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The Role of *Culicoides* Midges as Vectors of Bluetongue Virus: A Mini Review

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ABSTRACT

Culicoides biting midges (Ceratopogonidae) are the primary biological vectors of Bluetongue virus (BTV). The BTV is an orbivirus that causes substantial economic losses in livestock worldwide. Although over 50 arboviruses have been isolated from *Culicoides* species, BTV remains the most economically impactful disease. The present study aimed to evaluate the vector-virus association, including vector competence, transmission dynamics, and environmental factors influencing the spread of BTV. Vector competence in *Culicoides* is determined by midgut infection and dissemination barriers, which vary significantly among species. Transmission efficiency is influenced by temperature, extrinsic incubation period, and host factors, with cattle serving as long-term reservoirs and sheep exhibiting greater disease severity. Understanding vector-virus associations is essential for predicting outbreaks and developing effective control methods, especially as climate change promotes vector spread.

Keywords: Arbovirus, Bluetongue virus, *Culicoides*, Transmission, Vector competence

INTRODUCTION

Culicoides (*C.*) biting midges serve as the primary biological vectors for the Bluetongue virus (BTV), a pathogen classified within the genus *Orbivirus* of the family *Sedoreoviridae* (formerly Reoviridae, Payan-Carreira and Simões, 2025). Bluetongue virus causes morbidity and mortality in domestic and wild ruminants, leading to significant economic losses in the livestock industry (Maclachlan et al., 2009; Rushton, 2015). Bluetongue virus disease is notifiable to the World Organization for Animal Health (WOAH; Purse et al., 2005).

Over the past two decades, climate change has facilitated the spread of *Culicoides* vector species into geographical regions above 50° latitude (northern areas), thereby contributing to the global increase in BTV prevalence (Maclachlan, 2011). The disease has now been reported in all continents except Antarctica, exhibiting a noticeable trend of spreading towards more northern regions (Zhugunissov et al., 2025). The present study aimed to examine the association between *Culicoides* midges and BTV, focusing on vector competence, transmission mechanisms, and factors influencing viral spread.

BLUETONGUE VIRUS: KEY FEATURES RELEVANT TO VECTOR TRANSMISSION

Bluetongue virus is a small icosahedral virus measuring approximately 70 nanometers in diameter, with a genome comprising 10 segments of double-stranded RNA (Patel and Roy, 2014; Payan-Carreira and Simões, 2025). The genome segments encode seven structural proteins (VP1-7) along with four nonstructural proteins (NS1-3 and 3A; Roy, 2017). The outer capsid protein VP2 is the principal determinant of serotype specificity and the primary target of neutralizing antibodies (Bissett and Roy, 2024).

So far, 28 distinct BTV serotypes have been identified globally (Bumbarov et al., 2020). The virus demonstrated considerable genetic diversity, resulting from mechanisms such as genetic drift, reassortment, and intragenic recombination (Sanders et al., 2022). Reassortment, which involves the exchange of genome segments between different viral serotypes, can influence viral replication kinetics, cytopathogenicity, and virulence (Coetzee et al., 2014). This has been documented not only in wild-type field strains but also in live weak vaccine serotypes, prompting concerns regarding disease management (Nomikou et al., 2015). Bluetongue virus serotypes were further divided into eastern and western topotypes based on their geographic origin, indicating a long-term evolutionary divergence with limited genetic

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exchange between the regions (Maan et al., 2010). The viral RNA-dependent RNA polymerase, which lacks proofreading ability, is prone to errors, leading to increased genetic variability (Payan-Carreira and Simões, 2025).

CULICOIDES VECTORS OF BLUETONGUE VIRUS

Out of approximately 1,400 described *Culicoides* species worldwide (Harrup et al., 2015), only about 30 have been recognized as vectors of BTV (Gomulski et al., 2006). The most widely accepted major vector species of the BTV include *C. imicola*, which is distributed across Africa, southern Europe, the Middle East, and Asia, *C. brevitarsis* in Australia, *C. bolitinos* in southern Africa, *C. obsoletus* across Europe and Asia, *C. scoticus* and *C. pulicaris* in Europe, *C. sonorensis* in North America, and *C. insignis* in Central and South America. The success and extent of BTV transmission depend on the presence and density of these vector populations in regions (Mellor et al., 2000). *Culicoides* distribution is associated with warm, humid, and muddy areas rich in organic matter, and adult activity is most pronounced from approximately one hour before sunset to one hour after sunrise.

