Bluetongue
Summary

Introduction

Bluetongue (BT) remains one of the most complex and impactful vector-borne viral diseases of ruminants worldwide. Caused by bluetongue virus (BTV), an Orbivirus transmitted by Culicoides biting midges, the disease continues to pose significant challenges for animal health systems.

Since the previous analysis published in 2019, the epidemiological landscape of bluetongue has evolved considerably. The emergence and rapid spread of novel serotypes—most notably BTV-3 and BTV-5 in Europe—together with recurrent incursions of previously circulating strains, have reaffirmed the transboundary nature of the disease. At the same time, climate change has increasingly shaped transmission dynamics by facilitating virus expansion into previously unaffected regions.

Despite major advances in diagnostics, surveillance and vaccination, bluetongue remains difficult to eradicate. Control strategies continue to rely heavily on vaccination and animal movement management, but key biological characteristics of the virus, particularly its ability to persist, overwinter and circulate as multiple serotypes, limit the effectiveness of current tools or make them not cost-effective.

Disease profile

Bluetongue virus belongs to the genus *Orbivirus* (family Sedoreoviridae) and possesses a segmented double-stranded RNA genome comprising ten segments encoding structural and non-structural proteins.

All BTV strains share conserved group-specific antigens, particularly VP7, which forms the basis of most serogroup-specific diagnostic assays. In contrast, the outer capsid protein VP2 is highly variable and defines serotype specificity.

To date, more than 36 BTV serotypes or genotypes have been described worldwide. Classical serotypes (BTV-1 to BTV-24) are regulated under national and international animal health legislation, whereas the so-called “atypical” serotypes (e.g. BTV-25, BTV-26, BTV-27) display distinct biological properties and are not regulated by law.

Bluetongue affects a wide range of domestic and wild ruminants. Sheep are most severely affected, often developing acute clinical disease, while cattle typically exhibit subclinical infection but act as major amplification hosts due to prolonged viraemia.

Transmission is predominantly vector-borne, resulting in strong seasonal patterns in temperate regions and more continuous circulation in tropical and subtropical areas.

The simultaneous circulation of multiple serotypes and topotypes creates favourable conditions for genomic reassortment, a frequent evolutionary mechanism in BTV. Reassortant strains may exhibit altered virulence, host range or vector competence, further complicating control strategies.

Risk

The whole of Europe must be considered at risk from further incursions of BTV.

Climate change, which expands the geographical range of vectors and enhance their adaptation to new environments, exacerbates this risk. Indeed, BTV has recently expanded its geographic range and is able to cross borders due to the wide distribution and long-distance dispersal of Culicoides vectors. Additionally, climate change has extended their seasonal activity and geographical range, with higher temperatures enhancing viral replication within vectors and increasing the likelihood of overwintering, thereby sustaining transmission in areas previously considered marginal for bluetongue.

The co-circulation of multiple BTV serotypes and topotypes increases the probability of reassortment, shaping viral evolution and facilitating the emergence of novel strains. This genetic and biological variability complicates surveillance, risk prediction and vaccine-based control strategies.

Host-related risk is particularly evident when BTV is introduced into immunologically naïve populations. Recent European outbreaks, notably those caused by BTV-3, have shown that cattle can experience significant clinical and production losses, challenging the traditional view of cattle as largely subclinical hosts.

Bluetongue also presents a substantial transboundary risk, as infected vectors can be transported over long distances by wind and viremic animals can introduce the virus into new areas.

Overall, the risk of bluetongue emergence and re-emergence is expected to increase, mainly driven by climate change and limited surveillance in endemic regions such as North Africa and sub-Saharan Africa. These factors underline the need for proactive cooperation with endemic countries to strengthen surveillance, preparedness and risk management strategies.

Diagnostics

Diagnostic tools for bluetongue are generally robust and widely available. Serological assays, primarily competitive ELISA targeting VP7, are routinely used for surveillance and trade purposes. Virus neutralisation tests remain the reference method for serotype-specific antibody detection, although they are laborious and require specialised infrastructure and more trained personnel. Molecular diagnostics, particularly real-time RT-PCR assays, represent the cornerstone of early detection and outbreak investigation. Both group-specific and serotype-specific assays are available for many classical serotypes, including those historically circulating in Europe. Nevertheless, the continuous emergence of novel strains and reassortants necessitates regular updating and validation of these assays.

