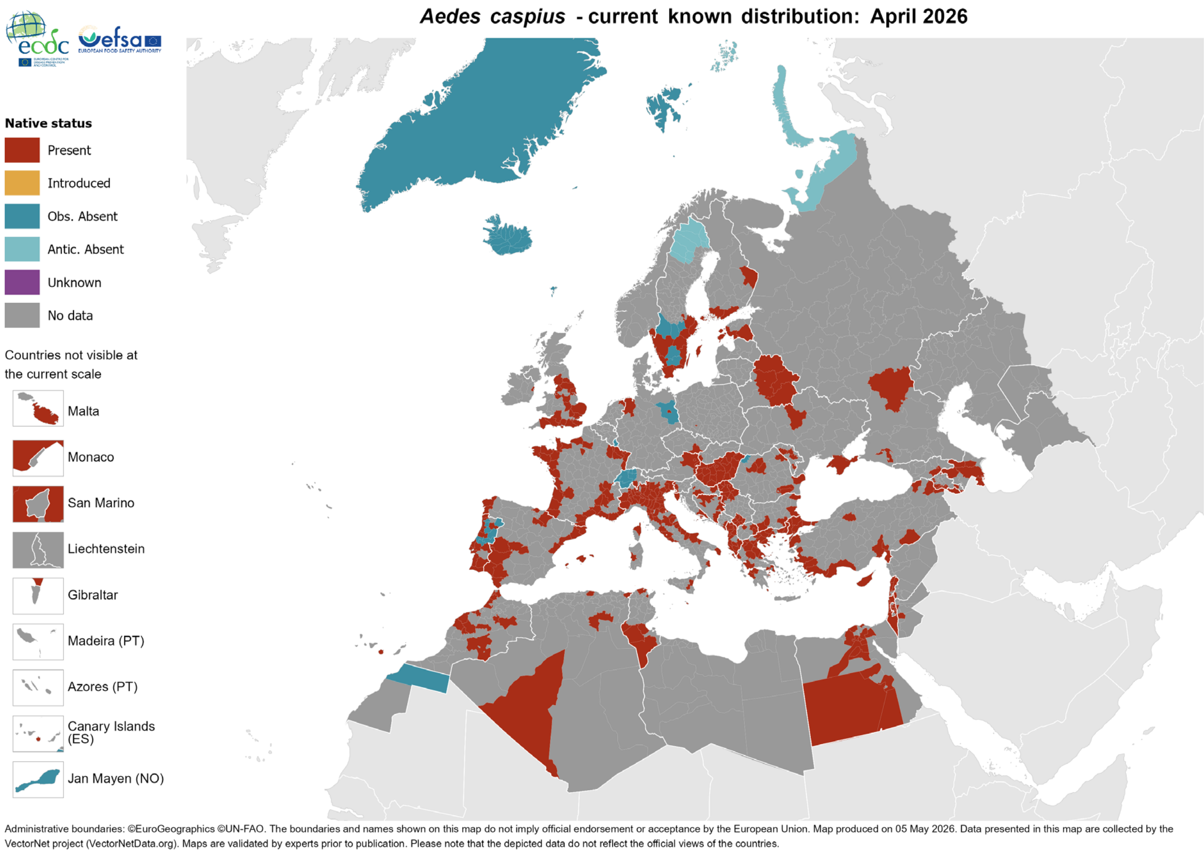

FIGURE 18 Vector Status maps of *Aedes caspius* provided by VectorNet (last updated in April 2026).

Figure 18 displays the geographic distribution of *Ae. caspius* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ae. caspius* can be used to assess the risk for RVFV for which it can be a potential biological vector.

3.2.3.4 | *Aedes detritus*

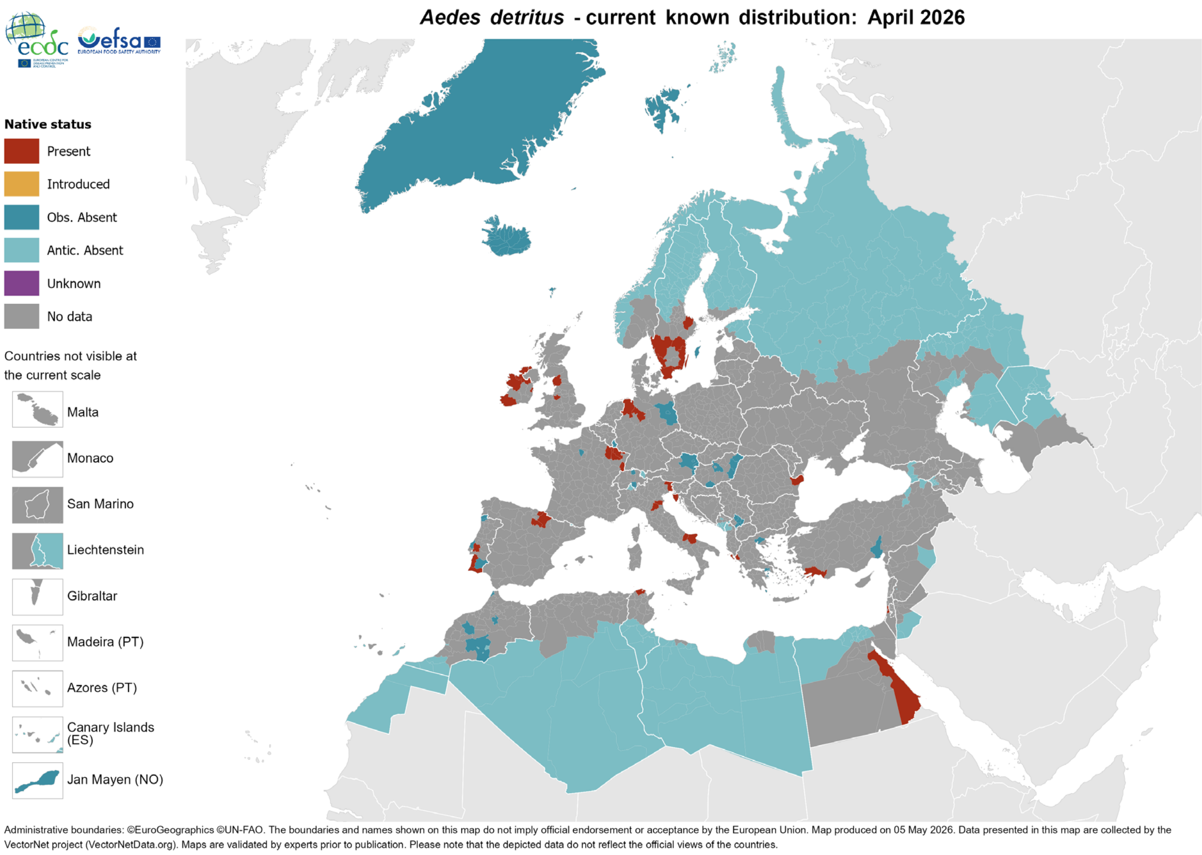

FIGURE 19 Vector Status maps of *Aedes detritus* provided by VectorNet (last updated in April 2026).

Figure 19 displays the geographic distribution of *Ae. detritus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ae. detritus* can be used to assess the risk for RVFV, VEEV, WNV for which it can be a potential biological vector.

3.2.3.5 | *Aedes japonicus*

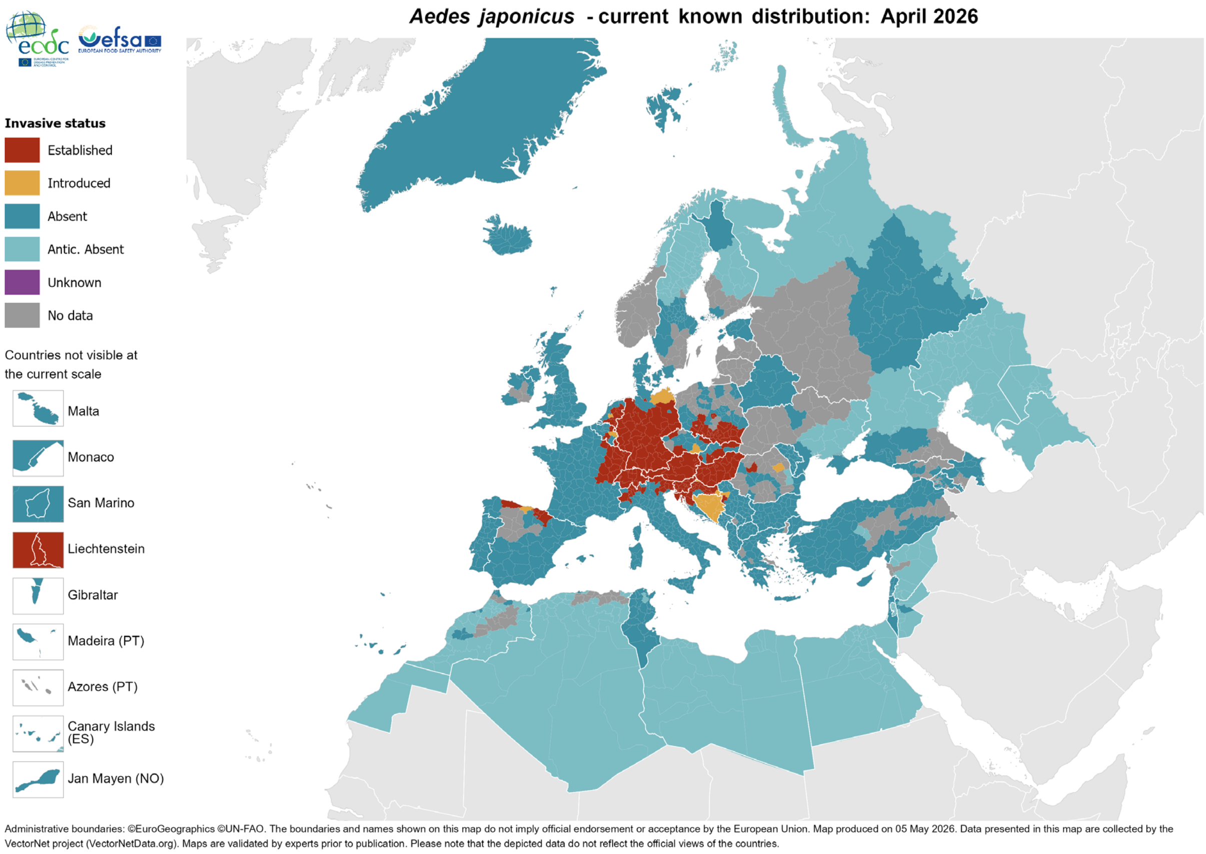

FIGURE 20 Vector Status maps of *Aedes japonicus* provided by VectorNet (last updated in April 2026).

Figure 20 displays the geographic distribution of *Ae. japonicus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ae. japonicus* can be used to assess the risk for EEEV, JEV, CVV for which it can be a potential biological vector.

3.2.3.6 | *Aedes vexans*

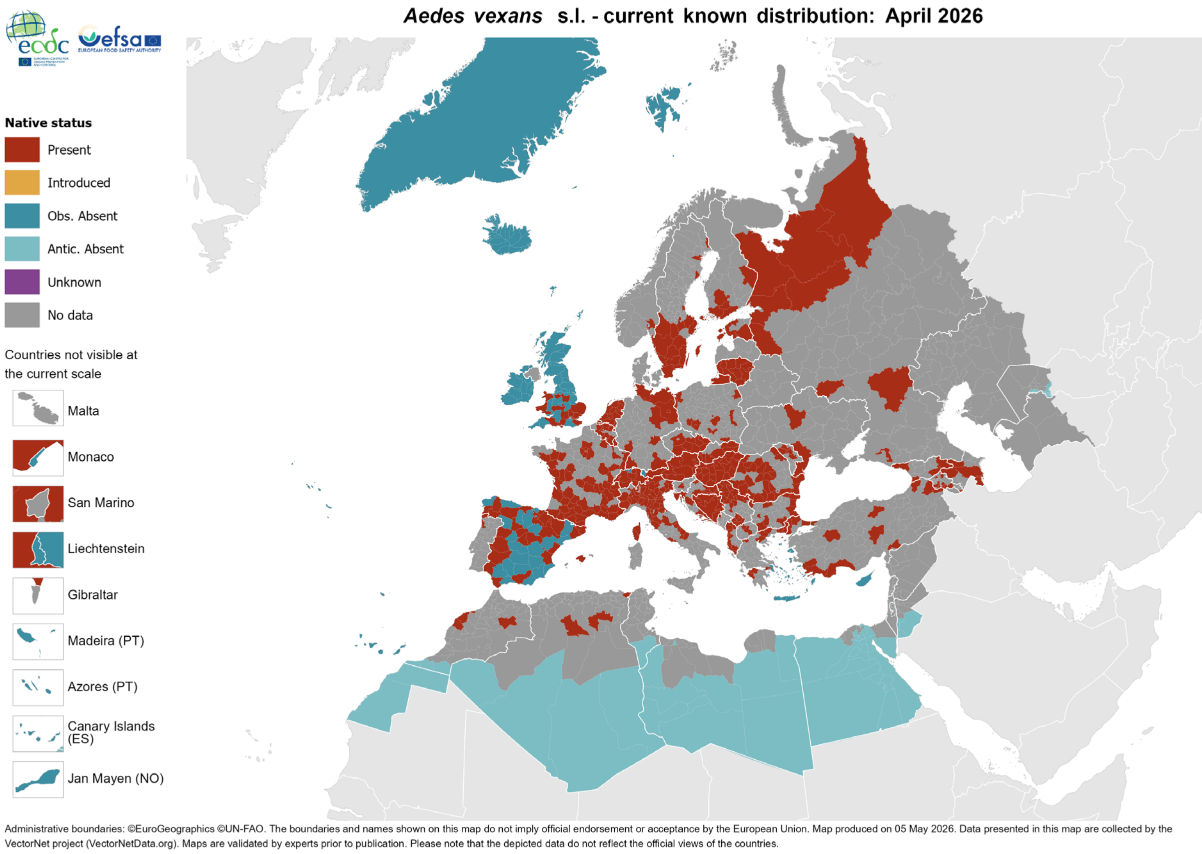

FIGURE 21 Vector Status maps of *Aedes vexans* provided by VectorNet (last updated in April 2026).

Figure 21 displays the geographic distribution of *Ae. vexans* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ae. vexans* can be used to assess the risk for EEEV, RVFV, VEEV WNV for which it can be a potential biological vector.

3.2.3.7 | *Culiseta annulata*

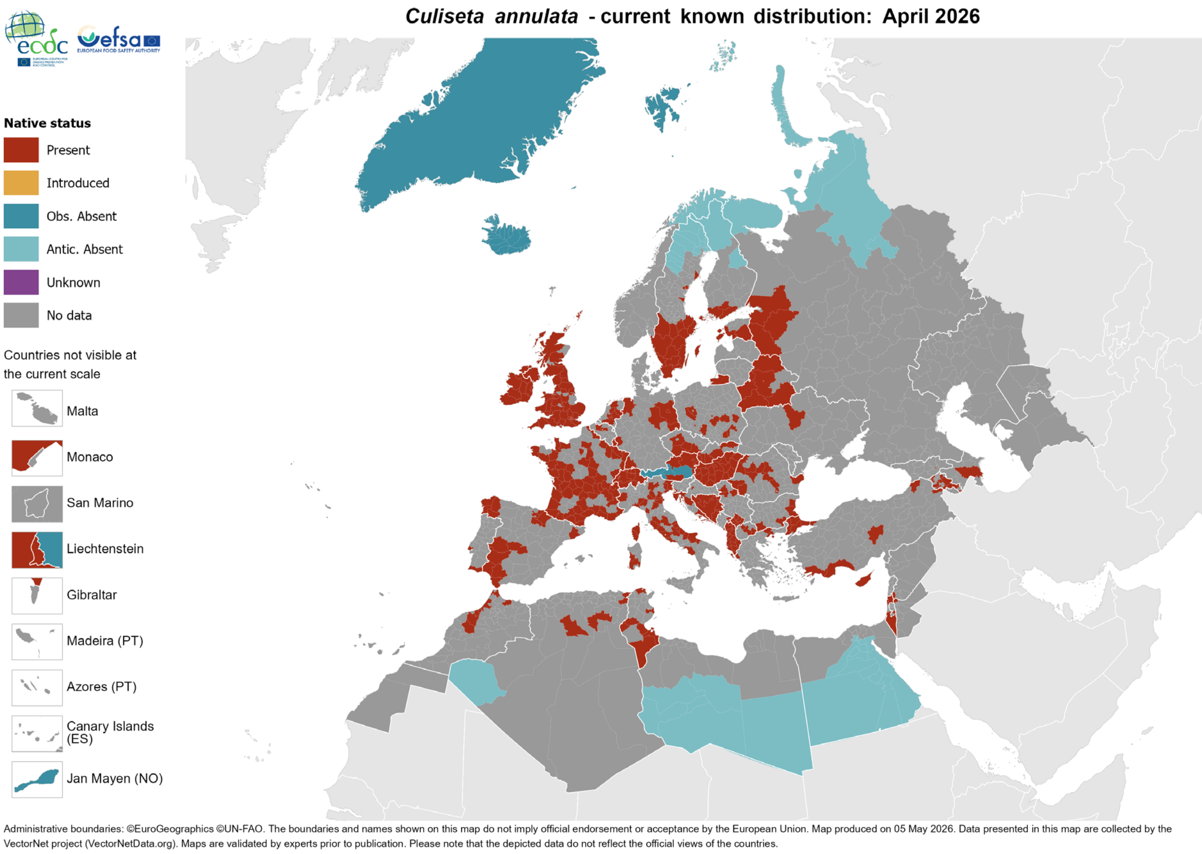

FIGURE 22 Vector Status maps of *Culiseta annulata* provided by VectorNet (last updated in April 2026).

