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# Viral *Culicoides*-borne diseases: an underestimated risk?

## *Maladies virales transmises par les* Culicoides *: un risque sous-estimé ?*

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**Abstract**

*Over the past two decades, three exotic arboviruses transmitted by* Culicoides *have been introduced into Europe. They are primarily responsible for bluetongue (BTV), Schmallenberg disease (SBV), and epizootic haemorrhagic disease (EHDV), which were previously absent. While the origin of EHDV contamination in French cattle is known, as it was first prevalent in Spain, the same cannot be said for the various serotypes of BTV that have appeared in Europe since 2006, or for SBV. However, it is necessary to better understand the risks of importing these exotic vector-borne viruses, which could find a local vector in Europe, in order to more effectively control these emerging diseases. This research is of utmost importance given that Oropouche fever, also transmitted by* Culicoides*, reappeared in human populations in South America in 2024. Some cases of emergence are well documented, but others remain to be elucidated. It is important to confirm or refute the hypothesis of introduction through the flower trade in the Netherlands, given the successive epizootic waves observed since 2006, particularly for bluetongue.*

***Keywords*:** Culicoides, *bluetongue, Schmallenberg disease, epizootic haemorrhagic disease, Oropouche fever, import, world flower market*

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Résumé

Au cours des deux dernières décennies, trois arbovirus exotiques transmis par les *Culicoides* ont été introduits en Europe. Ils sont responsables de la fièvre catarrhale ovine (BTV), de la maladie de Schmallenberg (SBV) et de la maladie hémorragique épizootique (EHDV), dont l'Europe était auparavant indemne. Si l'origine de la contamination par l'EHDV chez les bovins français est connue, puisqu'elle fut d'abord prévalente en Espagne, il n'en va pas de même pour les différents sérotypes de BTV apparus en Europe depuis 2006, ni pour le SBV. Il est toutefois nécessaire de mieux comprendre les risques d'importation de ces virus exotiques transmis par des vecteurs, qui pourraient trouver un relais avec des vecteurs indigènes en Europe, afin de mieux contrôler ces maladies émergentes. Ces recherches sont d'autant plus essentielles que la fièvre d'Oropouche, également transmise par les *Culicoides*, est réapparue chez l'Homme en Amérique du Sud en 2024. Certains cas d'émergence sont bien documentés, mais d'autres restent à élucider. Il importe de confirmer ou d'infirmer l'hypothèse d'une introduction par le commerce des fleurs aux Pays-Bas, face aux vagues successives observées depuis 2006, notamment pour la fièvre catarrhale ovine.

**Mots-clés** : *Culicoides*, fièvre catarrhale ovine, maladie de Schmallenberg, maladie hémorragique épizootique, fièvre d'Oropouche, importation, marché mondial des fleurs

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# Introduction

In recent years, the increase in trade and travel has led to a rise in the prevalence of emerging and re-emerging diseases in both humans and animals. Most of these diseases affect multiple species, and approximately 75% of them are zoonotic, emerging at the intersection of wildlife, domestic animals, and humans. On 24 November 2009, physicians and veterinarians gathered at the French *National Academy of Medicine* (ANM) for a session on "*Risks of importation and establishment of exotic infectious diseases in Europe*," *exploring the concept of "One Health*," which remains highly relevant today. Questions were addressed at the time about the impact of climate change, in the context of the local and regional threat posed by the establishment of *Aedes albopictus* in Italy and southern France, and the resulting risk of chikungunya and dengue fever. Nail was put on the underestimated risks of vector-borne diseases (Brugère Picoux & Rey 2010).

Over the last two decades, three exotic arboviruses transmitted by *Culicoides* have been introduced into Europe, despite the continent having been previously free of them. These are the agents responsible for bluetongue (BT with various serotypes), Schmallenberg disease (SB), and epizootic hemorrhagic disease (EHD) in cattle. The emergence of these epizootics has been a significant economic disaster for livestock farmers and has demonstrated the possibility of an autochthonous relay for these ruminant diseases. Among the 83 species of *Culicoides* known in Europe, several are suspected of transmitting these viruses, including *Cu. imicola*, *Cu. obsoletus*, *Cu. scoticus*, *Cu. punctatus*, *Cu. dewulfi*, *Cu. pulicaris*, *Cu. chiopterus* (Carpenter *et al.* 2013; Cuellar *et al.* 2018).

While the origin of EHD contamination in French cattle is known, as it was prevalent in Spain, the same cannot be said for the various BTV serotypes that have appeared in Europe since 2006, or for SBV. However, further research is required to better understand the risks associated with the introduction and establishment of these exotic vector-borne viruses in Europe.

The geographical origins of certain primary bluetongue outbreaks underscore the potential role of air travel in their spread, although introduction via road and sea transport must also be considered (e.g. exotic flowers?). Similar to epidemiological studies on diseases transmitted by mosquitoes or ticks, it is essential to employ similar methods to accurately determine the precise origin of these exotic *Culicoides*-transmitted viruses, thereby preventing new epizootic outbreaks. This research is all the more important given the recent re-emergence of *Culicoides*-transmitted Oropouche fever in humans in South America in 2024. A scenario similar to that of BT must be avoided or drastically mitigated for public health reasons.