Important diagnostic gaps remain. No commercial serological DIVA (Differentiating Infected from Vaccinated Animals) tests are currently available, nor are serotype specific ELISAs, limiting the ability to conduct serological surveillance in vaccinated populations. Field-deployable diagnostics, such as pen-side tests and isothermal amplification methods (e.g. LAMP-PCR), remain well underdeveloped.

Vaccines

Vaccination remains the most effective tool for bluetongue control. Both live attenuated and inactivated vaccines have been used historically, although live vaccines are no longer authorised in Europe due to safety concerns, including reversion to virulence, transplacental transmission and reassortment with field strains.

Inactivated vaccines are currently the only commercially available option in Europe. They have proven highly effective in controlling past epidemics, including the major BTV-8 outbreak in northern Europe and more recent BTV-3 incursions. However, these vaccines are serotype-specific, often require two doses and periodic revaccination, and lack DIVA capability. Production is largely demand-driven, resulting in limited availability ahead of outbreaks. While emergency authorisation mechanisms exist, they remain reactive rather than anticipatory.

Next-generation vaccine platforms—including subunit vaccines, virus-like particles, vectored vaccines and mRNA-based approaches—offer promising avenues for safer, multivalent and potentially DIVA-compatible vaccines. However, these technologies have not yet reached commercial deployment and require further research on their effectiveness against BT.

Pharmaceuticals

No specific antiviral treatments are available for bluetongue. Disease management relies entirely on supportive care at animal level and preventive measures at population level. Although antiviral compounds could theoretically be developed based on a deeper understanding of BTV replication and host–virus interactions, their practical role in field conditions is expected to remain limited compared with vaccination and surveillance.

Knowledge gaps

Despite decades of research, important knowledge gaps persist, particularly in relation to pathogenesis, immunology, vaccinology, epidemiology and disease control. One of the most significant uncertainties concerns the mechanisms of virus persistence and overwintering. The relative contribution of vertebrate hosts, insect vectors and environmental factors to long-term virus maintenance remains incompletely understood and may vary according to serotype, topotype and ecological context.

From a diagnostic perspective, the absence of commercial serological DIVA assays represents a critical limitation, particularly in vaccinated populations and in the context of international trade. While molecular diagnostics are highly effective, their continuous adaptation to emerging and reassortant strains is essential.

In addition, rapid, field-deployable diagnostic tools remain largely unavailable, constraining early detection in resource-limited or remote settings.

Important gaps also persist in the understanding of vector biology. The ecology, population dynamics and vector competence of different Culicoides species, and how these may be influenced by anticipated climate change and extreme weather events, require further investigation. Improved knowledge in this area is essential for predictive modelling and risk-based surveillance.

Finally, global surveillance remains uneven, with limited and discontinuous monitoring in many endemic regions. Insufficient data sharing and incomplete genomic datasets hinder early warning, preparedness and coordinated responses to emerging threats.

Conclusions

Bluetongue remains a persistent and evolving threat to global ruminant health. While major progress has been achieved in diagnostics and vaccination, recent outbreaks have demonstrated that current tools are insufficient to fully anticipate and prevent disease emergence. The existence and co-circulation of multiple serotypes, vector ecology, knowledge gaps in epidemiology in endemic regions neighbouring Europe and climate-driven changes continue to undermine long-term control efforts.

Vaccination remains the cornerstone of bluetongue control, but future strategies must move beyond serotype-specific approaches.

Investment in multivalent, DIVA-compatible vaccines and strengthened genomic surveillance are essential. Enhanced international collaboration, particularly with endemic regions, will be critical to improve early warning systems and preparedness.

Although eradication of bluetongue is unrealistic under current conditions, a coordinated, science-based and forward-looking approach can substantially reduce disease impact and improve resilience against future incursions.

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