Figure 22 displays the geographic distribution of *Cs. annulata* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cs. annulata* can be used to assess the risk for JEV for which it can be a potential biological vector.

3.2.3.8 | *Culex antennatus*

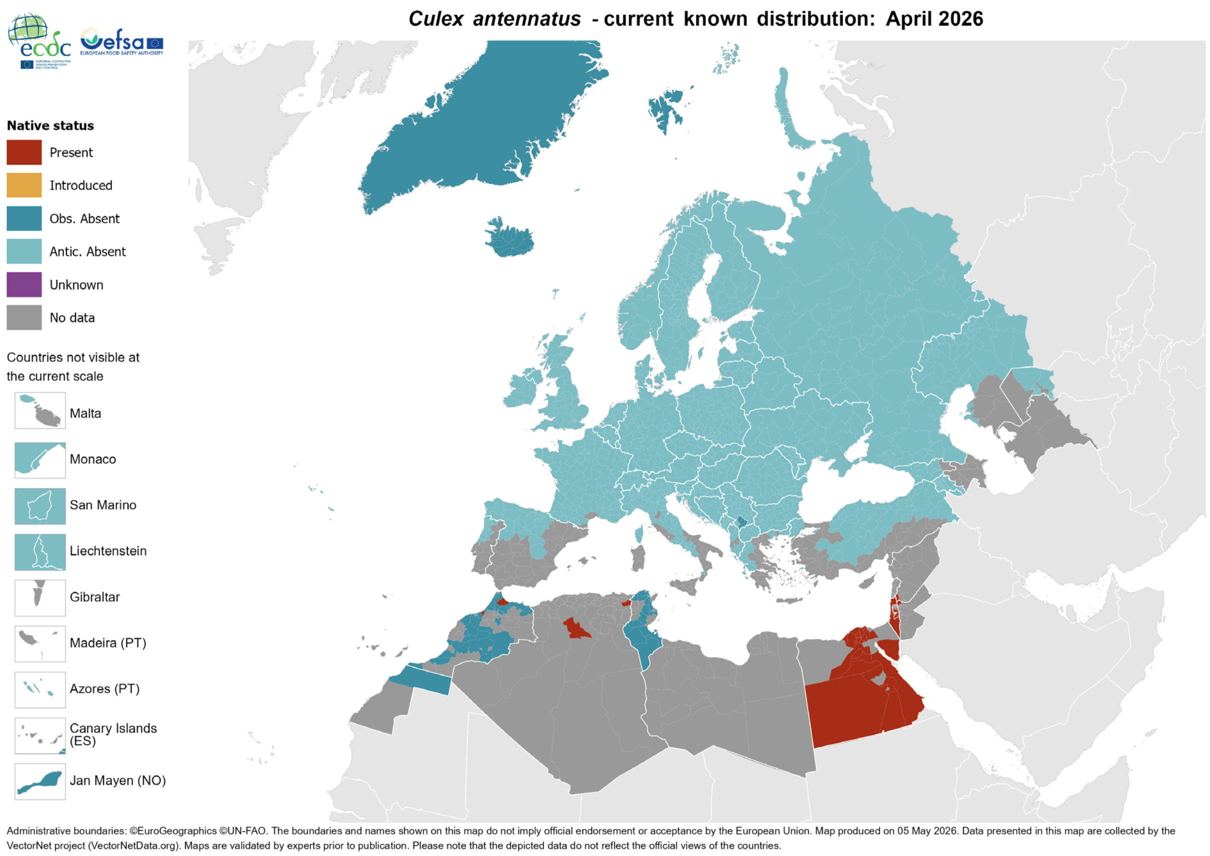

FIGURE 23 Vector Status maps of *Culex antennatus* provided by VectorNet (last updated in April 2026).

Figure 23 displays the geographic distribution of *Cx. antennatus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. antennatus* can be used to assess the risk for RVFV for which it can be a potential biological vector.

3.2.3.9 | *Culex modestus*

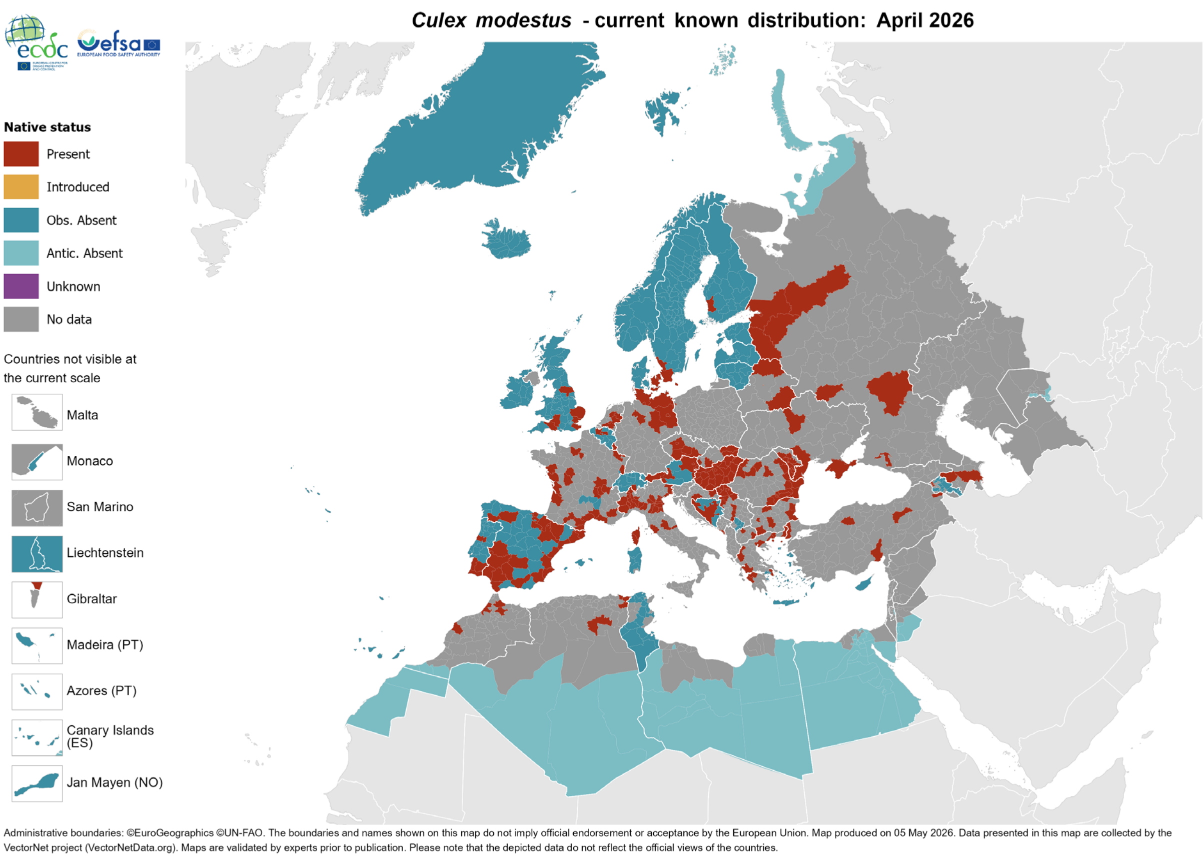

FIGURE 24 Vector Status maps of *Culex modestus* provided by VectorNet (last updated in April 2026).

Figure 24 displays the geographic distribution of *Cx. modestus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. modestus* can be used to assess the risk for WNV for which it can be a potential biological vector.

3.2.3.10 | *Culex prexiguus/univittatus*

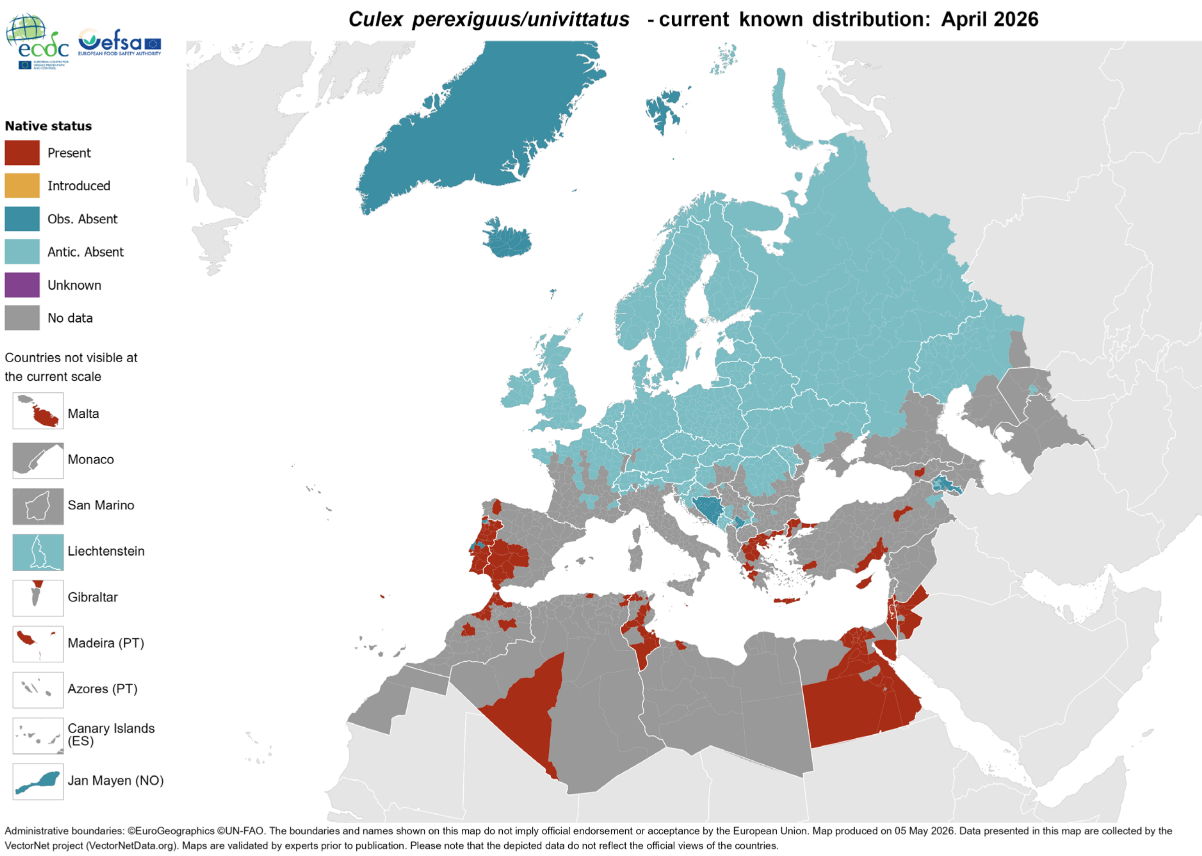

FIGURE 25 Vector Status maps of *Culex perexiguus/univittatus* provided by VectorNet (last updated in April 2026).

Figure 25 displays the geographic distribution of *Cx. perexiguus/univittatus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. perexiguus/univittatus* can be used to assess the risk for SBV and WNV, for which it can be a highly likely biological vector, and for CVV, SLEV and VEEV for which it can be a potential biological vector.

3.2.3.11 | *Culex pipiens group*

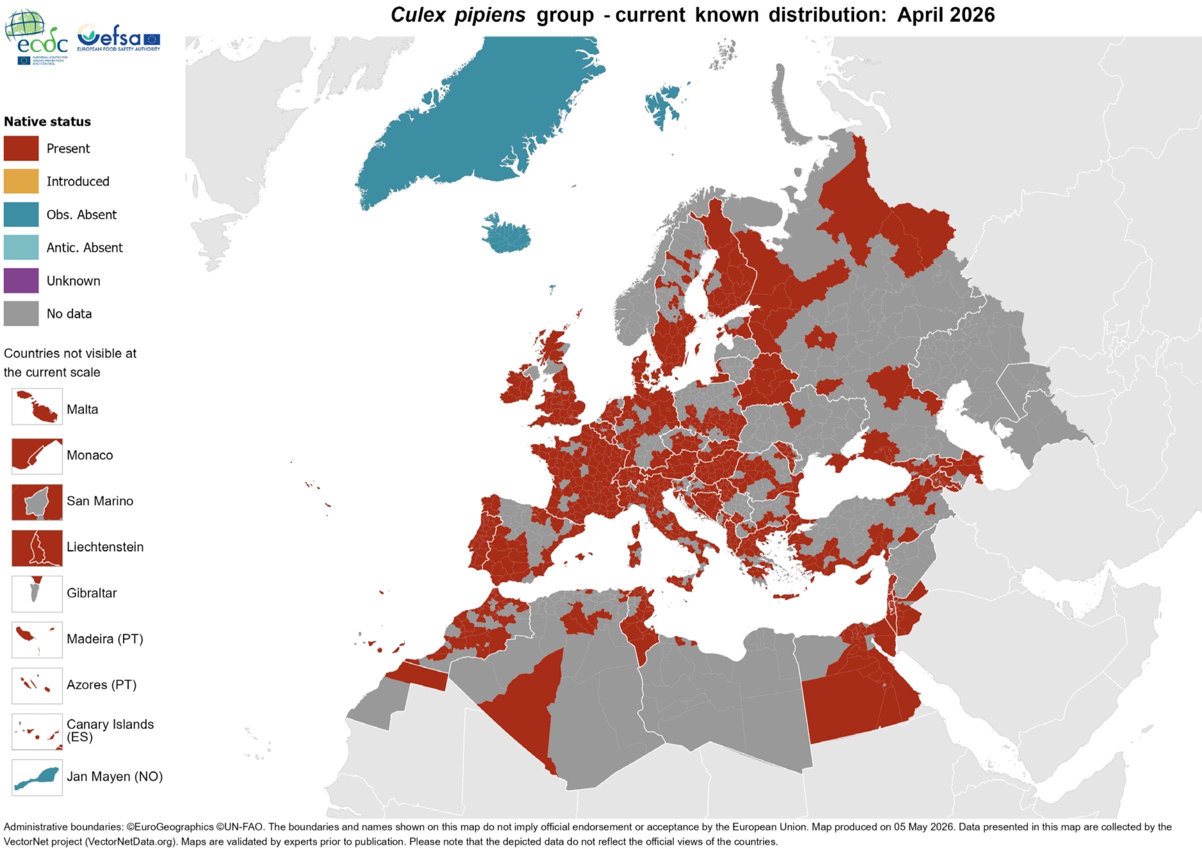

FIGURE 26 Vector Status maps of *Culex pipiens group* provided by VectorNet (last updated in April 2026).

Figure 26 displays the geographic distribution of *Cx. pipiens group* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. pipiens group* can be used to assess the risk for JEV, SBV and WNV, for which it can be a highly likely biological vector, and for RVFV, SLEV and VEEV for which it can be a potential biological vector.