## *Main animal diseases transmitted by* Culicoides

Since their introduction in Europe in 1998, vector-borne pathogens transmitted by *Culicoides* have been neglected. The main diseases concerned are caused by different Orbiviruses—e.g. BTV, EHDV, and African horse sickness virus (AHSV)—and the Orthobunyavirus SBV. The severity of the symptoms observed in ruminants, such as hyperthermia, hemorrhagic lesions, abortions, and congenital malformations, has often justified the implementation of emergency vaccination campaigns to stop the geographical spread of the virus.

### *Bluetongue (BT)*

The BT virus comprises numerous serotypes; the most common ones, numbered 1 to 24, are transmitted by *Culicoides*, while 12 others, numbered 25 to 36, were identified later. The related disease, already present in Africa, Asia, and America, reached the Mediterranean region in 1998. It is highly likely that *Culicoides* present and circulating in neighboring countries, such as Tunisia, were carried by the sirocco wind to Sicily, Sardinia, and Corsica. The wind is also probably responsible for spreading BTV from Morocco to Spain and then throughout Europe (Zientara *et al.* 2013).

### *Emergence of BTV 8 in 2006 in the Netherlands, Belgium, and Germany*

The unexpected emergence of serotype 8 (BTV 8) in the Maastricht region in 2006 surprised epidemiological experts. BTV-8 was first described in the Netherlands (European Commission 2006a); it was subsequently identified a few days later in Germany (European Commission 2006b) and near in Belgium near Maastricht (Saegerman *et al.* 2010). Its rapid spread indicated transmission by indigenous European vectors and justified the implementation of emergency vaccination. However, although a specific vaccination protocol was designed, it was delayed due to a lack of vaccine doses (avis de l'Anses 2007-SA-0295).

In parallel with this surprising emergence in northern Europe, it should be noted that BTV 1, previously present in Spain, had also reached France, necessitating emergency vaccination against this serotype.

### *Emergence of BTV 6 in 2008 in the Netherlands and Germany*

In October 2008, a new serotype, BTV 6, was detected in the Netherlands and Germany, and was identified by the European Community Reference Laboratory (ECRL) at the Pirbright Institute in the UK. It was a South African vaccine virus (Eschbaumer *et al.* 2010). The restriction zone established when the first case was reported in the Netherlands extended beyond the Dutch border into Lower Saxony, which was very quickly affected (Eschbaumer 2010).

### *Emergence of BTV 11 in Belgium in 2008*

The search for the cause of a cow abortion in Belgium led to the detection of a new virus, BTV 11 (de Clercq *et al.* 2009). Although the source of the infection remains unknown, it is worth noting that this virus was found in the same geographical area where BTV 8 and BTV 6 emerged in 2006 and 2008, respectively. A few cattle were tested positive. It is possible that infected animals may have benefited from some protection through vaccination against BTV 8.

### *Emergence of BTV 14 in Poland in 2012*

A new serotype originating from a vaccine strain (BTV 14) appeared in Poland in 2012. It was found in Russia, Lithuania, and Spain (in an animal imported from Lithuania). All cases were subclinical (Orłowska *et al.* 2016).

### *Emergence of BTV 3 in 2023 in the Netherlands and Germany (Figure 1)*

Since August 5, 2024, France has been experiencing a new serotype (BTV 3), which had previously emerged in the Netherlands (Holwerda *et al.* 2004). This required the implementation of an emergency insect control campaign combined with specific vaccination. This BTV 3 strain first appeared in Germany on 12 October 2023 in the district of Kleve, located near the Dutch border. It then spread during the seasonal activity of the vectors in spring 2024 (Voigt *et al.* 2024). It should be noted that an autogenous vaccine used in Germany against BTV 3 caused a few additional cases of vaccine-associated BT.