VECTOR COMPETENCE FOR BLUETONGUE VIRUS

Vector competence refers to an arthropod vector's ability to acquire, become infected with, and biologically transmit an arbovirus to a susceptible host (Carpenter et al., 2015). Competence varies significantly between different *Culicoides* species and even among individuals within a single species. For instance, only a specific proportion of *C. sonorensis* individuals can be orally infected with BTV (Jennings and Mellor, 1987).

Barriers to Bluetongue virus infection in *Culicoides*

The underlying variations in vector competence are attributed to intrinsic barriers, which include genetically determined immunological and physiological factors (Tabachnick, 1991). These barriers function at multiple stages of viral infection (Muntzer, 2017). The midgut infection barrier prevents the virus from entering or replicating within midgut epithelial cells, leaving individuals unaffected. The dissemination barrier (DB), also known as the midgut escape barrier, functions by preventing the virus from replicating in the midgut, spreading into the hemocoel, or causing infection in secondary tissues. The salivary gland barrier prevents virus transmission via saliva during subsequent blood meals, even when the virus has reached the salivary glands. Finally, the transovarial transmission barrier signified that infected females are unable to vertically transmit the virus to their offspring. The midgut is widely considered the primary determinant of vector competence and might even be the only tissue that affects the BTV infection outcomes in *Culicoides* (Fu et al., 1999).

Extrinsic incubation period

The extrinsic incubation period is the earliest time at which the virus is excreted into saliva and becomes infectious. The length of the extrinsic incubation period is influenced by viral strain, ambient temperature, viral dose ingested, vector type, body size, and nutritional status (Wittmann et al., 2002). The shortest documented incubation period for BTV is 4 days, observed with BTV-9 in *Culicoides*, whereas BTV-10 may require up to 15 days in *C. sonorensis* maintained at 25°C (Wittmann et al., 2002; Carpenter et al., 2011).

Bluetongue virus infection and dissemination in *Culicoides*

The transmission cycle initiates when female *Culicoides* ingest BTV while feeding on an infected host's blood. Then the virus replicates in both invertebrate vectors and vertebrate host cells, facilitating reproduction and transmission. Previous findings on *C. sonorensis* have reported the transmission pathway of BTV through the vector (Weaver et al., 1991; Fu et al., 1999). Following blood ingestion, virions enter the midgut, where the outer capsid protein VP2 is cleaved by intestinal proteases. Within approximately one hour, midgut epithelial cells become infected via either clathrin-mediated endocytosis or macropinocytosis (Mellor et al., 2000). Over approximately three days, viral particles replicate and spread from cell to cell within the midgut epithelium until reaching a limiting titer. Subsequently, viral particles disseminate into the hemocoel and then infect and replicate in secondary tissues, including neural tissues, the foregut, Malpighian tubules, ommatidia of the compound eyes, the fat body, the antennae, oocytes, and epithelial cells. Viral particles then enter the distal lateral lobes of the salivary glands, where they replicate and are secreted from acinar cells into saliva, a stage that lasts at least two days. Once salivary gland cells are infected, BTV is transmitted to the next host during subsequent blood feeding (Mellor et al., 2000; Muntzer, 2017).

Host factors affecting Bluetongue virus transmission

Successful vector transmission depends not only on vector competence but also on host susceptibility to BTV infection (Figure 1). Due to differences in the innate immune response, sheep exhibit significantly greater disease severity than cattle (Maclachlan, 2011; 2014). Higher and earlier levels of interferon type I (IFN-1) are associated with lower BTV titers, suggesting that early viral replication is more effective in sheep cells than in cattle cells (Hardy et al., 2023). Extended viremia in cattle makes them significant epidemiological reservoirs for BTV transmission, as indicated in Table 1 (Saminathan et al., 2020; Rodríguez-Martín et al., 2021).