3.2.3.12 | *Culex torrentium*

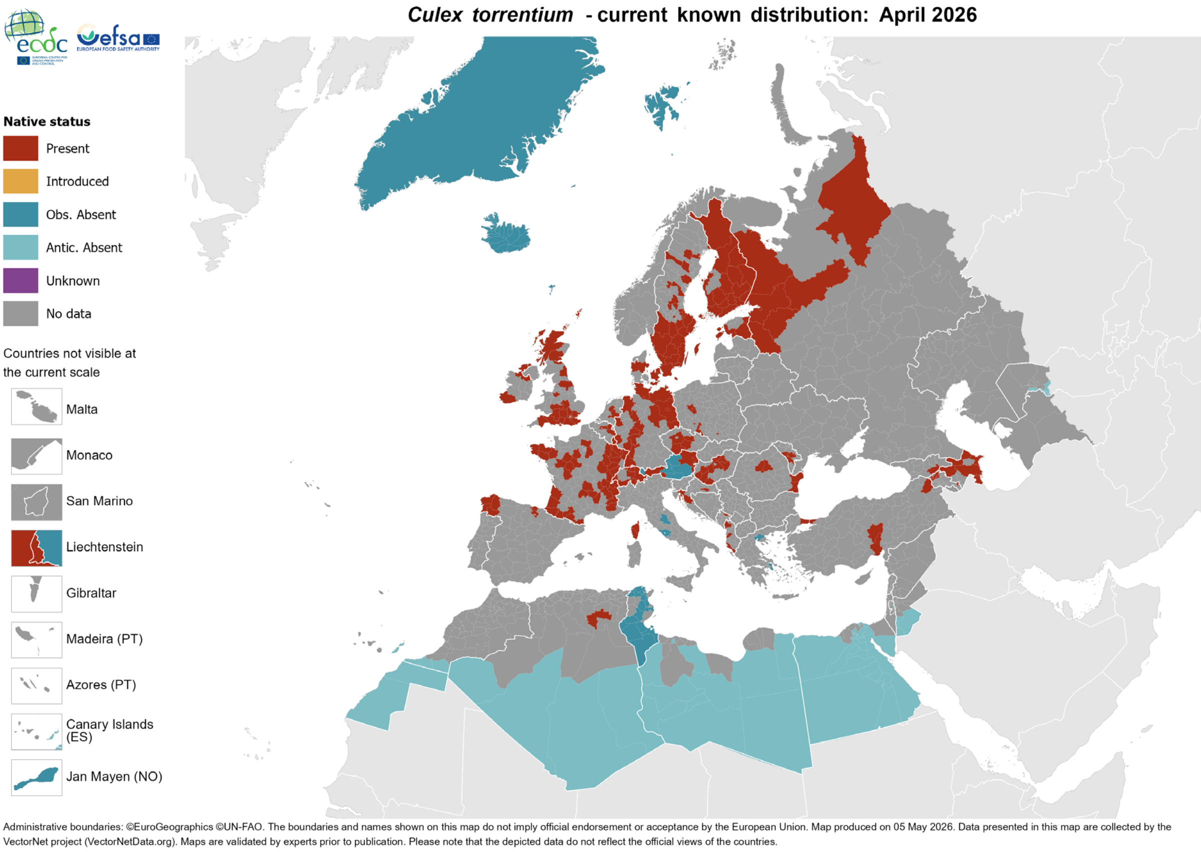

FIGURE 27 Vector Status maps of *Culex torrentium* provided by VectorNet (last updated in April 2026).

Figure 27 displays the geographic distribution of *Cx. torrentium* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. torrentium* can be used to assess the risk for WNV for which it can be a potential biological vector.

3.2.3.13 | *Culex tritaeniorhynchus*

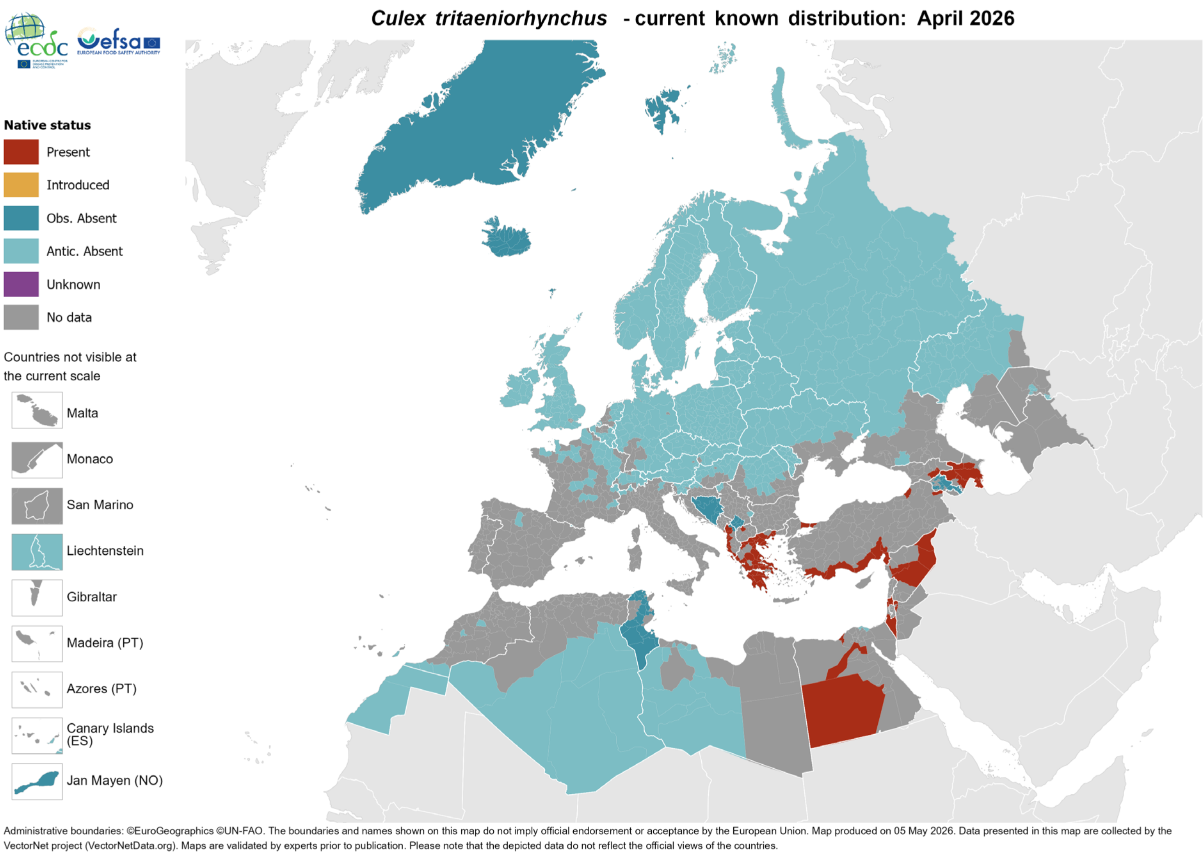

FIGURE 28 Vector Status maps of *Culex tritaeniorhynchus* provided by VectorNet (last updated in April 2026).

Figure 28 displays the geographic distribution of *Cx. tritaeniorhynchus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Cx. tritaeniorhynchus* can be used to assess the risk for JEV, for which it can be a highly likely biological vector, and for RVFV for which it can be a potential biological vector.

3.2.4 | Sandflies

3.2.4.1 | *Phlebotomus mascittii*

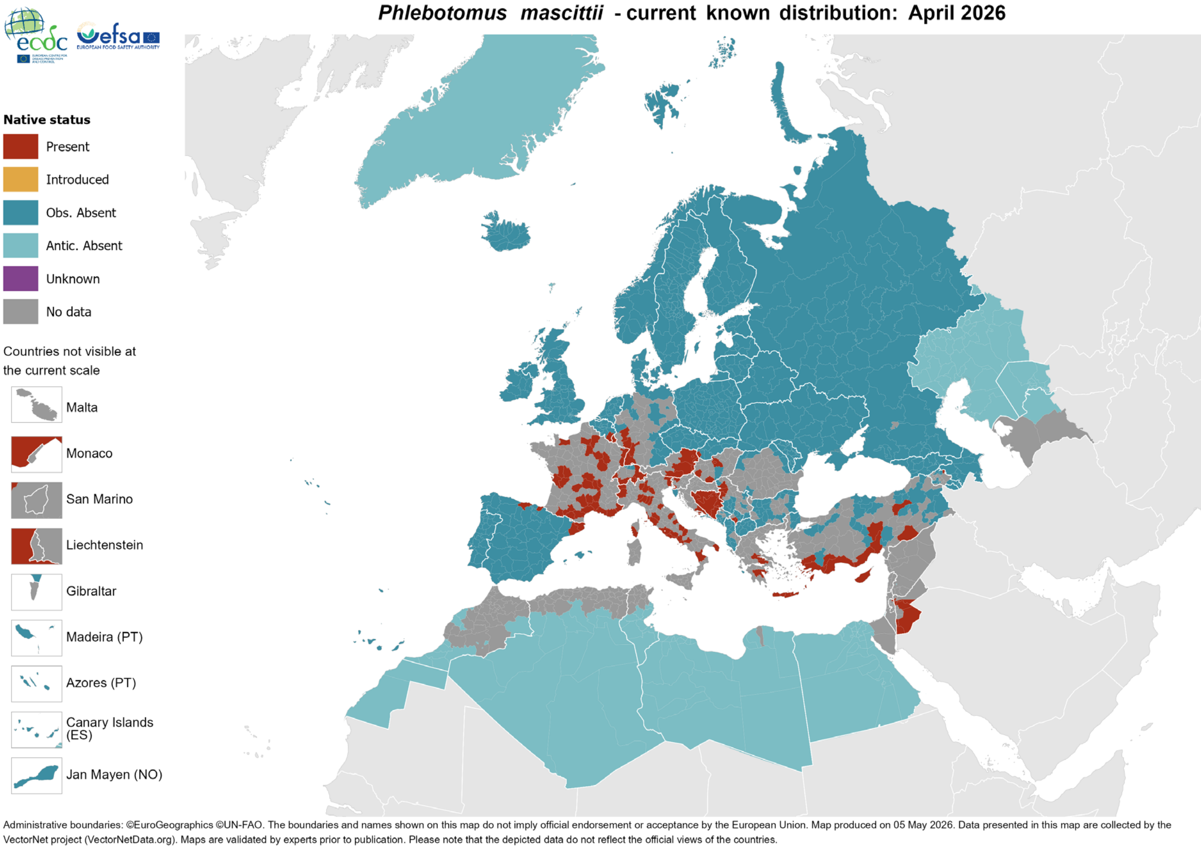

FIGURE 29 Vector Status maps of *Phlebotomus mascittii* provided by VectorNet (last updated in April 2026).

Figure 29 displays the geographic distribution of *Ph. mascittii* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ph. mascittii* can be used to assess the risk for *L. infantum* for which it can be a potential biological vector.

3.2.4.2 | *Phlebotomus neglectus*

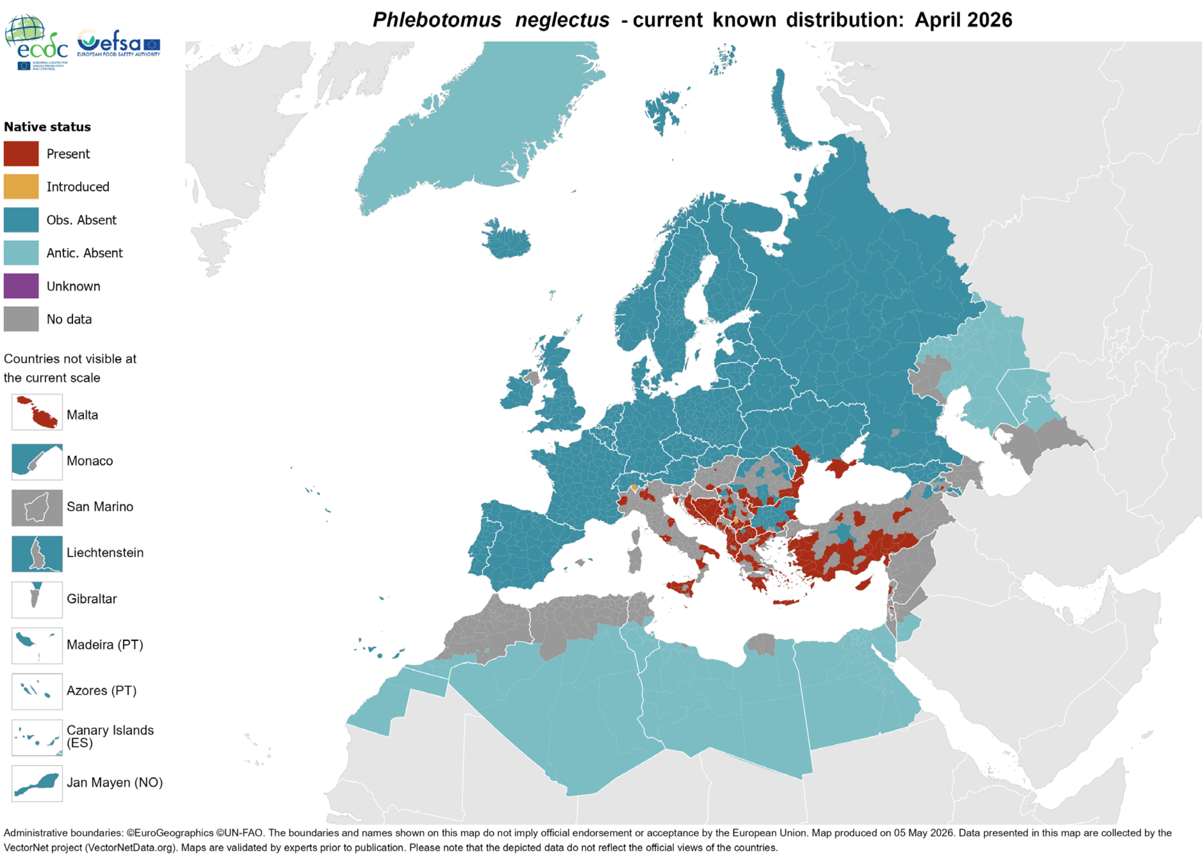

FIGURE 30 Vector Status maps of *Phlebotomus neglectus* provided by VectorNet (last updated in April 2026).

Figure 30 displays the geographic distribution of *Ph. neglectus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ph. neglectus* can be used to assess the risk for *L. infantum* for which it can be a potential biological vector.

3.2.4.3 | *Phlebotomus papatasi*

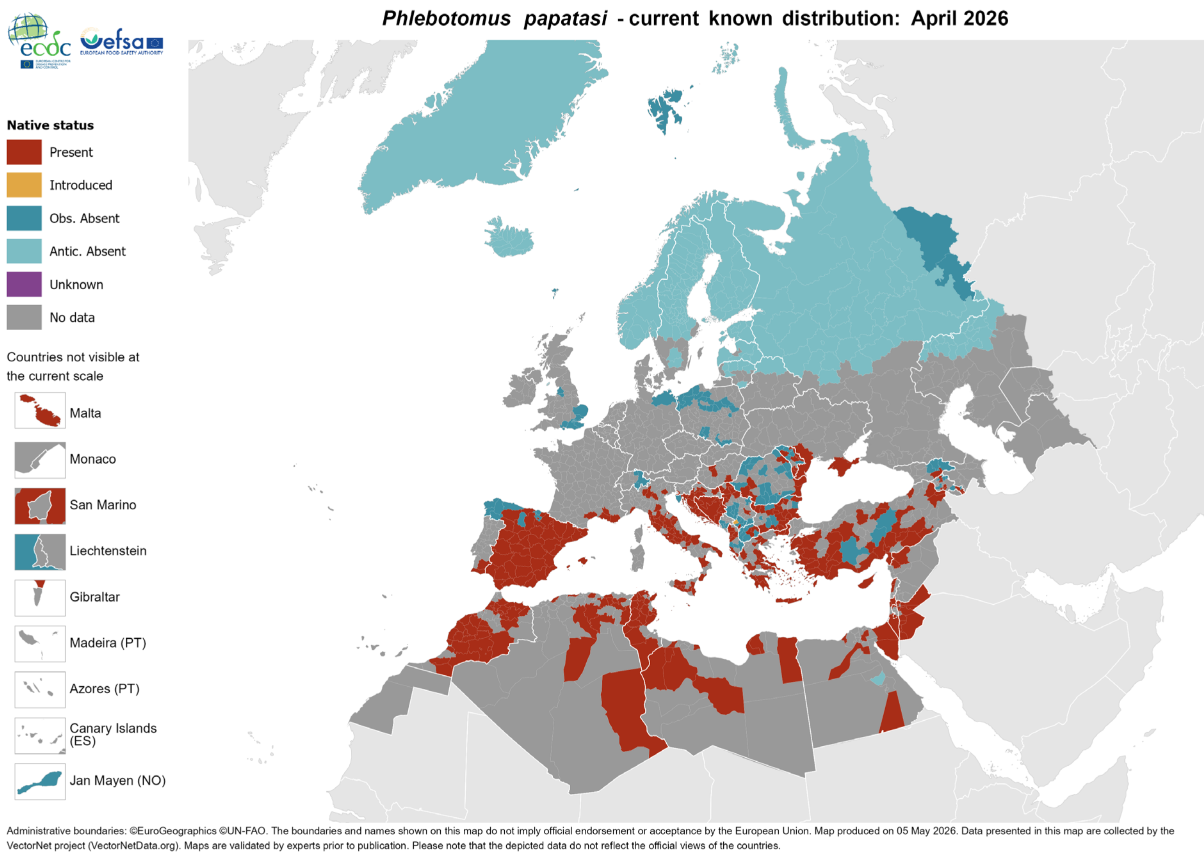

FIGURE 31 Vector Status maps of *Phlebotomus papatasi* provided by VectorNet (last updated in April 2026).