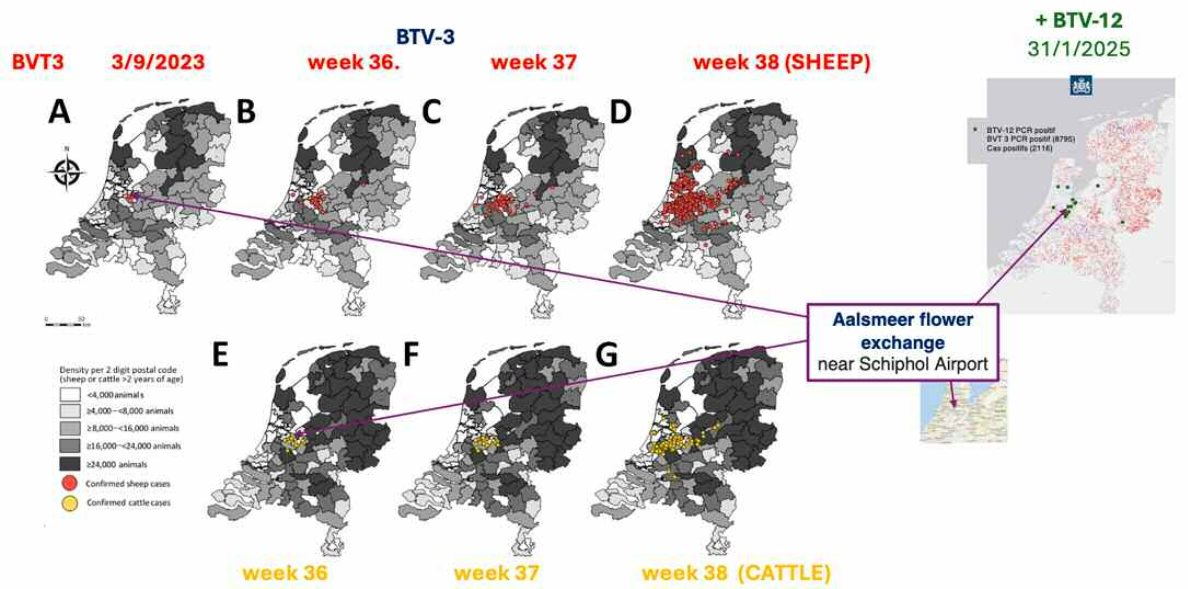


***Figure 1**. First isolations in the Netherlands of serotypes BTV 3 (in 2023) and BTV 12 (in 2024). Dutch Ministry of Agriculture (Holwerda* et al. *2004)*

***Emergence of BTV 12 in the Netherlands in 2024***

In December 2024, a new serotype (BTV 12) was identified in sheep that had been vaccinated against BTV 3. This demonstrates that the epidemics are not over (van den Brom *et al.* 2025). The latest BTV 12 outbreak was limited to just over a dozen cases in the Netherlands in 2024. In the absence of a vaccine for this serotype, and given that an outbreak was observed in the UK in February 2025, a high level of vigilance is required across Europe to track this serotype.

***Special case of the epidemiology of bluetongue in France***

Other BTV serotypes have been isolated in France. Of particular note is serotype 4, which is present in Corsica (likely originating from Sardinia) and was introduced via viremic cattle to Haute-Savoie in 2017.

BT is an ongoing issue: emergency vaccination during the 2006 BTV 8 epidemic enabled France to regain its disease free status, which was lost again when the virus re-emerged in 2015 (De Clercq *et al.* 2021). The 2006 BTV 8 strain remained present in an enzootic form, rarely causing clinical signs. However, a new strain of the same serotype emerged in Aveyron in September 2023, which was clinically more severe. Research conducted by the National Reference Laboratory (LNR) for BTV at the Animal Health Laboratory, ANSES (French Agency for Food, Environmental and Occupational Health & Safety), revealed that the 2023 BTV 8 strain was genetically similar to those circulating in Africa and the Middle East.

***Significance of the number of serotypes introduced into Europe since 1998***

In total, several BTV serotypes (1, 2, 3, 4, 6, 8, 9, 11, 12, 14, 25, 27) have contaminated Europe in the last two decades. The origin of several of these serotypes in Europe remains unclear.

## Schmallenberg disease (SB)

SB, which is caused by an orthobunyavirus that was first identified in Schmallenberg, Germany, emerged in the Netherlands in the Maastricht region and in Germany during the summer of 2011. It followed a similar geographical pattern to the 2006 BT epidemic, affecting 27 countries; however, the origin of the virus was never officially identified (Wernicke *et al.* 2014; Wernicke & Beer 2017). SBV is similar to Akabane virus, which is named after the neighborhood in Japan where it was first identified. It is also characterized by its teratogenic effect in ruminants. SBV is also closely related to the Oropouche virus (OROV), which is responsible for a re-emerging human disease in South America and the Caribbean in 2024. The emergence of SBV, a previously unknown virus, prompted the World Organisation for Animal Health (WOAH) to update its alert system for emerging animal diseases that require reporting. France was affected at the end of January 2012.

## Epizootic hemorrhagic disease (EHD)

EHDV is an arbovirus that affects cattle and certain wild ruminants, mainly white-tailed deer (*Odocoileus virginianus*) in the USA. It should be noted, however, that this is not the case in France for this species. Sheep, goats, and camelids may also be susceptible. EHD is found worldwide, including North America, South America, Asia, and Africa. Europe was free of the disease until 2022.It first appeared in countries in the Mediterranean region (gradually spreading to the countries of the Maghreb, Sicily, and the Iberian Peninsula).. France saw its first outbreak (serotype EHDV 8) in September 2023 in the Pyrénées-Atlantiques county. This was likely due to the presence of the virus in Spain, which was transmitted by wind-borne *Culicoides* (Bibard *et al.* 2024). An emergency vaccination campaign was launched in a restricted area to halt the spread of the epidemic. Within 10 days, by 28 September 2023, the National Reference Laboratory (LNR) for BTV at the Animal Health Laboratory, ANSES, had mobilized a network of 14 laboratories (and subsequently more than 50) to carry out thousands of PCR tests to diagnose EHD (Zientara 2025, personal communication).

## African horse sickness

Europe is currently free of African horse sickness, but the causative arbovirus (AHSV), which is very similar to that of BT, is also transmitted by *Culicoides*. The risk cannot be ruled out, as the disease was imported to a Spanish zoo via infected zebras from Namibia in 1987 (Mellor *et al.* 1990). Portugal was subsequently infected. The first appearance of this disease in Thailand in 2020 is also thought to be due to the importation of South African zebras (Nelson *et al.* 2022).

## Routes of introduction of these viruses transmitted by Culicoides

Given the significant economic consequences of these viral diseases affecting ruminants and equines, it is important to understand the risks associated with the introduction of these viruses transmitted by *Culicoides*. While some cases of emergence are well documented, others remain to be elucidated (Maintiens *et al.* 2008; Carpenter *et al.* 2013; Napp *et al.* 2013; Brugère-Picoux & Angot 2020).