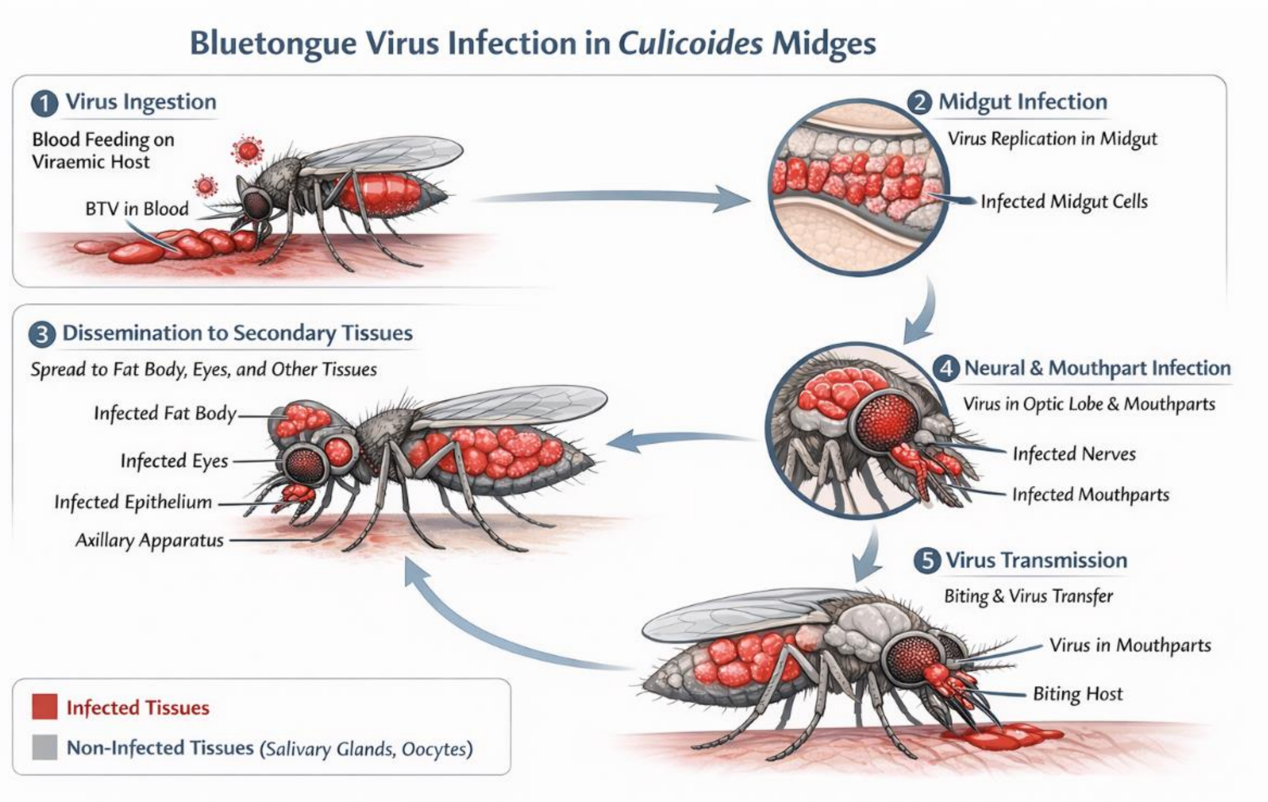

Figure 1. Bluetongue virus infection and dissemination in *Culicoides* midges. Bluetongue virus enters the midgut after blood feeding, replicates in epithelial cells, disseminates to secondary and neural tissues, and is transmitted via infected mouthparts during subsequent blood meals (Designed by the author).

Table 1. Duration of detectable viremia varies according to host species and Bluetongue virus serotype

Host	Viremia duration
Sheep	14-54 days
Goats	19-54 days
Cattle	Up to 100 days

ENVIRONMENTAL FACTORS INFLUENCING BLUETOUNGE VIRUS–*CULICOIDES* ASSOCIATION

The distribution and persistence of BTV are dependent on the presence or absence of adult *Culicoides* (Nayduch et al., 2014). Essential environmental factors include temperature, seasonality, and climate change.