Figure 31 displays the geographic distribution of *Ph. papatasi* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ph. papatasi* can be used to assess the risk for *L. infantum* for which it can be a potential biological vector.

3.2.4.4 | *Phlebotomus perfiliewi*

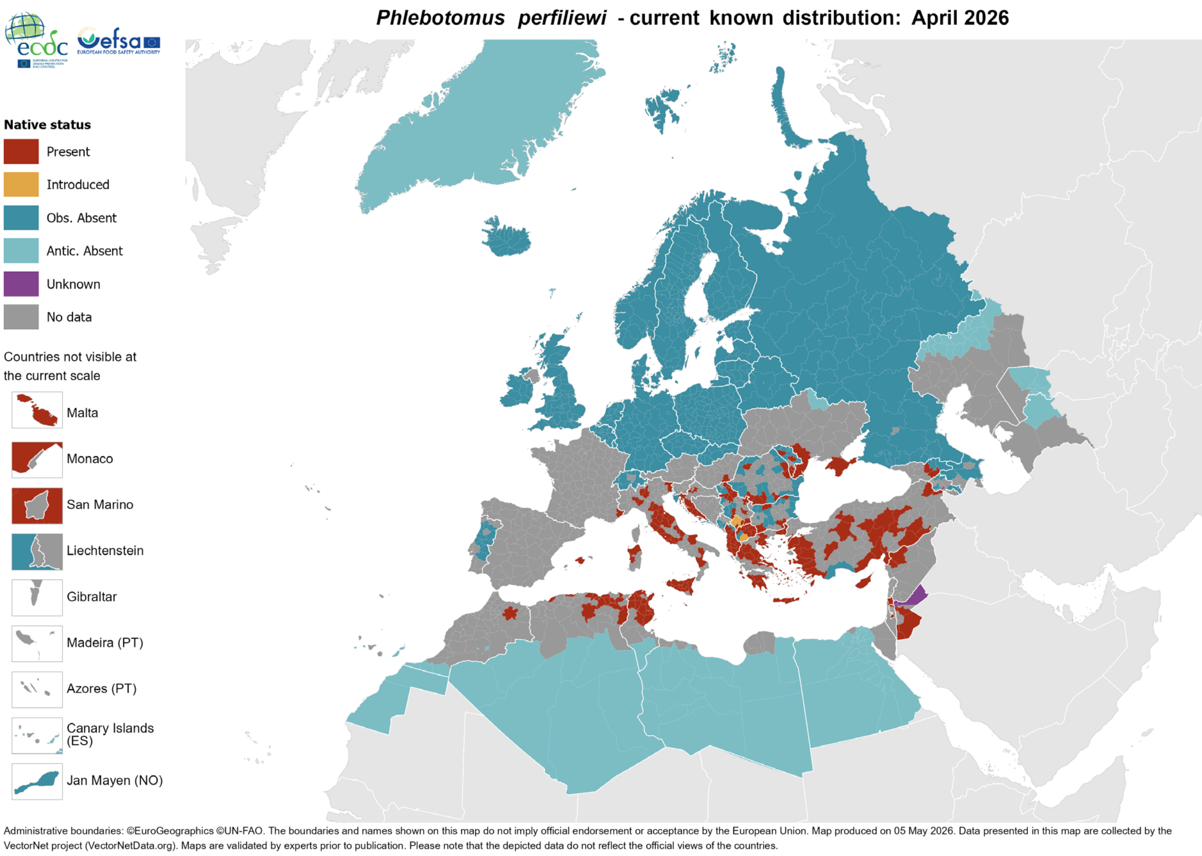

FIGURE 32 Vector Status maps of *Phlebotomus perfiliewi* provided by VectorNet (last updated in April 2026).

Figure 32 displays the geographic distribution of *Ph. perfiliewi* according to the vector status maps produced by VectorNet in . The geographic distribution data of *Ph. perfiliewi* can be used to assess the risk for *L. infantum* for which it can be a potential biological vector.

3.2.4.5 | *Phlebotomus perniciosus*

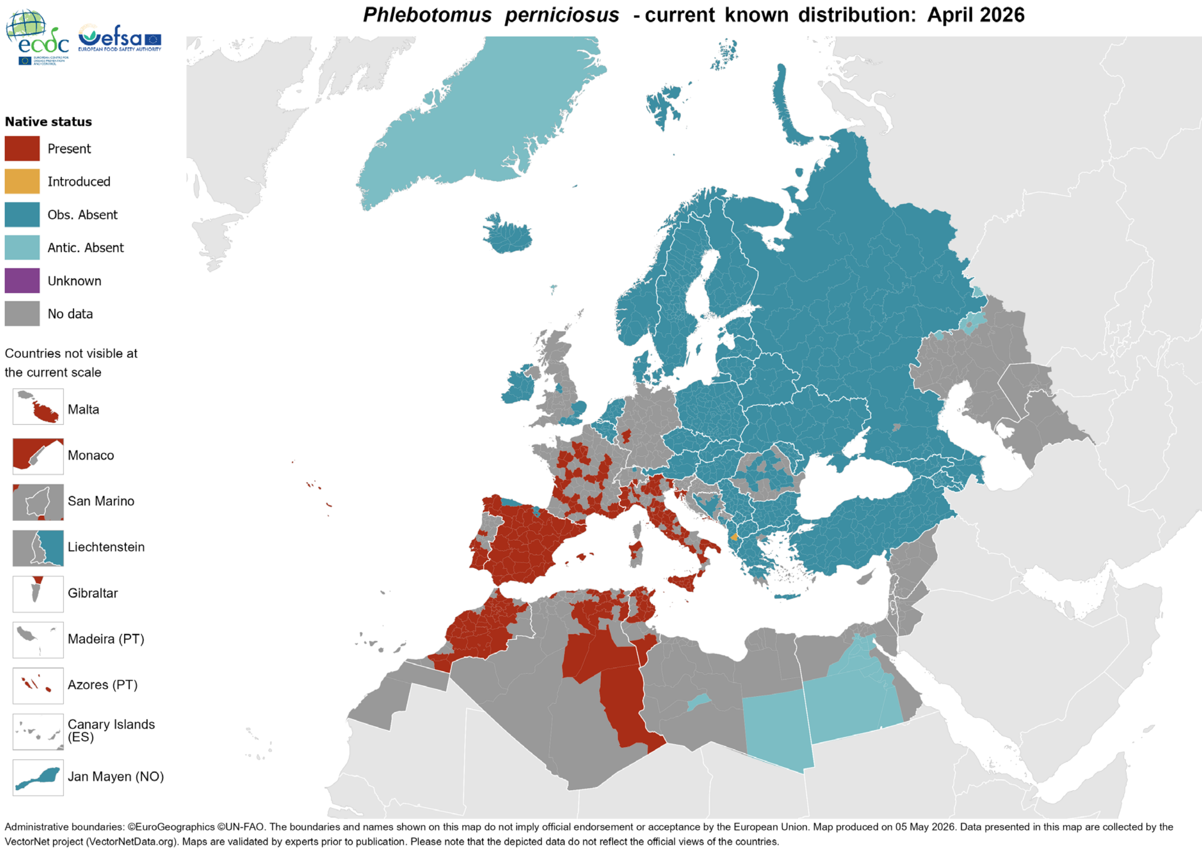

FIGURE 33 Vector Status maps of *Phlebotomus perniciosus* provided by VectorNet (last updated in April 2026).

Figure 33 displays the geographic distribution of *Ph. perniciosus* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ph. perniciosus* can be used to assess the risk for *L. infantum*, for which it can be a highly likely biological vector.

3.2.4.6 | *Phlebotomus tobbi*

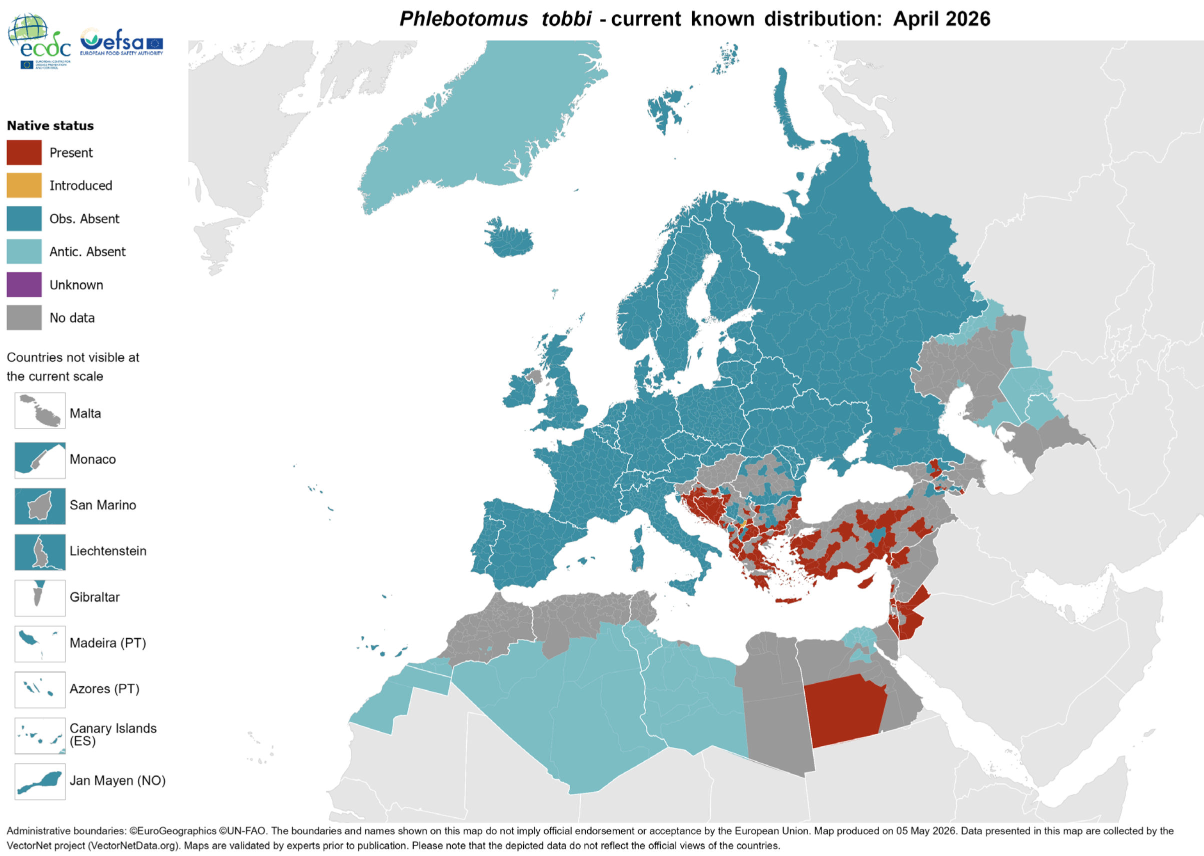

FIGURE 34 Vector Status maps of *Phlebotomus tobbi* provided by VectorNet (last updated in April 2026).

Figure 34 displays the geographic distribution of *Ph. tobbi* according to the vector status maps produced by VectorNet in March 2026. The geographic distribution data of *Ph. tobbi* can be used to assess the risk for *L. infantum* for which it can be a potential biological vector.

4 | CONCLUSIONS

4.1 | Biological vector transmission

- The SLR identified arthropod species with a highly **likely vector competence status** for eight pathogens, based on worldwide evidence from field observations and laboratory studies.
  - For all of these pathogens, vector species occur in the EU or neighbouring countries with vector distribution maps available for use in the risk assessment. These pathogens are: bluetongue virus, *Borrelia burgdorferi* s.l., Japanese encephalitis virus, *L. infantum*, Rift Valley fever virus, Schmallenberg virus, tick-borne encephalitis virus and West Nile virus.

- The SLR identified arthropod species with a **potential vector competence** status for 16 pathogens, based on worldwide evidence from either field or laboratory studies.
  - For all of these pathogens, vector species occur in the EU or neighbouring countries, and EU level vector distribution maps are available for use in the risk assessment. These pathogens are: African horse sickness virus, Akabane virus, Bluetongue virus, *Borrelia burgdorferi s.l.*, Cache Valley virus, Crimean–Congo haemorrhagic fever virus, epizootic haemorrhagic disease virus, Japanese encephalitis virus, *L. infantum*, Rift Valley fever Virus, Schmallenberg virus, St. Louis encephalitis virus, tick-borne encephalitis virus, Venezuelan equine encephalitis virus, West Nile virus and Western equine encephalitis virus.

- The SLR did not identify any highly likely or potential biological vector species for bovine ephemeral fever virus, *Coxiella burnetii*, Eastern equine encephalitis virus, Shuni virus and vesicular stomatitis virus. Expert opinion was used to identify potential vector species that could occur in the EU for those pathogens.

4.2 | Mechanical vector transmission

- The narrative literature review identified vector species classified as having a **highly likely competence status**, with vector species that occur in the EU or neighbouring countries. These pathogens are *Besnoitia besnoiti*, LSDV and *T. vivax*
- The narrative literature review identified vector species classified as having a **potential competence status** with vector species occur in the EU or neighbouring countries. These pathogens are *Besnoitia besnoiti*, EIAV, LSDV and *T. vivax*.
- The narrative review did not identify any highly likely or potential mechanical vector species for *Trypanosoma evansi* with vector species that occur in the EU or neighbouring countries. Expert opinion was used to identify potential vector species that could occur in the EU for this pathogen.
- For mechanically transmitted pathogens, vector distribution status maps are not available for the EU or neighbouring countries. However, geographical distribution is not considered a limiting factor for the risk assessment, as these vectors are widely distributed in the EU

4.3 | Uncertainty and limitations

- The limited availability of eligible experimental evidence for some pathogens is mainly due to
  - Strict biosafety requirements for working with some pathogens (e.g. Crimean–Congo haemorrhagic fever virus), which limit laboratory transmission studies.
  - Limited knowledge of vector involvement under natural field conditions for some pathogens (e.g. *C. burnetii*, the causative agent of Q-fever and Shuni virus), resulting in few targeted studies.
  - Insufficient methodological detail in some field studies – particularly the absence of confirmation that analysed female vectors were unfed – leading to their exclusion under the SLR eligibility criteria.