***Wind-borne transmission of Culicoides***
We have previously ascertained the probable origin of the first cases of BT that appeared in the circum-Mediterranean region via the wind (Stokes *et al.* 2016). This wind also explains the ease with which infected vectors spread, particularly across borders.

***Importation of infected hosts***
Most often, these are zoo animals, as was the case with the introduction of African horse sickness to Spain. Similarly, Haute-Savoie was contaminated by BTV 4 following the introduction of an infected cow from Corsica. However, it is essential to consider animal transports throughout Europe, their origins, and transit sites, particularly.

***Disease caused by an indigenous or imported vaccine strain***
An example of this occurred in Germany in 2023, with an autogenous vaccine against BTV-3, and in the Netherlands in 2008, with an insufficiently attenuated vaccine strain against South African BTV 6.

***Transport of* Culicoides *via a commercial network***
The potential transport of infected *Culicoides* via commercial trade networks is a significant aspect of BT epidemiology that has not yet been adequately considered. However, the spread of pathogens via trade is well known, as seen in the transport of tiger mosquitoes. For example, tires transported from one continent to another act as water reservoirs, facilitating the reproduction of mosquitoes. Air traffic has often been implied in the importation of certain exotic diseases into the airport environment (e.g. malaria).

While the trade in plants and flowers is often cited for the associated risks of importing pathogens for these plants, it is also responsible for introducing insects or other animal species, such as the northern Andean tree frog (*Dendropsophus norandinus*) and the Sicilian lizard (*Podarcis siculus*), which has become an invasive species (Hinsley & Petrovan 2025). As these discoveries are random, the risks associated with these imports are certainly underestimated. The risk of importing pathogen vectors via flowers, which can lead to the contamination of native insects, has been mainly studied in relation to bee diseases (Adler *et al.* 2021). However, other pollinating insects, such as *Culicoides*, have been overlooked, despite the fact that they can carry agents of human or animal diseases. Compared to mosquitoes, *Culicoides* are often overlooked due to their small size. Therefore, the available data on these vectors is rather limited. We cannot rule out the possibility of orbivirus transmission through the presence of these viruses in organic matter associated with plants where *Culicoides* are found, via their excrement, eggs, or nymphs.

***The Netherlands, a hub for the world flower trade***

Several index cases of BT and SB have often emerged in the Netherlands, which is the hub of the world flower trade. This may be associated with the importation of *Culicoides* pollinating insects. While some flowers may be transported by road over short distances, the majority arriving in this global Dutch trade hub transit through platforms located near airports to facilitate the rapid transit of these perishable products.

*The chronology of the emergence of index cases of BT and SB in the Netherlands is shown in parallel with the evolution of flower markets* (**Figure 2**)

The index cases of BTV 8 appeared in the Netherlands in 2006, and then rapidly spread to Germany and Belgium, in the same geographical area where the index cases occurred in these countries in 2008, during the emergence of BTV 6. The same was true for the emergence of SB in the Netherlands in 2011. This geographical location is in the province of Limburg, in the south of the Netherlands, near Maastricht and not far from Venlo. According to Boyer (2012), Venlo was still the global hub for flower auctions at that time.

On 1 January 2008, the merger of flower markets, including those in Venlo and Aalsmeer, with the company "FloraHolland" resulted in the formation of a new flower exchange (Cessou 2007). This auction is located in Aalsmeer, nicknamed the "Wall Street of flowers," 15 km far from Schiphol International Airport near Amsterdam.

Alongside this regrouping, "*The Venlo market chose to focus on fruit and vegetables, and FloraHolland abandoned the flower auction. Curiously, it was in this city that the Netherlands organised the 'Floriade,' a huge horticultural exhibition that takes place only once every ten years, from April to October 2012. However, FloraHolland has maintained a flower market in the same region through a partnership with the German company Landgard. This market is located 10 minutes from Venlo, but on the German side of the border in Herongen.*" (Boyer 2012). The maintenance of a large flower market near Venlo could explain the emergence of SBV in 2011, which spread across Europe, similar to BTV 8 and BTV 6.

The emergence of BTV 3 in 2023 and BTV 12 in 2024 near the current world flower trading hub in Aalsmeer further supports the hypothesis of airborne importation of *Culicoides*, which has not yet been formally ruled out. This is particularly pertinent given that the reasons for the arrival of these viruses in the Netherlands were unclear 20 years ago.