Temperature

Under laboratory conditions, *C. imicola* larvae develop in 11-21 days at 20°C, 9-12 days at 25°C, and 7-9 days at 28°C. Egg and pupa development require 1-5 days, depending on temperature (Veronesi et al., 2009). In natural environments, larval development spans 10-60 days during summer and can extend through winter.

Seasonality

In Europe, active adult *Culicoides* were observed from February in oceanic climates to May in continental climates. The population peaks typically occur from May through September, with a secondary peak in the autumn following rainfall in Mediterranean climates. Populations decline in October or November, corresponding with the onset of winter temperatures (Veronesi et al., 2009). The seasonally vector-free period is defined as the duration during which the risk of BTV transmission is exceedingly low (EC, 2007).

Climate change

Mild, warm climates facilitate BTV survival during winter by expanding *Culicoides* habitats and sustaining vector activity. The emergence of multiple BTV serotypes (1, 2, 4, 9, and 16) into new regions, including Mediterranean Europe, since 1998 has led to major economic losses (Takken et al., 2007). Notably, the disease was detected in Norway in 2009, representing its farthest northern spread (Sperlova and Zendulkova, 2011).

GEOGRAPHIC SPREAD OF BLUETOUNGE VIRUS IN RELATION TO *CULICOIDES* DISTRIBUTION

Initially, BTV outbreaks were linked to tropical, subtropical, and temperate regions between 35°S and 40°N, aligning with climatic conditions conducive to *Culicoides* breeding (Sperlova and Zendulkova, 2011). Climate change has led to the expansion of *Culicoides* habitats into higher latitudes, facilitating the spread of BTV (Maclachlan, 2011). Since its initial identification in Africa in the late eighteenth century, BTV has been documented across all continents except Antarctica (Saminathan et al., 2020). Dissemination to new regions began in 1998 across the Mediterranean region of Europe (Takken et al., 2007). Previous isolated cases in Cyprus, the Greek islands, and the Iberian Peninsula likely resulted from wind-driven spread of infected *Culicoides* originating from Israel, Turkey, or North Africa (Purse et al., 2005).

CONCLUSION

The association between *Culicoides* midges and BTV represented a significant economic burden on global livestock production. Although the *Culicoides* genus comprises approximately 1,400 recognized species, only about 30 have been implicated in BTV transmission, with *C. imicola*, *C. obsoletus*, and *C. sonorensis* among the most notable vectors. Vector competence was influenced by physiological barriers, primarily the midgut infection barrier and viral dissemination barriers, which differed significantly across different species and among individuals within a population. Furthermore, species-specific differences in innate immune responses, with sheep exhibiting greater disease severity than cattle, underscore the importance of host factors in BTV transmission dynamics. The extrinsic incubation period, typically ranging from 4 to 15 days, was significantly influenced by ambient temperature and viral genotype. In vertebrates, cattle play a significant role in sustaining viral circulation, as they can remain viremic for up to 100 days and serve as strong reservoir hosts. Climate factors have enabled these vectors to move into higher latitudes, leading to the emergence of BTV in previously unaffected areas. Elucidating the specific associations between *Culicoides* species and circulating BTV serotypes is therefore important for refining predictive outbreak models and designing regionally adapted intervention strategies. Future studies should focus on regional vector competence investigations and surveillance of emerging vector-virus interactions.

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Authors' contributions

Ivana Zuber Bogdanović was responsible for conceptualization, literature collection, data interpretation, manuscript writing, review and editing, visualization, and final approval of the manuscript.The author read and approved the final edition of the manuscript before publication.

Availability of the data and materials

No new data were created or analyzed in this study. This study is a review of existing literature, and all referenced materials are cited in the reference list.

Competing interests

The author declared no conflict of interest.

Ethical considerations

The author reviewed potential ethical issues, including data falsification, multiple publications and submissions, redundancy, plagiarism, consent for publication, and misconduct, prior to publication. No AI tools were used in preparing and writing the manuscript.

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