DISEASE GLOSSARY

Causative agent	Abbreviation	Disease	Abbreviation
African horse sickness virus	AHSV	African horse sickness	AHS
Akabane virus	AKAV	Akabane	AKA
Besnoitia besnoiti	*B. besnoiti*	Besnoitiosis	Besno
Bluetongue virus	BTV	Bluetongue	BT
Borrelia burgdorferi s.l.	*B. burgdorferi* s.l.	Lyme Disease	Lyme
Bovine ephemeral disease virus	BEFV	Bovine ephemeral fever	BEF
Cache Valley virus	CVV	Cache valley/Bunyamwera disease	Cache
Coxiella burnetii	*C. burnetii*	Q-fever	Q-fever
Crimean Congo haemorrhagic fever virus	CCHFV	Crimean Congo haemorrhagic fever	CCHF
Eastern equine encephalitis virus	EEEV	Eastern equine encephalitis	EEE
Epizootic haemorrhagic disease virus	EHD V	Epizootic haemorrhagic disease	EHD
Equine infectious anaemia virus	EIA	Equine infectious anaemia	EIA
Japanese encephalitis virus	JEV	Japanese encephalitis	JEV
Leishmania infantum	*L. infantum*	Leishmaniosis	*Leishmania*
Lumpy skin disease virus	LSDV	Lumpy skin disease	LSD
Rift Valley fever virus	RVFV	Rift Valley fever	RVF
Schmallenberg virus	SBV	Schmallenberg	SB
Shuni virus	SHUV	Shuni	Shuni
St Louis encephalitis virus	SLE	St Louis encephalitis	SLE
Tick-borne encephalitis virus	TBEV	Tick-borne encephalitis	TBE
Trypanosoma vivax	*T. vivax*	Trypanosomiasis	Tryp
Trypanosoma evansi	*T. evansi*	Surra	Surra
Venezualan equine encephalitis virus	VEEV	Venezualan equine encephalitis	VEE
Vesicular stomatitis virus	VSV	Vesicular stomatitis	VS
West Nile virus	WNV	West Nile fever	WNF
Western equine encephalitis virus	WEEV	Western equine encephalitis	WEE

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APPENDIX A

Protocol to address Term of Reference 1.2

ToR 1.2.	Question	Evidence needs	Data collection	Reporting methods	Links to updated information/visualisation
1.2.1.	Which arthropod species are likely ***competent vectors*** with evidence of transmitting any of the 25 VBDs (worldwide)	• Evidence of pathogen detection in arthropods isolated in the **field** • Evidence of pathogen transmission under **laboratory** conditions	• SLR on vector competence	Classification of vector competence using data generated through SLR: Field detection OR laboratory detection – potential; field detection AND laboratory detection – highly likely competent vector.	Link to published external report with vector competence SLR protocol and results and in Disease Profiles
1.2.2.	What is the ***geographic distribution*** in the EU and neighbouring countries of those arthropod species that are likely competent	• Evidence of geographical information on presence, absence, or unknown status, summarised for relatively large subnational units	• SLR on geo-distribution • Surveillance data in VectorNet GBIF portal • Historical VN data	Mapping geographical vector status of polygons (NUTS 3 or 2 depending on the specific countries)	Link to VectorNet maps on ECDC and EFSA's website

APPENDIX B

Evidence for vector status for 25 selected vector-borne diseases

B.1 | Evidence collected by Systematic Literature Review and expert opinion on the vector status of biological vectors

The results are presented following the taxonomic classifications reported in the studies identified through the SLR.

Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
AHS	*C. chiopterus*	Potential	0	0	YES	YES	Expert opinion	This species has been implicated temporally and spatially in past outbreaks of AHS in Spain and Portugal.
	C. imicola	Potential	0	0	YES	YES	Expert opinion	
	C. obsoletus complex[a]	Potential	0	1	YES	YES	SLR	Maurer et al. (2021)
AKAV	*C. imicola*	Potential	1	0	YES	YES	SLR	Şevik (2017)
	C. oxystoma	Potential	0	1	NO	NO	SLR	Yanase et al. (2019)
	C. tainanus	Potential	0	1	NO	NO	SLR	Yanase et al. (2019)
BEFV	*C. chiopterus*	Potential	0	0	YES	YES	Expert opinion	According to Stokes et al. (2020), there are more field evidence for Culicoides to be vectors in Africa than mosquitos. Meanwhile, mosquitoes seem more important in Australia (Anopheles).
	C. dewulfi	Potential	0	0	YES	YES	Expert opinion	
	C. imicola	Potential	0	0	YES	YES	Expert opinion	
	C. obsoletus complex[a]	Potential	0	0	YES	YES	Expert opinion	
	C. sonorensis	Potential	0	1	NO	NO	SLR	Stokes et al. (2020)
***Borrelia burgdorferi* s.l.**	*Am. testudinarium*	Potential	1	0	NO	YES	SLR	Ashour et al. (2023)
	D. marginatus	Potential	5	0	NO	YES	SLR	del Cerro et al. (2022), Bona et al. (2021), Sherifi et al. (2018), Nunes et al. (2016), Michelet et al. (2016)
	D. reticulatus	Potential	24	0	YES	YES	SLR	Ciebiera et al. (2024), Goletic et al. (2024), Panteleienko et al. (2023), Buczek et al. (2023), del Cerro et al. (2022), Grochowska et al. (2022), Pańczuk et al. (2022), Martinescu et al. (2022), Grochowska et al. (2021), Pawełczyk et al. (2021), Dunaj et al. (2021), Dwużnik-Szarek et al. (2021), Kniazeva, Baysal, et al. (2021); Kniazeva, Pogotskaya, et al. (2021), Michalski et al. (2021), Michalski et al. (2020), Capligina et al. (2020), Kohn et al. (2019), Sprong et al. (2019), Namina et al. (2019), Ben and Lozynskyi (2019), Roczen-Karczmarz et al. (2018), Sukara et al. (2018), Zajac et al. (2017), Espi et al. (2017)
	D. silvarum	Potential	1	0	NO	NO	SLR	Pukhovskaya et al. (2019)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Haemaphysalis spp.	Potential	10	0	NO	YES	SLR	Dwużnik-Szarek et al. (2021), Pukhovskaya et al. (2019), Bona et al. (2021), del Cerro et al. (2022), Borşan et al. (2021), Palomar et al. (2017), Espi et al. (2017), Rataud et al. (2022), Špitalská et al. (2021)
	H. aegyptium	Potential	1	0	NO	YES	SLR	Norte et al. (2022)
	H. anatolicum	Potential	1	0	NO	NO	SLR	Polat et al. (2021)
	H. concinna	Potential	2	0	NO	YES	SLR	Dwużnik-Szarek et al. (2021), Pukhovskaya et al. (2019)
	H. dromedarii	Potential	3	0	NO	NO	SLR	Ashour et al. (2023), Yousery et al. (2024), Senbill et al. (2024)
	H. inermis	Potential	2	0	NO	YES	SLR	Bona et al. (2021), del Cerro et al. (2022)
	H. japonica douglasi	Potential	1	0	NO	NO	SLR	Pukhovskaya et al. (2019)
	H. lusitanicum	Potential	2	0	YES	YES	SLR	Díaz-Cao et al. (2022), Nunes et al. (2016)
	H. marginatum	Potential	3	0	YES	YES	SLR	Ashour et al. (2023), Cicculli et al. (2019), Mancini et al. (2019)
	H. punctata	Potential	4	0	NO	YES	SLR	del Cerro et al. (2022), Borşan et al. (2021), Palomar et al. (2017)
	H. rufipes	Potential	1	0	NO	YES	SLR	Rollins, Schaper, et al. (2021)
	Ixodes spp.	Highly likely	242	12	YES	YES	SLR	Norte et al. (2020), Sabitova et al. (2018), McCoy et al. (2023), Michalik et al. (2020), Rar et al. (2019), Špitalská et al. (2021), Wodecka et al. (2022), Wodecka et al. (2016), Rataud et al. (2022), Wilhelmsson et al. (2020), Palomar et al. (2017), Heylen, Fonville, et al. (2017), Philippe et al. (2024), Wodecka et al. (2022), Zanet et al. (2020), Abdullah et al. (2018), Szekeres et al. (2019), Jahfari et al. (2017), Waindok et al. (2017), Davies et al. (2017), Gern et al. (1991), Daněk et al. (2024), Selmi et al. (2024), Knoll et al. (2021), Hauck et al. (2019), Rar et al. (2017), Zakham et al. (2023), Bugmyrin et al. (2022), Sormunen et al. (2020), Pakanen et al. (2020); Capligina et al. (2020), Grigoryeva, Miteva, et al. (2019), Namina et al. (2019), Rar et al. (2019), Jansen et al. (2019), Pukhovskaya et al. (2019), Laaksonen et al. (2018), Rar et al. (2017), Laaksonen et al. (2017), Sormunen et al. (2016), Sun and Xu (2003), Sato and Nakao (1997), Hoxha et al. (2025), Gajda-Sawicka et al. (2024), Haidar-Ahmad et al. (2025), Ivanova-Aleksandrova et al. (2024), Lindso et al. (2024), Rusňáková Tarageľová et al. (2024), Balážová et al. (2024), Berthén et al. (2024), Rosso et al. (2024), Dillon et al. (2024), Kiewra et al. (2024), Vikentjeva et al. (2024), Hartemink et al. (2024), Dwużnik-Szarek et al. (2024), Philippe et al. (2024), Guardone et al. (2024), Asman et al. (2024), Menzano et al. (2024), Omeragić et al. (2024), Zubriková et al. (2024),

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
								Ciebiera et al. (2024), Dyczko et al. (2024), Rousseau et al. (2024), Daněk et al. (2024), Liberska et al. (2024), Janzén et al. (2024), Habib et al. (2024), Selmi et al. (2024), Kiran et al. (2024), Pańczuk et al. (2024), Van Gestel et al. (2024), Melis et al. (2024), Panteleienko et al. (2023), Sawczyn-Domańska et al. (2023), Buczek et al. (2023), Carlströmer Berthén et al. (2023), Susnjar et al. (2023), Köhler et al. (2023), Wodecka and Kolomiiets (2023), Banovic et al. (2023), Dvořáková et al. (2023), Hansford et al. (2023), Grassi et al. (2023), Stegmüller et al. (2023), Petráš et al. (2023), Zakham et al. (2023), Kazimírová et al. (2023), Wojcicka et al. (2022), Šujanová et al. (2022), Richtrová et al. (2022), Bugmyrin et al. (2022), Uusitalo et al. (2022), van Duijvendijk et al. (2022), Ebani et al. (2022), Wodecka et al. (2022), Morozov et al. (2022), Kubiak et al. (2022), Schoetta et al. (2017); Schötta et al. (2023), Król et al. (2022), del Cerro et al. (2022), Blazhev et al. (2022), Grochowska et al. (2022), Dyczko et al. (2022), Răileanu et al. (2022), Ivanović et al. (2022), Springer et al. (2022), Kocon et al. (2022), Bourdin et al. (2022), Sonnberger et al. (2022), Orkun (2022), Martinescu et al. (2022), Hansford et al. (2022), Gandy et al. (2022), Lemoine et al. (2022), Rataud et al. (2022), Medlock et al. (2022), Boyer et al. (2022), Garcia-Vozmediano et al. (2022), Musilová et al. (2022), Bona et al. (2021), Olsthoorn et al. (2021), Polat et al. (2021), Fabri et al. (2021), Pawełczyk et al. (2021), Pittermannová et al. (2021), Răileanu et al. (2021), Cafiso et al. (2021), Knoll et al. (2021), Luu et al. (2021), Borşan et al. (2021), Markowicz et al. (2021), Bregnard et al. (2021), Asman et al. (2021), Hartemink et al. (2021), Kovryha et al. (2021), Cull et al. (2021), Levytska et al. (2021), Alafaci et al. (2021), Bertola et al. (2021), Hoffmann et al. (2021), Dwużnik-Szarek et al. (2021), Hansford et al. (2021), Kniazeva, Pogotskaya, et al. (2021), Michalski et al. (2021), Millins et al. (2021), Špitalská et al. (2021), Rollins, Schaper, et al. (2021), Gandy et al. (2021), Nebbak et al. (2021), Wilhelmsson et al. (2020), Zintl et al. (2020), Sormunen et al. (2020), Michalski et al. (2020), Garcia-Vozmediano et al. (2020), Capligina et al. (2020), Mtierová et al. (2020), Hvidsten et al. (2020), Sprong et al. (2020), Okeyo et al. (2020), Lebert et al. (2020), Pedersen et al. (2020), Hauck et al. (2020), Răileanu et al. (2020), Zanet et al. (2020), Springer et al. (2020), Zubriková et al. (2020), Orkun et al. (2020),

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
								Michalik et al. (2020), Cicculi et al. (2019), Klitgaard et al. (2019), Vaculová et al. (2019), Klemola et al. (2019), Asman et al. (2019), Martello et al. (2019), Grigoryeva, Miteva, et al. (2019), Hauck et al. (2019), Namina et al. (2019), Heylen et al. (2019), Lejal et al. (2019), Lernout et al. (2019), Makenov et al. (2019), Remesar et al. (2019), Ben and Lozynskyi (2019), Ćakić et al. (2019), Rogovskyy et al. (2019), Kubiak et al. (2019), Hönig et al. (2019), Lambert et al. (2019), Akl et al. (2019), Mysterud et al. (2019), Galfsky et al. (2019), Fedoniuk et al. (2019), Millet et al. (2019), Pospisilova et al. (2019), Layzell et al. (2018), Abdullah et al. (2018), Andersson et al. (2018), Page et al. (2018), Karasartova et al. (2018), Roczen-Karczmarz et al. (2018), Szekeres et al. (2019), Millins et al. (2018), Coipan et al. (2018), Mysterud et al. (2018), Chvostáč et al. (2018), Ehrmann et al. (2018), Rogovskyy et al. (2018), Weiner et al. (2018), Sormunen et al. (2018), Laaksonen et al. (2018), Kazimírová et al. (2018), Mori et al. (2018), Geurden et al. (2018), Pajoro et al. (2018), Blazejak et al. (2018), Kjelland et al. (2018), Sukara et al. (2018), Rosà et al. (2018), Sherifi et al. (2018), Da Rold et al. (2018), Nader et al. (2018), Ruyts et al. (2018), Hofmeester et al. (2017), Raileanu et al. (2017), Jahfari et al. (2017), Krstic et al. (2017), Bonnet et al. (2017), Szekeres et al. (2017), Waindok et al. (2017), Marchant et al. (2017), Hornok et al. (2017), Laaksonen et al. (2017), Hansford et al. (2017), Adamska and Skotarczak (2017), Takken et al. (2017), Palomar et al. (2017), Didyk et al. (2017), Kybicova et al. (2017), Briciu et al. (2017), Wagemakers et al. (2017), Obiegala et al. (2017), Delgado et al. (2017), Hamsikova et al. (2017), Schoetta et al. (2017), Hofhuis et al. (2017), Heylen, Fonville, et al. (2017), Jensen et al. (2017), Díaz et al. (2017), Pistone et al. (2017), Kowalec et al. (2017), Oechslin et al. (2017), Honig et al. (2017), Morganti et al. (2017), Davies et al. (2017), Ruyts et al. (2016), Sormunen et al. (2016), Daniel, Rudenko, et al. (2016), Potkonjak et al. (2016), Piksa et al. (2016), Krstic et al. (2016), Millins et al. (2016), Ragagli et al. (2016), Tarageľová et al. (2016), Wojcik-Fatla et al. (2016), Paul et al. (2016), Skotarczak et al. (2016), Vourc'h et al. (2016), Gryczynska and Welc-Faleciak (2016), Wodecka et al. (2016), Espi et al. (2017), Nunes et al. (2016), Durand et al. (2017), Moutailler et al. (2016), van Duijvendijk et al. (2016), van Duijvendijk et al. (2016), Wodecka et al. (2014), Hu et al. (2001), Kahl et al. (1998), Dolan et al. (1998), Gern and Rais (1996)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	I. arboricola	Potential	1	0	NO	YES	SLR	Špitalská et al. (2021)
	I. ariadnae	Potential	1	0	NO	YES	SLR	Michalik et al. (2020)
	I. canisuga	Potential	2	0	NO	YES	SLR	Wodecka et al. (2022), Wodecka et al. (2016)
	I. cf. *kaiseri*	Potential	1	0	NO	YES	SLR	Wodecka et al. (2016)
	I. frontalis	Potential	4	0	NO	YES	SLR	Rataud et al. (2022), Wilhelmsson et al. (2020), Palomar et al. (2017), Heylen et al. (2017)
	I. hexagonus	Highly likely	8	1	NO	YES	SLR	Philippe et al. (2024), Wodecka et al. (2022), Zanet et al. (2020), Abdullah et al. (2018), Szekeres et al. (2019), Jahfari et al. (2017), Waindok et al. (2017), Davies et al. (2017), Gern et al. (1991)
	I. inopinatus	Potential	4	0	NO	YES	SLR	Danek et al. (2024), Selmi et al. (2024), Knoll et al. (2021), Hauck et al. (2019)
	I. kaiseri	Potential	1	0	NO	YES	SLR	Wodecka et al. (2022)
	I. pacificus	Potential	0	1	NO	NO	SLR	Couper et al. (2020)
	I. pavlovskyi	Potential	2	0	NO	NO	SLR	Rar et al. (2019), Rar et al. (2017)
	I. persulcatus	Highly likely	14	2	YES	YES	SLR	Zakham et al. (2023), Bugmyrin et al. (2022), Sormunen et al. (2020), Pakanen et al. (2020), Capligina et al. (2020), Grigoryeva et al. (2019), Namina et al. (2019), Rar et al. (2019), Jaenson et al. (2019), Pukhovskaya et al. (2019), Laaksonen et al. (2018), Rar et al. (2017), Laaksonen et al. (2017), Sormunen et al. (2016), Sun et al. (2003), Sato et al. (1997)
	I. persulcatus × *I. pavlovskyi*	Potential	1	0	YES	YES	SLR	Rar et al. (2019)
	I. ricinus	Highly likely	234	6	YES	YES	SLR	Hoxha et al. (2025), Gajda-Sawicka et al. (2024), Haidar-Ahmad et al. (2025), Ivanova-Aleksandrova et al. (2024), Lindso et al. (2024), Rusňáková Tarageľová et al. (2024), Balážová et al. (2024), Berthén et al. (2024), Rosso et al. (2024), Dillon et al. (2024), Kiewra et al. (2024), Vikentjeva et al. (2024), Hartemink et al. (2024), Dwużnik-Szarek et al. (2024), Philippe et al. (2024), Guardone et al. (2024), Asman et al. (2024), Menzano et al. (2024), Omeragić et al. (2024), Zubriková et al. (2024), Ciebiera et al. (2024), Dyczko et al. (2024), Rousseau et al. (2024), Daněk et al. (2024), Liberska et al. (2024), Janzén et al. (2024), Habib et al. (2024), Selmi et al. (2024), Kiran et al. (2024), Pańczuk et al. (2024), Van Gestel et al. (2024),