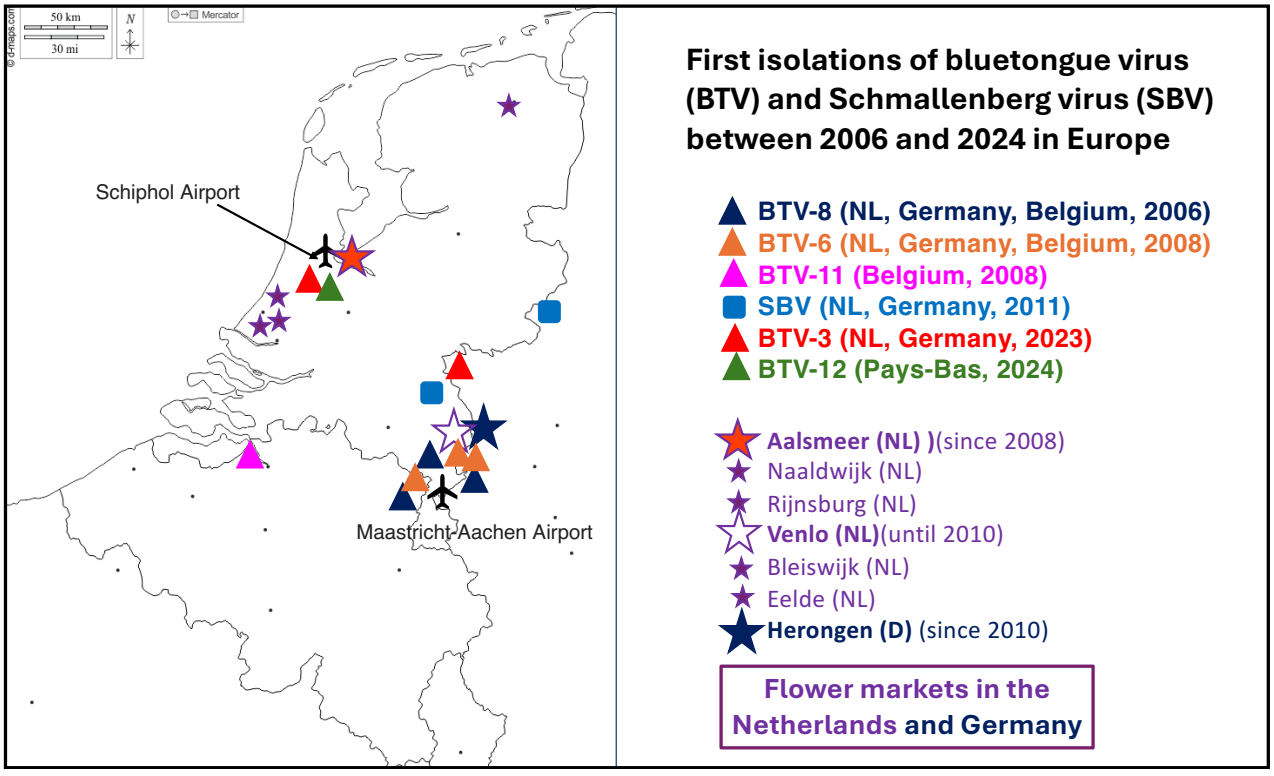


***Figure 2.*** *Chronology of the emergence of index cases of BT and SB in the Netherlands, alongside the development of flower markets*

*How can the hypothesis of a risk linked to the flower trade be confirmed in order to clarify the origin of BT and SV in this country?*
*"It is evident that the limited surveillance measures applied to flower imports by air—such as the trapping of* Culicoides *near containers, within cargo aircraft transporting flowers, at the Aalsmeer auction, or in other flower markets—fail to provide additional insights necessary to address this question."*

This hypothesis is not new; we previously proposed it after BTV 8 and BTV 6 first emerged in the Netherlands (Brugère-Picoux & Angot 2012).

Admittedly, studies on ticks and mosquitoes have been a priority until now, but the economic problems associated with BT, EHD, and SB justify investigating the origins of this emergence of diseases and establishment in Europe over the past 20 years (Figure 3).

In Europe, the importance of *Culicoides* in public health is limited to the nuisance caused by their bites, which are mainly inflicted by a single species, *Cu. impunctatus* (Carpenter *et al.* 2013).

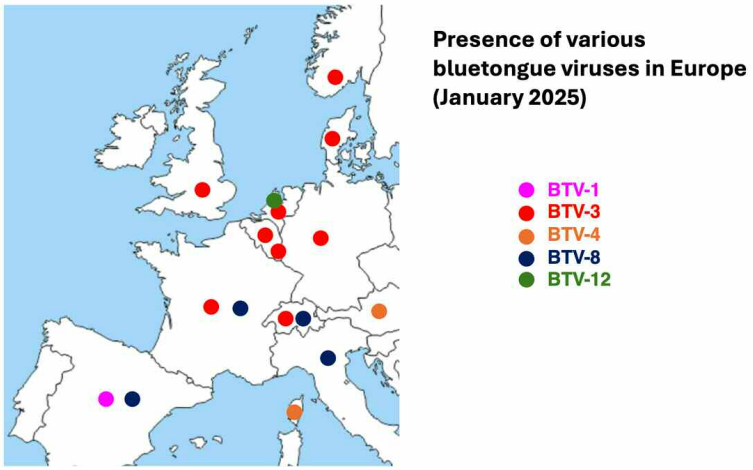


***Figure 3.*** *The presence of different BTV in Europe in January 2025*

## Re-emergence of Oropouche disease in 2024

The current threat posed by OROV, primarily transmitted to humans by a culicoid midge, underscores the need to investigate the risk factors for the introduction and establishment of this vector, which has been largely neglected until now.

Few viruses recognize *Culicoides* as their primary vector and are transmitted to humans. The best-known example is OROV, which spread in 2024 to infected and previously unaffected countries, resulting in more severe clinical manifestations, such as death, miscarriages, and microcephaly. This demonstrates that the importance of this viral disease may have been underestimated. The infection of travelers from the Americas and Europe justified the issuance of a global alert. However, uncertainties regarding the epidemiology of arboviruses and the vector competence of *Culicoides* make it impossible to assess the risk of OROV entering Europe (Brugère-Picoux *et al.* 2025). The main vector of OROV across the Atlantic is *Cu. paraensis*, which has not yet been identified in Europe. But can the possibility of *Cu. impunctatus* acting as a relay for OROV in Europe be formally ruled out? Nevertheless, the risk seems lower given the seasonal activity of this *Culicoides* species, as opposed to the year-round activity of *Cu. paraensis* in Brazil.