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
								Melis et al. (2024), Panteleienko et al. (2023), Sawczyn-Domańska et al. (2023), Buczek et al. (2023), Carlströmer Berthén et al. (2023), Susnjar et al. (2023), Köhler et al. (2023), Wodecka and Kolomiiets (2023), Banovic et al. (2023), Dvořáková et al. (2023), Hansford et al. (2023), Grassi et al. (2023), Stegmüller et al. (2023), Petráš et al. (2023), Zakham et al. (2023), Kazimírová et al. (2023), Wojcicka et al. (2022), Šujanová et al. (2022), Richtrová et al. (2022), Bugmyrin et al. (2022), Uusitalo et al. (2022), van Duijvendijk et al. (2022), Ebani et al. (2022), Wodecka et al. (2022), Morozov et al. (2022), Kubiak et al. (2022), Schötta et al. (2023), Król et al. (2022), del Cerro et al. (2022), Blazhev et al. (2022), Grochowska et al. (2022), Dyczko et al. (2022), Răileanu et al. (2022), Ivanović et al. (2022), Springer et al. (2022), Kocon et al. (2022), Bourdin et al. (2022), Sonnberger et al. (2022), Orkun (2022), Martinescu et al. (2022), Hansford et al. (2022), Gandy et al. (2022), Lemoine et al. (2022), Rataud et al. (2022), Medlock et al. (2022), Boyer et al. (2022), Garcia-Vozmediano et al. (2022), Musilová et al. (2022), Bona et al. (2021), Olsthoorn et al. (2021), Polat et al. (2021), Fabri et al. (2021), Pawełczyk et al. (2021), Pittermannová et al. (2021), Răileanu et al. (2021), Cafiso et al. (2021), Knoll et al. (2021), Luu et al. (2021), Borşan et al. (2021), Markowicz et al. (2021), Bregnard et al. (2021), Asman et al. (2021), Hartemink et al. (2021), Kovryha et al. (2021), Cull et al. (2021), Levytska et al. (2021), Alafaci et al. (2021), Bertola et al. (2021), Hoffmann et al. (2021), Dwużnik-Szarek et al. (2021), Hansford et al. (2021), Kniazeva, Pogotskaya, et al. (2021), Michalski et al. (2021), Millins et al. (2021), Špitalská et al. (2021), Rollins, Yeyin, et al. (2021), Gandy et al. (2021), Nebbak et al. (2021), Wilhelmsson et al. (2020), Zintl et al. (2020), Sormunen et al. (2020), Michalski et al. (2020), Garcia-Vozmediano et al. (2020), Capligina et al. (2020), Mtierová et al. (2020), Hvidsten et al. (2020), Sprong et al. (2020), Okeyo et al. (2020), Lebert et al. (2020), Pedersen et al. (2020), Hauck et al. (2020), Răileanu et al. (2021), Zanet et al. (2020), Springer et al. (2020), Zubriková et al. (2020), Orkun et al. (2020), Michalik et al. (2020), Cicculli et al. (2019), Klitgaard et al. (2019), Vaculová et al. (2019), Klemola et al. (2019), Asman et al. (2019), Martello et al. (2019), Grigoryeva, Miteva, et al. (2019), Hauck et al. (2019), Namina et al. (2019), Heylen et al. (2019), Lejal et al. (2019), Lernout et al. (2019),

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
								Makenov et al. (2019), Remesar et al. (2019), Ben and Lozynskyi (2019), Ćakić et al. (2019), Rogovskyy et al. (2019), Kubiak et al. (2019), Hönig et al. (2019), Lambert et al. (2019), Akl et al. (2019), Mysterud et al. (2019), Galfsky et al. (2019), Fedoniuk et al. (2019), Millet et al. (2019), Pospisilova et al. (2019), Layzell et al. (2018), Abdullah et al. (2018), Andersson et al. (2018), Page et al. (2018), Karasartova et al. (2018), Roczen-Karczmarz et al. (2018), Szekeres et al. (2019), Millins et al. (2018), Coipan et al. (2018), Mysterud et al. (2018), Chvostáč et al. (2018), Ehrmann et al. (2018), Rogovskyy et al. (2018), Weiner et al. (2018), Sormunen et al. (2018), Laaksonen et al. (2018), Kazimírová et al. (2018), Mori et al. (2018), Geurden et al. (2018), Pajoro et al. (2018), Blazejak et al. (2018), Kjelland et al. (2018), Sukara et al. (2018), Rosà et al. (2018), Sherifi et al. (2018), Da Rold et al. (2018), Nader et al. (2018), Ruyts et al. (2018), Hofmeester et al. (2017), Raileanu et al. (2017), Jahfari et al. (2017), Krstic et al. (2017), Bonnet et al. (2017), Szekeres et al. (2017), Waindok et al. (2017), Marchant et al. (2017), Hornok et al. (2017), Laaksonen et al. (2017), Hansford et al. (2017), Adamska and Skotarczak (2017), Takken et al. (2017), Palomar et al. (2017), Didyk et al. (2017), Kybicova et al. (2017), Briciu et al. (2017), Wagemakers et al. (2017), Obiegala et al. (2017), Delgado et al. (2017), Hamsikova et al. (2017), Schoetta et al. (2017), Hofhuis et al. (2017), Heylen, Fonville, et al. (2017), Jensen et al. (2017), Díaz et al. (2017), Pistone et al. (2017), Kowalec et al. (2017), Oechslin et al. (2017), Honig et al. (2017), Morganti et al. (2017), Davies et al. (2017), Ruyts et al. (2016), Sormunen et al. (2016), Daniel, Rudenko, et al. (2016), Potkonjak et al. (2016), Piksa et al. (2016), Krstic et al. (2016), Millins et al. (2016), Ragagli et al. (2016), Tarageľová et al. (2016), Wojcik-Fatla et al. (2016), Paul et al. (2016), Skotarczak et al. (2016), Vourc'h et al. (2016), Gryczynska and Welc-Faleciak (2016), Wodecka et al. (2016), Espi et al. (2017), Nunes et al. (2016), Durand et al. (2017), Moutailler et al. (2016), van Duijvendijk et al. (2016), Wodecka et al. (2014), Hu et al. (2001), Kahl et al. (1998), Dolan et al. (1998), Gern and Rais (1996)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	I. ricinus/inopinatus	Potential	2	0	YES	YES	SLR	Daněk et al. (2024), Glass et al. (2022)
	I. scapularis	Potential	0	3	NO	NO	SLR	Dolan et al. (1998), Couper et al. (2020), Dolan et al. (2017)
	I. simplex	Potential	1	0	NO	YES	SLR	Michalik et al. (2020)
	I. uriae	Potential	1	0	NO	NO	SLR	McCoy et al. (2023)
	I. vespertilionis	Potential	1	0	NO	YES	SLR	Michalik et al. (2020)
	Rh. annulatus	Potential	3	0	NO	YES	SLR	Polat et al. (2021), Senbill et al. (2024), Mancini et al. (2019)
	Rh. bursa	Potential	2	0	NO	YES	SLR	Mancini et al. (2019), Espi et al. (2017)
	Rh. rutilus	Potential	1	0	NO	NO	SLR	Senbill et al. (2024)
	Rh. sanguineus	Potential	6	0	YES	YES	SLR	Ahmed et al. (2024), Elhelw et al. (2021), Balti et al. (2021), Zanet et al. (2020), Abdullah et al. (2018), Nunes et al. (2016)
	Rh. turanicus	Potential	1	0	NO	NO	SLR	Orkun et al. (2019)
	C. fulvus	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. imicola	Highly likely	1	1	YES	YES	SLR	Federici et al. (2019), Fujisawa et al. (2021)
	C. obsoletus complex[a]	Highly likely	2	1	YES	YES	SLR	Vanbinst et al. (2009), De Deken et al. (2008), Paslaru et al. (2018)
	C. obsoletus group[b]	Highly likely	2	1	YES	YES	SLR	Vanbinst et al. (2009), De Deken et al. (2008), Paslaru et al. (2018)
	C. orientalis	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. oxystoma	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. pulicaris	Potential	1	0	YES	YES	SLR	Vanbinst et al. (2009)
	C. sonorensis	Potential	0	4	NO	NO	SLR	Veronesi et al. (2020), Sanders et al. (2022), Baylis et al. (2008), Reeves et al. (2009)
	C. tainanus	Potential	1	0	NO	NO	SLR	Duan et al. (2019)
BTV	*C. dewulfi*	Potential	0	0	YES	YES	Expert opinion	This species has been implicated in BTV outbreaks in Italy (Goffredo et al. 2015).
	C. fulvus	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. imicola	Highly likely	1	1	YES	YES	SLR	Federici et al. (2019), Fujisawa et al. (2021)
	C. obsoletus complex[a]	Highly likely	2	1	YES	YES	SLR	Vanbinst et al. (2009), De Deken et al. (2008), Paslaru et al. (2018)
	C. obsoletus group[b]	Highly likely	2	1	YES	YES	SLR	Vanbinst et al. (2009), De Deken et al. (2008), Paslaru et al. (2018)
	C. orientalis	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. oxystoma	Potential	1	0	NO	NO	SLR	Fujisawa et al. (2021)
	C. pulicaris	Potential	1	0	YES	YES	SLR	Vanbinst et al. (2009)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	C. sonorensis	Potential	0	4	NO	NO	SLR	Veronesi et al. (2020), Sanders et al. (2022), Baylis et al. (2008), Reeves et al. (2009)
	C. tainanus	Potential	1	0	NO	NO	SLR	Duan et al. (2019)
CCHFV	*H. aegyptium*	Potential	1	0	YES	YES	SLR	Kar et al. (2020)
	H. anatolicum	Potential	1	0	NO	NO	SLR	Petrova et al. (2013)
	H. asiaticum	Potential	1	0	NO	NO	SLR	Voorhees et al. (2018)
	H. marginatum	Potential	2	0	YES	YES	SLR	Akyildiz et al. (2021), Orkun et al. (2017)
Coxiella burnetii	*D. marginatus*	Potential	0	0	YES	YES	Expert opinion	Pathogen was isolated from these tick species under field conditions in Slovakia (Rehácek et al., 1991). Applying similar criteria as for B. burgdorferi (pathogen detection under field conditions in ticks of any physiological state supports these species' vector competence for *C. burnetii*.
	D. reticulatus	Potential	0	0	YES	YES	Expert opinion	
	Ha. concinna	Potential	0	0	YES	YES	Expert opinion	
	Ha. inermis	Potential	0	0	YES	YES	Expert opinion	
	Ha. punctata	Potential	0	0	YES	YES	Expert opinion	
	I. ricinus	Potential	0	0	YES	YES	Expert opinion	Being a generalist pathogen (it could be found in a wide diversity of ticks. Even if the role in transmission is unclear (ticks may play a role in the sylvatic cycle. Several species have been detected positive to C. burnetti in the field Celina SS and Cerný J (2022), Rehácek et al. (1991) (although it was not specified whether the ticks were non-engorged. Applying similar criteria as for *B. burgdorferi* (pathogen detection under field conditions in ticks of any physiological state supports *I. ricinus* vector competence.
CVV	*Ae. aegypti*	Potential	0	2	YES	YES	SLR	Chan et al. (2020), Ayers et al. (2019)
	Ae. albopictus	Potential	0	3	YES	YES	SLR	Dieme, Ngo, et al. (2022), Chan et al. (2020), Ayers et al. (2019)
	Ae. japonicus	Potential	0	2	YES	YES	SLR	Chan et al. (2020), Yang et al. (2018)
	Ae. triseriatus	Potential	0	1	NO	NO	SLR	Chan et al. (2020)
	An. gambiae	Potential	1	0	NO	NO	SLR	Ajamma et al. (2018)
	An. quadrimaculatus	Potential	0	1	NO	NO	SLR	Dieme, Ngo, et al. (2022)
	Cx. tarsalis	Potential	0	1	NO	NO	SLR	Ayers et al. (2018)
	Cx. univittatus	Potential	1	0	YES	YES	SLR	Ajamma et al. (2018)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
EHDV								
	C. chiopterus	Potential	0	0	YES	YES	Expert opinion	
	C. dewulfi	Potential	0	0	YES	YES	Expert opinion	
	C. imicola	Potential	0	0	YES	YES	Expert opinion	EHDV is similar to other arboviruses transmitted by the same vector species. Also Bluetongue virus (BTV) and Epizootic haemorrhagic disease virus (EHDV) (are both members of the Sedoreoviridae family and Orbivirus genus. Quaglia et al. (2023) reported collecting EHDV-8 positive parous female pools of *C. imicola (C. obsoletus complex (C. pulicaris (C. newsteadi* and *C. bysta* in EHD affected farms in Sardinia.
	C. insignis	Potential	0	1	NO	NO	SLR	McGregor, Kenney, and Connelly (2021), McGregor, Erram, et al. (2021)
	C. obsoletus complex[a]	Potential	0	1	YES	YES	SLR	Maurer et al. (2021)
	C. sonorensis	Potential	0	2	NO	NO	SLR	McGregor et al. (2019), Reeves et al. (2009)
EEEV	*Ae. albopictus*	Potential	0	1	YES	YES	Expert opinion	
	Ae. japonicus	Potential	0	1	YES	YES	Expert opinion	
	Ae. vexans	Potential	0	0	YES	YES	Expert opinion	*Aedes vexans* (#3) was positive for EEEV: females were sorted by species and physiological status (unfed (blood-fed (gravid) (Oliver et al., 2018).
	Cs. melanura	Potential	1	0	NO	NO	SLR	
JEV	*Ae. aegypti*	Potential	0	1	YES	YES	SLR	van den Hurk et al. (2003)
	Ae. albopictus	Potential	0	1	YES	YES	SLR	Hernandez-Triana et al. (2022)
	Ae. japonicus	Potential	0	1	YES	YES	SLR	Faizah et al. (2020)
	Ae. notoscriptus	Potential	0	1	NO	NO	SLR	van den Hurk et al. (2003)
	Ae. purpureus	Potential	0	1	NO	NO	SLR	van den Hurk et al. (2003)
	Ae. vigilax	Highly likely	1	1	NO	NO	SLR	van den Hurk et al. (2003), Johansen et al. (2001)
	An. sinensis	Potential	1	0	NO	NO	SLR	Li et al. (2017)
	Cx. annulirostris	Potential	0	2	NO	NO	SLR	Johnson et al. (2009), van den Hurk et al. (2003)
	Cx. annulus	Potential	1	0	NO	NO	SLR	Okuno et al. (1973)
	Cx. gelidus	Potential	0	1	NO	NO	SLR	Johnson et al. (2009)
	Cx. pipiens	Highly likely	1	1	YES	YES	SLR	Hameed et al. (2019), Fang et al. (2019)
	Cx. pipiens pipiens							
		Potential	0	1	YES	YES	SLR	Folly et al. (2021)
	Cx. quinquefasciatus	Potential	0	4	NO	NO	SLR	Huang et al. (2016), Karna and Bowen (2019), Hernandez-Triana et al. (2022), van den Hurk et al. (2003)
	Cx. sitiens	Potential	0	1	NO	NO	SLR	van den Hurk et al. (2003)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Cx. sitiens group	Highly likely	1	2	NO	NO	SLR	Johansen et al. (2001), Johnson et al. (2009), van den Hurk et al. (2003)
	Cx tritaeniorhynchus	Highly likely	6	1	YES	YES	SLR	Faizah et al. (2020), Li et al. (2017), Chu et al. (2017), Samuel et al. (2018), Deng et al. (2020), Fang et al. (2021), Okuno et al. (1973)
	Cx. vishnui	Potential	1	0	NO	NO	SLR	Sahu et al. (2018)
	Cs. annulata	Potential	0	1	NO	YES	SLR	Chapman et al. (2020)
	Ma. septempunctata	Potential	0	1	NO	NO	SLR	van den Hurk et al. (2003)
	Ma. uniformis	Potential	0	1	NO	NO	SLR	van den Hurk et al. (2003)
L. infantum	*E. cortelezii*	Potential	2	0	NO	NO	SLR	Carvalho et al. (2022), Capucci et al. (2023)
	E. edwardsi	Potential	2	0	NO	NO	SLR	Serra et al. (2022), Capucci et al. (2023)
	E. firmatoi	Potential	1	0	NO	NO	SLR	Carvalho et al. (2022)
	Lu. cavernicola	Potential	1	0	NO	NO	SLR	Carvalho et al. (2022)
	Lu. cortelezzii s.l.	Potential	1	0	NO	NO	SLR	Lara-Silva et al. (2015
	Lu. cruzi	Potential	0	1	NO	NO	SLR	Falcao de Oliveira et al. (2017)
	Lu. lloydi	Potential	1	0	NO	NO	SLR	Lara-Silva et al. (2015
	Lu. longipalpis	Highly likely	7	3	NO	NO	SLR	Dos Santos Nogueira et al. (2019), Galvis-Ovallos, Casanova, et al. (2017), Batista et al. (2020), Mota et al. (2019), Moya et al. (2017), Carvalho et al. (2022), Acardi et al. (2010), Lara-Silva Fde et al. (2015), Rodrigues et al. (2016), Capucci et al. (2023)
	Lu. migonei	Potential	1	0	NO	NO	SLR	Rodrigues et al. (2016)
	Lu. renei	Potential	1	0	NO	NO	SLR	Carvalho et al. (2022)
	M. quinquefer	Potential	1	0	NO	NO	SLR	Moya et al. (2017)
	N. whitmani	Potential	2	0	NO	NO	SLR	Moya et al. (2017), Capucci et al. (2023)
	Pa. lutziana	Potential	1	0	NO	NO	SLR	Capucci et al. (2023)
	Ph. longicuspis	Potential	2	0	NO	NO	SLR	Mhaidi et al. (2018), Barhoumi et al. (2016)
	Ph. mascittii	Highly likely	1	1	YES	YES	SLR	Obwaller et al. (2016), Sádlová et al. (2026)*
	Ph. neglectus	Potential	2	0	YES	YES	SLR	Karaku et al. (2017), Latrofa et al. (2018)
	Ph. papatasi	Potential	2	0	YES	YES	SLR	Latrofa et al. (2018), Barhoumi et al. (2016)
	Ph. perfiliewi	Potential	1	0	YES	YES	SLR	Barhoumi et al. (2016)
	Ph. perniciosus	Highly likely	6	1	YES	YES	SLR	Remadi et al. (2018), Weslati et al. (2022), Bennai et al. (2018), Gonzalez et al. (2017), Latrofa et al. (2018), Mhaidi et al. (2018), Barhoumi et al. (2016)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Ph. tobbi	Potential	2	0	YES	YES	SLR	Karaku et al. (2017), Karakus et al. (2019)
	Pi. fischeri	Potential	0	1	NO	NO	SLR	Galvis-Ovallos, Casanova, et al. (2017)
	S. minuta	Potential	3	0	NO	YES	SLR	Pereira et al. (2017), Latrofa et al. (2018), Barhoumi et al. (2016)
RVFV	*Ae. albopictus*	Potential	0	1	YES	YES	SLR	Brustolin et al. (2017)
	Ae. aegypti	Highly likely	1	3	YES	YES	SLR	Wichgers Schreur et al. (2021), Campbell et al. (2022), Kading et al. (2014), Kumalija et al. (2021)
	Ae. caspius	Potential	0	1	YES	YES	SLR	Lumley et al. (2018)
	Ae. detritus	Potential	0	1	Yes	YES	SLR	Lumley et al. (2018)
	Ae. durbanensis	Potential	1	0	NO	NO	SLR	van den Bergh et al. (2022)
	Ae. melanimon	Potential	0	1	NO	NO	SLR	Hartman et al. (2021)
	Ae. vexans	Potential	0	5	YES	YES	SLR	Hartman et al. (2021), Birnberg et al. (2019), Ndiaye El et al. (2016), Turell et al. (2008), Turell et al. (2010)
	An. coustani	Potential	0	1	NO	NO	SLR	Nepomichene et al. (2018)
	Cs. inornata	Potential	0	1	NO	NO	SLR	Hartman et al. (2021)
	Cx. antennatus	Potential	0	1	YES	NO	SLR	Nepomichene et al. (2018)
	Cx. erraticus	Potential	0	2	NO	NO	SLR	Turell et al. (2008), Turell et al. (2010)
	Cx. erythrothorax	Potential	0	1	NO	NO	SLR	Turell et al. (2010)
	Cx. nigripalpus	Potential	0	1	NO	NO	SLR	Turell et al. (2010)
	Cx. pipiens	Potential	0	3	YES	YES	SLR	Zakhia et al. (2018), Vloet et al. (2017), Turell et al. (2010)
	Cx. pipiens s.l.	Potential	1	0	YES	YES	SLR	Kumalija et al. (2021)
	Cx. pipiens molestus	Potential	0	1	YES	YES	SLR	Talavera et al. (2018)
	Cx. pipiens pipiens	Potential	0	1	YES	YES	SLR	Lumley et al. (2018)
	Cx. pipiens pipiens × molestus	Potential	0	2	YES			
						YES	SLR	Lumley et al. (2018), Brustolin et al. (2017)
	Cx. poicilipes	Potential	0	1	NO	NO	SLR	Ndiaye El et al. (2016)
	Cx. quinquefasciatus	Potential	0	1	NO	NO	SLR	Ndiaye El et al. (2016)
	Cx. tarsalis	Potential	0	5	NO	NO	SLR	Campbell et al. (2022), Dodson et al. (2017), Bergren et al. (2021), Hartman et al. (2021), Turell et al. (2010)
	Cx. tritaeniorhynchus	Potential	0	1	YES	YES	SLR	Jupp et al. (2002)
	Cx. zombaensis	Potential	0	1	NO	NO	SLR	Turell et al. (2007)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
SBV								
	C. chiopterus	Potential	1	0	YES	YES	SLR	Balenghien et al. (2014)
	C. imicola	Potential	0	1	YES	YES	SLR	Pages et al. (2018)
	C. nubeculosus	Potential	1	0	NO	YES	SLR	Balenghien et al. (2014)
	C. obsoletus	Potential	0	1	YES	YES	SLR	Pages et al. (2018)
	C. obsoletus complex[a]	Highly likely	3	1	YES	YES	SLR	Sohier et al. (2017), Elbers et al. (2015), Balenghien et al. (2014), Pages et al. (2018)
	C. obsoletus group[b]	Highly likely	4	1	YES	YES	SLR	Sohier et al. (2017), Elbers et al. (2015), Balenghien et al. (2014), Pages et al. (2018), Kameke et al. (2016)
	C. pulicaris	Potential	1	0	YES	YES	SLR	Balenghien et al. (2014)
	C. sonorensis	Potential	0	1	NO	NO	SLR	Veronesi et al. (2013)
SHUV	*C. chiopterus*	Potential	0	0	YES	YES	Expert opinion	Virus isolated from biting midges and mosquitoes in Africa. Oral susceptibility for infection of *Culicoides* was demonstrated (but not for mosquitoes (Möhlmann et al. (2018).
	C. dewulfi	Potential	0	0	YES	YES	Expert opinion	
	C. imicola	Potential	0	0	YES	YES	Expert opinion	
	C. obsoletus/scoticus	Potential	0	0	YES	YES	Expert opinion	
SLEV	*Cx. interfor*	Potential	0	1	NO	NO	SLR	Beranek et al. (2020)
	Cx. quinquefasciatus	Potential	0	3	NO	NO	SLR	Beranek et al. (2020), Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005)
	Cx. pipiens	Potential	0	1	YES	YES	SLR	Reisen et al. (2008
	Cx. pipiens s.l.	Potential	0	0	YES	YES	Expert opinion	We assume SLEV is very similar to WNV (they share Culex spp. transmission and same hosts. There are some indicators that Cx. pipiens plays a role (minor compared to the other Cx spp. in the Americas). Gallichotte et al. (2024).
	Cx. nigripalpus	Potential	0	1	NO	NO	SLR	Richards, Anderson, Lord, and Tabachnick (2012)
	Cx. saltanensis	Potential	0	1	NO	NO	SLR	Beranek et al. (2020)
	Cx. stigmatosoma	Potential	0	2	NO	NO	SLR	Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005)
	Cx. tarsalis	Potential	0	2	NO	NO	SLR	Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005)
	Cx. univittatus	Potential	0	0	YES	YES	Expert opinion	