## Another risk: is a reassortment between OROV and SBV possible?

When SBV first appeared in Europe, one of the primary concerns was the zoonotic risk associated with this emerging disease, given the similarities between SBV and OROV (Brugère-Picoux & Angot 2012). The British health authorities advised pregnant women to avoid contact with sick animals. However, European authorities considered that there was no zoonotic risk. However, the possibility of reassortment between OROV and SBV viruses is considered likely. This could lead to the emergence of a new Simbu virus with zoonotic potential (Wesselmann *et al.* 2024).

Unlike BT, SB has remained endemic in continental Europe. SBV appeared to have been eliminated after its emergence in 2011, but the virus was observed to recirculate in summer 2014 and again in 2016 in Germany. The significant presence of the virus led to a resurgence of congenital malformations in non-immune cattle during the following winter (Wernicke *et al.* 2015).

When BTV-3 appeared in Germany in 2023, testing of *Culicoides* trapped in contaminated areas near the Dutch border (in North Rhine-Westphalia and Lower Saxony) confirmed the persistence of high SBV vector circulation (Voigt *et al.* 2024). Today, SBV has an endemic status in Central Europe (Zeiske *et al.* 2025).

## Conclusion

The problem of animal diseases transmitted by *Culicoides* is a constant concern in Europe. In France, in January 2025, all departments were infected with EHDV, BTV 8, BTV 4, or BTV 3, with two or three of these viruses potentially present in the same department at the same time (the BT vaccination campaign will mainly target serotypes 1, 3, and 8).
The survival of *Culicoides* during the winter period (overwintering) may raise concerns about the potential spread of BTV 12, which emerged in the Netherlands at the end of 2024. Unvaccinated wild ruminants may continue to serve as a reservoir for the virus. Other viruses may emerge in Europe in animals (e.g. a new serotype of BTV or AHSV) or even in humans (e.g. OROV), but it is not known when.

These viral outbreaks in Northern Europe, particularly in the Netherlands, require serious investigations to assess the risk of new emerging infections for both animals and humans. Finding the origin of these outbreaks would address a long-standing knowledge gap. The hypothesis that viruses may have been introduced through the flower trade requires thorough investigation. However, if this is the case, insect control of commercial flowers could create another public health problem.

In a "One Health" approach, it is crucial to maintain knowledge sharing between veterinarians and physicians regarding animal or human vector-borne diseases with zoonotic potential. This requires the development of improved surveillance and prevention strategies for these diseases, regardless of whether their vectors are mosquitoes, ticks, or *Culicoides*.

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## Conflicts of interest

*The authors declare that they have no conflicts of interest.*

## References


• Adler, L. S., Irwin, R. E., McArt, S. H., & Vannette, R. L. (2021). Floral traits affecting the transmission of beneficial and pathogenic pollinator-associated microbes. *Current Opinion in Insect Science*, 44, 1–7. https://doi.org/10.1016/j.cois.2020.08.006

• Bibard, A., Martinetti, D., Picado, A., Chalvet-Monfray, K., & Porphyre, T. (2024). Assessing the Risk of Windborne Dispersal of *Culicoides* Midges in Emerging Epizootic Hemorrhagic Disease Virus Outbreaks in France. *Transboundary and Emerging Diseases*, 2024, 5571195. https://doi.org/10.1155/2024/5571195

• Boyer, P. (2012). Les Pays-Bas, plaque tournante du marché mondial des fleurs. Available at: https://www.la-croix.com/Actualite/Economie-Entreprises/Economie/Les-Pays-Bas-plaque-tournante-du-marche-mondial-des-fleurs-_NP_-2012-04-29-800572

• Brugère-Picoux, J. & Rey, M. (2010). Les maladies infectieuses exotiques : risques d'importation et d'implantation en Europe. *Rapport de l'Académie nationale de Médecine. Médecine Sciences Publications (Lavoisier)*, 226 p. ISBN: 9782257204202. Available at: https://www.academie-medecine.fr/les-maladies-infectieuses-exotiques-risques-dimportation-et-dimplantation-en-europe/

• Brugère-Picoux, J. & Angot, J. L. (2012). La progression du virus Schmallenberg en Europe: une nouvelle maladie d'élevage des ruminants. *Bulletin de l'Académie vétérinaire de France*, 165(1), 5-8. https://www.persee.fr/doc/bavf_0001-4192_2012_num_165_1_9593

• Brugère-Picoux, J. & Angot, J. L. (2020). Biodiversité et maladies émergentes. *Bulletin de l'Académie vétérinaire de France*, 173, 117-127. https://www.persee.fr/doc/bavf_0001-4192_2020_num_173_1_12953

• Brugère-Picoux, J., Bourhy, H., Rosolen, S., Angot, J.L., Buisson, Y., Rodhain, F. Jarlier V, & Malvy D. (2025). Réémergence en Amérique du Sud du virus Oropouche dont le principal vecteur est un culicoïde : faut-il s'inquiéter ? *Bulletin de l'Académie nationale de Médecine*, *209*(6), 847-858. https://doi.org/10.1016/j.banm.2025.04.018