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
TBEV	*D. nuttallii*	Potential	1	0	NO	NO	SLR	Kholodilov et al. (2019)
	D. reticulatus	Highly likely	11	1	YES	YES	SLR	Krol et al. (2024), Sidorenko et al. (2024), Pautienius et al. (2021), Sidorenko et al. (2021), Capligina et al. (2020), Ott et al. (2020), Lickova et al. (2020), Chitimia-Dobler et al. (2019), Ben and Lozynskyi (2019), Zajac et al. (2017), Biernat et al. (2016), Karbowiak et al. (2016)
	D. reticulatus	Potential	0	1	NO	YES	SLR	Lickova et al. (2020)
	D. silvarum	Potential	2	0	NO	NO	SLR	Kholodilov et al. (2019), Pukhovskaya et al. (2018)
	H. concinna	Potential	1	0	NO	YES	SLR	Pukhovskaya et al. (2018)
	H. inermis	Potential	0	1	NO	YES	SLR	Lickova et al. (2020)
	H. japonica douglasi	Potential	1	0	NO	NO	SLR	Pukhovskaya et al. (2018)
	Ixodes sp.	Highly likely	52	4	NO	YES	SLR	Rar et al. (2019), Belova et al. (2023), Tkachev et al. (2017), Rar et al. (2017), Bakhvalova et al. (2016), Rar et al. (2019), Belova et al. (2023), Bugmyrin et al. (2022), Kholodilov et al. (2022), Capligina et al. (2020), Rar et al. (2019), Kholodilov et al. (2019), Pukhovskaya et al. (2018), Tkachev et al. (2017), Rar et al. (2017), Laaksonen et al. (2017), Bakhvalova et al. (2016), Vikentjeva et al. (2024), Zubriková et al. (2024), Król et al. (2024), Sidorenko et al. (2024), Bakker et al. (2024), Lamsal et al. (2023), Stegmüller et al. (2023), Zakham et al. (2023), Belova et al. (2023), Esser et al. (2022), Bugmyrin et al. (2022), Topp et al. (2022), Pautienius et al. (2021), Borde et al. (2021), Fares et al. (2021), Sidorenko et al. (2021), Gethmann et al. (2020), Capligina et al. (2020), Vikse et al. (2020), Bournez et al. (2020), Ott et al. (2020), Król et al. (2020), Alfano et al. (2020), Zubriková et al. (2020), Holding et al. (2020), Lickova et al. (2020), Liebig et al. (2020), Smura et al. (2019), Chitimia-Dobler et al. (2019), Andersen et al. (2019), Agergaard et al. (2019), Makenov et al. (2019), Ben and Lozynskyi (2019), Boelke et al. (2019), Casati Pagani et al. (2019), Hönig et al. (2019), Dekker et al. (2019), Sormunen et al. (2018), Gondard et al. (2018), Bestehorn et al. (2018), Kjelland et al. (2018), Soleng et al. (2018), Laaksonen et al. (2017), Rieille et al. (2017), Potkonjak et al. (2017), Daniel, Rudenko, et al. (2016), Daniel, Danielova, et al. (2016), Henningsson et al. (2016), Jaaskelainen et al. (2016), Gonzalez et al. (2022)
	I. pavlovskyi	Potential	4	0	NO	NO	SLR	Tkachev et al. (2017), Rar et al. (2017), Bakhvalova et al. (2016), Rar et al. (2019)

(Continued)

Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	I. persulcatus	Highly likely	10	1	YES	YES	SLR	Belova et al. (2023), Bugmyrin et al. (2022), Kholodilov et al. (2022), Capligina et al. (2020), Rar et al. (2019), Kholodilov et al. (2019), Pukhovskaya et al. (2018), Tkachev et al. (2017), Rar et al. (2017), Laaksonen et al. (2017), Bakhvalova et al. (2016)
	I. persulcatus × *I. pavlovskyi*	Potential	1	0	YES	YES	SLR	Rar et al. (2019)
	I. ricinus	Highly likely	44	4	YES	YES	SLR	Vikentjeva et al. (2024), Zubriková et al. (2024), Król et al. (2024), Sidorenko et al. (2024), Bakker et al. (2024), Lamsal et al. (2023), Stegmüller et al. (2023), Zakham et al. (2023), Belova et al. (2023), Esser et al. (2022), Bugmyrin et al. (2022), Topp et al. (2022), Pautienius et al. (2021), Borde et al. (2021), Fares et al. (2021), Sidorenko et al. (2021), Gethmann et al. (2020), Capligina et al. (2020), Vikse et al. (2020), Bournez et al. (2020), Ott et al. (2020), Król et al. (2020), Alfano et al. (2020), Zubriková et al. (2020), Holding et al. (2020), Lickova et al. (2020), Liebig et al. (2020), Smura et al. (2019), Chtimia-Dobler et al. (2019), Andersen et al. (2019), Agergaard et al. (2019), Makenov et al. (2019), Ben and Lozynskyi (2019), Boelke et al. (2019), Casati Pagani et al. (2019), Hönig et al. (2019), Dekker et al. (2019), Sormunen et al. (2018), Gondard et al. (2018), Bestehorn et al. (2018), Kjelland et al. (2018), Soleng et al. (2018), Laaksonen et al. (2017), Rieille et al. (2017), Potkonjak et al. (2017), Daniel, Danielova, et al. (2016); Daniel, Rudenko, et al. (2016), Henningsson et al. (2016), Jaaskelainen et al. (2016)
	I. ricinus × *I. persulcatus*	Highly likely	0	1	YES	YES	SLR	Belova et al. (2023)
VEEV	*Ae. detritus*	Potential	0	1	YES	YES	SLR	Chapman et al. (2020)
	Ae. vexans	Potential	0	0	YES	YES	Expert opinion	The virus is reported to be transmitted by a wide range of mosquito genera during epizootic events (Culex (Psorophora (Ochlerotatus and there is lab evidence of replication in Ae. albopictus Fernández et al. (2003) and Aedes spp. has been related to urban outbreaks.
	Cx. gnomatos	Potential	0	1	NO	NO	SLR	Turell et al. (2006)
	Cx. gnomatos/ vomerifer	Potential	0	1	NO	NO	SLR	Turell et al. (2006)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Cx. pipiens	Highly likely	0	0	YES	YES	Expert opinion	The virus is reported to be transmitted by a wide range of mosquito genera during epizootic events (*Culex* (*Psorophora* (*Ochlerotatus* and there is lab evidence of replication in *Ae. albopictus* Fernández et al. (2003) and *Aedes* spp. has been related to urban outbreaks. The same as highly likely for WNV, while *Ae. albopictus* for urban areas only
	Cx. pipiens s.l.	Potential	0	0	YES	YES	Expert opinion	
	Cx. taeniopus	Potential	0	1	NO	NO	SLR	Deardorff and Weaver (2010)
	Cx. univittatus	Potential	0	0	YES	YES	Expert opinion	The virus is reported to be transmitted by a wide range of mosquito genera during epizootic events (*Culex* (*Psorophora* (*Ochlerotatus* and there is lab evidence of replication in Ae. albopictus Fernández et al. (2003) and *Aedes* spp. has been related to urban outbreaks. The same as Highly likely for WNV, while *Ae. albopictus* for urban areas only
	Ps. columbiae	Potential	0	1	NO	NO	SLR	Moncayo et al. (2008)
VSV	*C. chiopterus*	Potential	0	0	YES	YES	Expert opinion	The virus could be mechanically and biologically transmitted by different groups of vectors, mosquitoes, sandflies, biting flies and *Culicoides*. The most probable candidates are *Culicoides* based on the type of feeding and link with large abundance. Black flies also candidates, but these vectors are not included in the opinion. Transovarial and cofeeding also mentioned for some vectors groups, but role not clear (Rozo-Lopez et al., 2018).
	C. dewulfi	Potential	0	0	YES	YES	Expert opinion	
	C. imicola	Potential	0	0	YES	YES	Expert opinion	
	C. obsoletus complex[a]	Potential	0	0	YES	YES	Expert opinion	
	C. sonorensis	Potential	0	3	NO	NO	SLR	Rozo-Lopez et al. (2022), Rozo-Lopez et al. (2021), Drolet et al. (2005)
WEEV	*Ae. aegypti*	Potential	0	1	YES	YES	SLR	Wang et al. (2012)
	Ae. albopictus	Potential	0	1	YES	YES	SLR	Wang et al. (2012)
	Cx. pallens	Potential	0	2	NO	NO	SLR	Wang et al. (2010), Wang et al. (2012)
	Cx. quinquefasciatus	Potential	0	1	NO	NO	SLR	Wang et al. (2012)
	Cx. tarsalis	Potential	0	2	NO	NO	SLR	Mahmood et al. (2006), Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
WNV	*Ae. albopictus*	Potential	0	2	YES	YES	SLR	Zhang et al. (2022), Holicki et al. (2022)
	Ae. australis	Potential	0	1	NO	NO	SLR	Kramer et al. (2011)
	Ae. canadensis	Potential	0	1	NO	NO	SLR	Turell et al. (2005)
	Ae. detritus	Potential	0	1	YES	YES	SLR	Blagrove et al. (2016)
	Ae. dorsalis	Potential	0	1	NO	YES	SLR	Goddard et al. (2002)
	Ae. japonicus	Potential	0	2	YES	YES	SLR	Veronesi et al. (2018), Wagner et al. (2018)
	Ae. kochi	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Ae. melanimon	Potential	0	1	NO	NO	SLR	Goddard et al. (2002)
	Ae. notoscriptus	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Ae. procax	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Ae. sierrensis	Potential	0	1	NO	NO	SLR	Goddard et al. (2002)
	Ae. taeniorhynchus	Potential	1	0	NO	NO	SLR	Blackmore et al. (2003)
	Ae. triseriatus	Potential	0	2	NO	NO	SLR	Erickson et al. (2006), Turell et al. (2005)
	Ae. vigilax	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Ae. vexans	Potential	0	3	YES	YES	SLR	Anderson et al. (2020), Goddard et al. (2002), Turell et al. (2005)
	Cq. linealis	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Cq. perturbans	Potential	0	1	NO	NO	SLR	Sardelis et al. (2001), Jansen et al. (2008), Ramirez et al. (2018)
	Cs. inornata	Potential	0	1	NO	NO	SLR	Goddard et al. (2002)
	Cs. melanura	Potential	1	0	NO	NO	SLR	Molaei et al. (2015)
	Cx. annulirostris	Potential	0	2	NO	NO	SLR	Jansen et al. (2008), Ramirez et al. (2018)
	Cx. bitaeniorhynchus	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Cx. erythrothorax	Potential	0	1	NO	NO	SLR	Goddard et al. (2002)
	Cx. gelidus	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Cx. incidens	Potential	0	1	NO	NO	SLR	Reisen, Barker, et al. (2006); Reisen, Fang, and Martinez (2006)
	Cx. modestus	Potential	0	2	YES	YES	SLR	Balenghien et al. (2008),Balenghien et al. (2007)
	Cx. neavei group	Highly likely	2	2	NO	NO	SLR	Fall et al. (2014), Lutomiah et al. (2011), Esteves et al. (2005) Figuerola et al. (2022)
	Cx. nigripalpus	Potential	0	2	NO	NO	SLR	Richards et al. (2011), Sardelis et al. (2001)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Cx. pipiens	Highly likely	3	19	YES	YES	SLR	Figuerola et al. (2022), Vogels et al. (2017), Romo et al. (2018), Wöhnke et al. (2020), Wagner et al. (2018), Koenraadt et al. (2019), Zakhia et al. (2018), Wang et al. (2020), Kenney et al. (2018), Balenghien et al. (2008), Bolling et al. (2012), Fortuna et al. (2015), Fros et al. (2015), Goddard et al. (2002), Kilpatrick et al. (2010), Kramer et al. (2011), Moudy et al. (2007), Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008), Richards, Anderson, Lord, Smartt, and Tabachnick (2012); Richards, Anderson, Lord, and Tabachnick (2012), Vaidyanathan et al. (2008), Vaidyanathan and Scott (2007), Tokarz and Smith (2020), Soltesz et al. (2017), Esteves et al. (2005), Lampman et al. (2006)
	Cx. pipiens s.l.	Highly likely	1	1	YES	YES	SLR	Bakhshi et al. (2020), Kampen et al. (2020)
	Cx. pipiens molestus	Potential	0	5	YES	YES	SLR	Vogels et al. (2016), Jansen et al. (2019), Holicki et al. (2020), Micieli et al. (2013), Nelms et al. (2013)
	Cx. pipiens pipiens	Potential	0	4	YES	YES	SLR	Vogels et al. (2016), Jansen et al. (2019), Holicki et al. (2020), Nelms et al. (2013)
	Cx. pipiens/restuans	Potential	1	0	YES	YES	SLR	Adelman et al. (2022)
	Cx. pipiens molestus × *Cx. quinquefasciatus*	Potential	0	1	YES	YES	SLR	Ciota et al. (2013)
	Cx. pipiens pipiens × *molestus*	Potential	0	1	YES	YES	SLR	Vogels et al. (2016)
	Cx. pipiens pipiens × *Cx. quinquefasciatus*	Potential	0	1	YES	YES	SLR	Ciota et al. (2013)
	Cx. perexiguus	Potential	1	0	YES	YES	SLR	Figuerola et al. (2022)
	Cx. pervigilans	Potential	0	1	NO	NO	SLR	Kramer et al. (2011)
	Cx. quinquefasciatus	Highly likely	1	19	NO	NO	SLR	McGregor, Erram, et al. (2021); McGregor, Kenney, and Connelly (2021), Romo et al. (2018), Giayetto et al. (2021), Maharaj et al. (2019), Blagrove et al. (2016), Shi et al. (2022), Ciota et al. (2013), Eastwood et al. (2011), Fall et al. (2014), Goddard et al. (2002), Jansen et al. (2008), Kramer et al. (2011), Lutomiah et al. (2011), Micieli et al. (2013),Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005); Reisen, Wheeler, et al. (2005), Reisen, Barker, et al. (2006); Reisen, Fang, and Martinez (2006), Richards et al. (2014), Sardelis et al. (2001), Riles et al. (2022), SLEV: Beranek et al. (2020), Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005); Reisen, Wheeler, et al. (2005)

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Vector-borne pathogen	Arthropod species	Vector status based on SLR	N_{Field} studies	N_{exp} studies	VectorNet map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
	Cx. restuans	Highly likely	1	2	NO	NO	SLR	Kilpatrick et al. (2010), Sardelis et al. (2001), Tokarz and Smith (2020), Lampman et al. (2006)
	Cx. salinarius	Potential	0	1	NO	NO	SLR	Sardelis et al. (2001)
	Cx. sitiens	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	Cx. stigmatosoma	Potential	0	4	NO	NO	SLR	Goddard et al. (2002), Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005); Reisen, Wheeler, et al. (2005), Reisen, Barker, et al. (2006); Reisen, Fang, and Martinez (2006)
	Cx. tarsalis	Potential	0	12	NO	NO	SLR	McGregor, Erram, et al. (2021); McGregor, Kenney, and Connelly (2021), Danforth et al. (2018), Danforth et al. (2016), Worwa et al. (2018), Worwa et al. (2019), Dodson et al. (2011), Dodson et al. (2012), Goddard et al. (2002), Moudy et al. (2007), Reisen, Barker, et al. (2008); Reisen, Fang, and Brault (2008); Reisen, Lothrop, et al. (2008), Reisen, Fang, and Martinez (2005); Reisen, Wheeler, et al. (2005), Reisen, Barker, et al. (2006); Reisen, Fang, and Martinez (2006)
	Cx. thriambus	Potential	0	1	NO	NO	SLR	Reisen, Barker, et al. (2006); Reisen, Fang, and Martinez (2006)
	Cx. torrentium	Potential	0	1	NO	YES	SLR	Jansen et al. (2019)
	Cx. univittatus	Highly likely	1	1	YES	YES	SLR	Lutomiah et al. (2011), Esteves et al. (2005)
	Cx. vansomereni	Potential	0	1	NO	NO	SLR	Lutomiah et al. (2011)
	V. carmenti	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	V. funerea	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)
	V. lineato	Potential	0	1	NO	NO	SLR	Jansen et al. (2008)

*Paper was identified by VectorNet expert after the SLR was carried out.

[a]*Culicoides obsoletus* complex includes *C. obsoletus* and *C. scoticus*. In some papers this is expressed as *Culicoides obsoletus/scoticus*.

[b]*Culicoides obsoletus* group includes *C. obsoletus*, *C. scoticus*, *C. montanus*, *C. chiopterus* and *C. dewulfi*.

B.2 | Evidence collected by Systematic Literature Review and expert opinion on the vector status of mechanical vectors

The results are presented following the taxonomic classifications reported in the studies identified through the narrative literature review.

Vector-borne pathogen	Arthropod species	Vector status based on SLR	$N_{exp\ studies}$	N_{path} studies	N_{epi} studies	N_{circ} studies	VectorNet Map	Presence in EU	Type of evidence	Source (bibliographic reference or reasoning for expert opinion)
Besnoitia besnoiti	*Stomoxys calcitrans*	Potential		3	1		NO	YES	NLR	Gollnick et al. (2015), Liénard et al. (2011), 2013), Sharif et al. (2019)
	Stomoxys spp.	Highly likely	1	1			NO	YES	NLR	Hornok et al. (2015), Sharif et al. (2019)
	Tabanidae	Potential			1		NO	YES	NLR	Hornok et al. (2015)
EIAV	*Stomoxys calcitrans*	Potential	1				NO	YES	NLR	Foil et al. (1983)
	Tabanidae	Potential			1		NO	YES	NLR	De Liberato et al. (2019)
LSDV	*A. aegypti*	Potential	1				NO	YES	NLR	Chihota et al. (2001)
	Haematobia irritans	Potential			1		NO	YES	NLR	Kahana-Sutin et al. (2016)
	Haematopota spp.	Potential	1				NO	YES	NLR	Sohier et al. (2019)
	Stomoxys calcitrans	Highly likely	2	3	1	1	NO	YES	NLR	Chihota et al. (2003), Gubbins (2019), Issimov et al. (2020), Kahana-Sutin et al. (2016), Paslaru et al. (2021), Sanz-Bernardo et al. (2022), Sohier et al. (2019)
Trypanosoma evansi	*Stomoxys* spp.[a]	Potential	1				NO	NO	NLR	Mihok et al. (1995)
	Stomoxys calcitrans	Potential	1				NO	YES	NLR	Mihok et al. (1995)
	Stomoxys niger[a]	Potential	1				NO	NO	NLR	Sumba et al. (1998)
	Stomoxys taeniatus[a]	Potential	1				NO	NO	NLR	Sumba et al. (1998)
Trypanosoma vivax	*Stomoxys* spp.[a]	Potential	1				NO	NO	NLR	Mihok et al. (1995)
	Tabanidae	Highly likely	1		2		NO	YES	NLR	Dávila et al. (2003), Desquesnes et al. (2009), Roeder et al. (1984)
	Stomoxys calcitrans	Potential	1				NO	YES	NLR	Mihok et al. (1995)
	Haematobosca[a]	Potential	1				NO	NO	NLR	Mihok et al. (1995)
	Atylotus agrestis[a]	Potential	2				NO	NO	NLR	Desquesnes and Dia (2003), Desquesnes et al. (2009)
	Atylotus fuscipes[a]	Potential	2				NO	NO	NLR	Desquesnes and Dia (2004), Desquesnes et al. (2009)
	Hippoboscidae	Potential			1		NO	YES	NLR	Roader et al. (1984)

[a]Only detected in species not found in Europe; NLR = narrative literature review.

APPENDIX C

Classification of data availability for selected vector-borne diseases

TABLE C.1 Number of publications identified through systematic literature reviews for select pathogens.

VBD	Publication count	Data availability
AHSV	66	++
AKAV	77	++
B. besnoiti	82	++
B. burgdorferi s.l.	486	+++
BEFV	67	++
BTV	380	+++
C. burnetii	217	+++
CCHFV	73	++
CVV	24	+
EEEV	31	+
EHDV	72	++
EIAV	55	++
JEV	79	++
L. infantum	560	+++
LSDV	87	++
RVFV	317	+++
SBV	84	++
SHUV	16	+
SLEV	212	+++
T. evansi	72	++
T. vivax	121	+++
TBEV	98	++
VEEV	31	+
VSV	33	+
WEEV	18	+
WNV	191	+++

Note: + 0–50; ++ 51–100; +++ > 100.

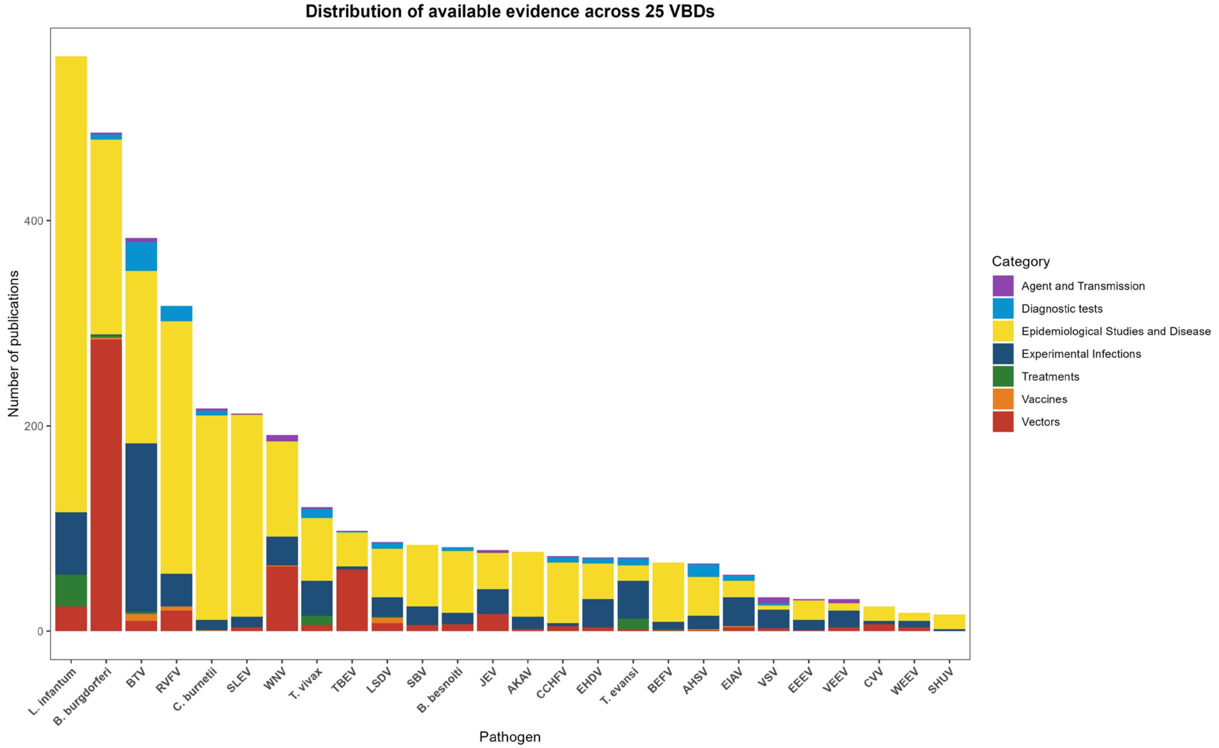

FIGURE C.1 Available evidence by category for the 25 vector-borne diseases (WEEV and EEEV are considered together). *Y*-axis refers to the publications that were considered eligible in the SLRs.

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