• Carpenter, S., Groschup, M. H., Garros, C., Felippe-Bauer, M. L., & Purse, B. V. (2013). *Culicoides* biting midges, arboviruses and public health in Europe. *Antiviral Research*, *100*(1), 102–113. https://doi.org/10.1016/j.antiviral.2013.07.020

• Carpenter, A., Ghai, R. R., Gary, J., Ritter, J. M., Carvallo, F. R., Diel, D. G., Martins, M., Murphy, J., Schroeder, B., Brightbill, K., Tewari, D., Boger, L., Gabel, J., Cobb, R., Hennebelle, J., Stanton, J. B., McCullough, K., Mosley, Y. C., Naikare, H. K., Radcliffe, R., … Wallace, R. M. (2021). Determining the role of natural SARS-CoV-2 infection in the

death of domestic pets: 10 cases (2020-2021). *Journal of the American Veterinary Medical Association*, *259*(9), 1032–1039. https://doi.org/10.2460/javma.259.9.1032
• Cessou, S. (2007). Une nouvelle Bourse aux fleurs éclôt aux Pays-Bas. Available at: https://www.liberation.fr/futurs/2007/12/31/une-nouvelle-bourse-aux-fleurs-eclot-aux-pays-bas_109779/
• Cuéllar, A. C., Kjær, L. J., Kirkeby, C., Skovgard, H., Nielsen, S. A., Stockmarr, A., Andersson, G., Lindstrom, A., Chirico, J., Lühken, R., Steinke, S., Kiel, E., Gethmann, J., Conraths, F. J., Larska, M., Hamnes, I., Sviland, S., Hopp, P., Brugger, K., Rubel, F., … Bødker, R. (2018). Spatial and temporal variation in the abundance of *Culicoides* biting midges (Diptera: *Ceratopogonidae*) in nine European countries. *Parasites & Vectors*, *11*(1), 112. https://doi.org/10.1186/s13071-018-2706-y
• De Clercq, K., Mertens, P., De Leeuw, I., Oura, C., Houdart, P., Potgieter, A. C., Maan, S., Hooyberghs, J., Batten, C., Vandemeulebroucke, E., Wright, I. M., Maan, N., Riocreux, F., Sanders, A., Vanderstede, Y., Nomikou, K., Raemaekers, M., Bin-Tarif, A., Shaw, A., Henstock, M., … Vandenbussche, F. (2009). Emergence of bluetongue serotypes in Europe, part 2: the occurrence of a BTV-11 strain in Belgium. *Transboundary and Emerging Diseases*, 56(9-10), 355–361. https://doi.org/10.1111/j.1865-1682.2009.01092.x
• De Clercq, K., Vandaele, L., Vanbinst, T., Riou, M., Deblauwe, I., Wesselingh, W., Pinard, A., Van Eetvelde, M., Boulesteix, O., Leemans, B., Gélineau, R., Vercauteren, G., Van der Heyden, S., Beckers, J. F., Saegerman, C., Sammin, D., de Kruif, A., & De Leeuw, I. (2021). Transmission of Bluetongue Virus Serotype 8 by Artificial Insemination with Frozen-Thawed Semen from Naturally Infected Bulls. *Viruses*, 13(4), 652. https://doi.org/10.3390/v13040652
• Eschbaumer, M., Hoffmann, B., Moss, A., Savini, G., Leone, A., König, P., Zemke, J., Conraths, F., & Beer, M. (2010). Emergence of bluetongue virus serotype 6 in Europe-German field data and experimental infection of cattle. *Veterinary Microbiology*, *143*(2-4), 189–195. https://doi.org/10.1016/j.vetmic.2009.11.040
• Eschbaumer, M. (2010): Recent Developments in Immunoprophylaxis, Diagnosis and Epizootiology of Bluetongue Virus in Germany. Dissertation, LMU München: Faculty of Veterinary Medicine. Available at: https://edoc.ub.uni-muenchen.de/12116/
• European Commission. (2006a). Bluetongue in the Netherlands confirmed. *Press release*, *18 August 2006*, IP/06/1112. Available at: https://ec.europa.eu/commission/presscorner/detail/en/ip_06_1112
• European Commission. (2006b). Bluetongue confirmed in Belgium and Germany. *Press release*, *21 August 2006*, IP/06/1113. Available at: https://ec.europa.eu/commission/presscorner/detail/en/ip_06_1113
• Hinsley, A., & Petrovan, S. (2025). The global plant trade is spreading invasive species to Europe. *The Conversation*. https://doi.org/10.64628/AB.tnp547qxd
• Holwerda, M., Santman-Berends, I. M. G. A., Harders, F., Engelsma, M., Vloet, R. P. M., Dijkstra, E., van Gennip, R. G. P., Mars, M. H., Spierenburg, M., Roos, L., van den Brom, R., & van Rijn, P. A. (2024). Emergence of Bluetongue Virus Serotype 3, the Netherlands, September 2023. *Emerging Infectious Diseases*, *30*(8), 1552–1561. https://doi.org/10.3201/eid3008.231331
• Mellor, P. S., Boned, J., Hamblin, C., & Graham, S. (1990). Isolations of African horse sickness virus from vector insects made during the 1988 epizootic in Spain. *Epidemiology and Infection*, *105*(2), 447–454. https://doi.org/10.1017/s0950268800048020
• Mintiens, K., Méroc, E., Mellor, P. S., Staubach, C., Gerbier, G., Elbers, A. R., Hendrickx, G., & De Clercq, K. (2008). Possible routes of introduction of bluetongue virus serotype 8 into the epicentre of the 2006 epidemic in north-western Europe. *Preventive Veterinary Medicine*, *87*(1-2), 131–144. https://doi.org/10.1016/j.prevetmed.2008.06.011
• Napp, S., García-Bocanegra, I., Pagès, N., Allepuz, A., Alba, A., & Casal, J. (2013). Assessment of the risk of a bluetongue outbreak in Europe caused by *Culicoides* midges introduced through intracontinental transport and trade networks. *Medical and Veterinary Entomology*, 27(1), 19–28. https://doi.org/10.1111/j.1365-2915.2012.01016.x
• Nelson, E., Thurston, W., Pearce-Kelly, P., Jenkins, H., Cameron, M., Carpenter, S., Guthrie, A., & England, M. (2022). A Qualitative Risk Assessment for Bluetongue Disease and African Horse Sickness: The Risk of Entry and Exposure at a UK Zoo. *Viruses*, 14(3), 502. https://doi.org/10.3390/v14030502
• Orłowska, A., Trebas, P., Smreczak, M., Marzec, A., & Zmudzinski, J. F. (2016). First detection of bluetongue virus serotype 14 in Poland. *Archives of Virology*, *161*(7), 1969–1972. https://doi.org/10.1007/s00705-016-2857-0
• Saegerman, C., Mellor, P., Uyttenhoef, A., Hanon, J. B., Kirschvink, N., Haubruge, E., Delcroix, P., Houtain, J. Y., Pourquier, P., Vandenbussche, F., Verheyden, B., De Clercq, K., & Czaplicki, G. (2010). The most likely time and place of introduction of BTV8 into Belgian ruminants. *PloS One*, *5*(2), e9405. https://doi.org/10.1371/journal.pone.0009405
• Stokes, J. E., Baylis, M., & Duncan, J. S. (2016). A freedom from disease study: Schmallenberg virus in the south of England in 2015. *The Veterinary Record*, *179*(17), 435. https://doi.org/10.1136/vr.103903
• Van den Brom, R., Santman-Berends, I., van der Heijden, M. G., Harders, F., Engelsma, M., van Gennip, R. G. P., Maris-Veldhuis, M. A., Feddema, A. J., Peterson, K., Golender, N., Spierenburg, M., van Rijn, P. A., & Holwerda, M. (2025). Bluetongue virus serotype 12 in sheep and cattle in the Netherlands in 2024 - A BTV serotype reported in Europe for the first time. *Veterinary Microbiology*, *301*, 110365. https://doi.org/10.1016/j.vetmic.2024.110365
• Voigt, A., Kampen, H., Heuser, E., Zeiske, S., Hoffmann, B., Höper, D., Holsteg, M., Sick, F., Ziegler, S., Wernike, K., Beer, M., & Werner, D. (2024). Bluetongue Virus Serotype 3 and Schmallenberg Virus in *Culicoides* Biting Midges, Western Germany, 2023. *Emerging Infectious Diseases*, *30*(7), 1438–1441. https://doi.org/10.3201/eid3007.240275
• Wernike, K., & Beer, M. (2017). Schmallenberg Virus: A Novel Virus of Veterinary Importance. *Advances in Virus Research*, *99*, 39–60. https://doi.org/10.1016/bs.aivir.2017.07.001
• Wernike, K., Conraths, F., Zanella, G., Granzow, H., Gache, K., Schirrmeier, H., Valas, S., Staubach, C., Marianneau, P.,

Kraatz, F., Höreth-Böntgen, D., Reimann, I., Zientara, S., & Beer, M. (2014). Schmallenberg virus-two years of experiences. *Preventive Veterinary Medicine*, *116*(4), 423–434. https://doi.org/10.1016/j.prevetmed.2014.03.021

• Wernike, K., Hoffmann, B., Conraths, F. J., & Beer, M. (2015). Schmallenberg Virus Recurrence, Germany, 2014. *Emerging Infectious Diseases*, *21*(7), 1202–1204. https://doi.org/10.3201/eid2107.150180

• Wesselmann, K. M., Postigo-Hidalgo, I., Pezzi, L., de Oliveira-Filho, E. F., Fischer, C., de Lamballerie, X., & Drexler, J. F. (2024). Emergence of Oropouche fever in Latin America: a narrative review. *The Lancet. Infectious Diseases*, *24*(7), e439–e452. https://doi.org/10.1016/S1473-3099(23)00740-5

• Zeiske, S., Kampen, H., Sick, F., Dähn, O., Voigt, A., Heuser, E., Beer, M., Werner, D., & Wernike, K. (2025). Monitoring of Schmallenberg virus, bluetongue virus and epizootic haemorrhagic disease virus in biting midges in Germany 2019-2023. *Parasites & Vectors*, *18*(1), 262. https://doi.org/10.1186/s13071-025-06913-w

• Zientara, S., & Sánchez-Vizcaíno, J. M. (2013). Control of bluetongue in Europe. *Veterinary Microbiology*, *165*(1-2), 33–37. https://doi.org/10.1016/j.vetmic.2013.01.010