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Review – One Health

Bovine Leukemia Virus and One Health: a Mini-Review of Emerging Evidence, Zoonotic Risks and Implications for Surveillance and Control

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HIGHLIGHTS

- BLV remains highly prevalent and impacts global cattle productivity.
- Molecular epidemiology reveals diverse genotypes and transmission patterns.
- Evidence suggests human exposure to BLV, but no confirmed infection.
- One Health framework is essential to assess zoonotic interfaces.
- Integrated surveillance is critical for effective control strategies

Abstract: Bovine Leukemia Virus (BLV) is a delta retrovirus widely distributed in cattle populations worldwide and is responsible for enzootic bovine leukosis, resulting in significant economic losses in the livestock industry. In recent years, increasing scientific interest has emerged regarding the potential implications of BLV beyond animal health, particularly within the One Health framework. This mini-review summarizes recent evidence (2020–2025) concerning BLV epidemiology, transmission routes, diagnostic advances, and potential interfaces between animal and human health. Recent studies have reported the detection of BLV DNA or antibodies in human tissues and blood samples, raising questions about possible human exposure. However, current evidence does not demonstrate active infection or a causal role of BLV in human disease. Therefore, while the available data suggests potential exposure pathways, the zoonotic significance of BLV remains uncertain. Continued interdisciplinary research integrating veterinary surveillance, molecular epidemiology, and public health perspectives will be essential to clarify the biological and epidemiological relevance of these findings.

Keywords: Bovine leukemia virus (BLV); One Health; zoonotic potential; epidemiological surveillance; control strategies.

INTRODUCTION

Enzootic bovine leucosis (EBL) is a chronic infectious disease caused by the Bovine Leukemia Virus (BLV), a retrovirus belonging to the Retroviridae family, genus Deltaretrovirus, and shares close genetic homology with the Human T-cell Leukemia Virus type 1 (HTLV-1) [1]. The infection is characterized by the integration of proviral DNA into the host cell genome, leading to long-term viral persistence. Most infected cattle remain asymptomatic or develop persistent lymphocytosis, while approximately 1–5% progress to malignant lymphoma or leukemia [2].

Although EBL has been successfully eradicated in most European countries through rigorous surveillance and eradication programs, recent studies have reported a resurgence or sustained high infection rates in several regions, including Argentina, Brazil, Canada, Japan, and the United States. This persistence suggests gaps in current control strategies, possible inter-herd reinfection, and environmental or trade-related factors that favor BLV dissemination [3].

In Brazil, epidemiological surveys have revealed substantial BLV burden, with prevalence estimates varying between 23% and 37% at the national level and reaching nearly 40% of animals in some southeastern regions. However, statistical data on bovine leukosis in Brazil remain fragmented due to isolated studies and regional variation in diagnostic coverage, which hinders reliable national estimates and impedes coordinated control programs [4].

Although initially regarded as an issue restricted to livestock health, recent research has broadened the understanding of BLV, highlighting its implications for animal productivity, food safety, and potential intersections with human health. The One Health framework, which emphasizes the interdependence among human, animal, and environmental health, provides a comprehensive perspective for assessing the multifaceted impact of BLV across species and ecosystems [5]. This multifaceted scenario encompasses immunological and epidemiological challenges as well as socioeconomic and environmental implications, demanding comprehensive, interdisciplinary analyses that extend beyond the traditional scope of veterinary medicine. Notably, in Latin America there are still no official mandatory programs for disease control, underscoring the need for policy development.

Accordingly, the present mini-review aims to integrate veterinary, epidemiological, molecular, and public health findings to guide surveillance policies and transdisciplinary research, with particular attention to the Brazilian context and other high-prevalence settings.

METHODS

Search strategy

This narrative mini-review was designed to provide a concise overview of the most recent advances (2020–2025) in the understanding of bovine leukemia virus (BLV) epidemiology, zoonotic risk, and its relevance within the One Health framework. A targeted literature search was conducted across major academic databases PubMed, Scopus, and Web of Science focusing on peer-reviewed studies in English that addressed BLV distribution, modes of transmission, diagnostic approaches, and potential human exposure. Rather than presenting a systematic synthesis, this work aims to deliver an updated and integrative perspective on current findings and research trends in this area.

Epidemiology and National/Global Prevalence

During the 19th century, early research reports described clinical symptoms consistent with Enzootic Bovine Leukosis (EBL) in cattle, the primary hosts of the disease. Subsequent investigations demonstrated that BLV could also infect other species such as sheep, goats, chickens, rabbits, and rodents, indicating a broader host range than initially believed [6,7].

As international trade in dairy and beef cattle expanded, BLV spread globally through the movement of animals and their derived products. Notably, higher infection rates were reported in Holstein breeds, accounting for approximately 49% of cases, possibly due to intensive breeding and management practices [8].

In Brazil, surveys investigating BLV seroprevalence have been performed throughout the country in dairy and beef herds, revealing infection rates that vary widely from as low as 9.2% to nearly 80%, depending on the region and production system. In the state of Santa Catarina, the most recent prevalence study by Rodakiewicz and coauthors (2018) evaluated Holstein, Jersey, and crossbred dairy cattle [9].

Recent studies highlight significant regional variations in BLV prevalence across Brazil. In the South region, Pereira and coauthors (2023) reported rates of 38.1% in animals and 64.5% in herds, emphasizing the persistence of the agent in highly technologically advanced production system [10]. In the Northeast, investigations in Paraíba by Ramalho and coauthors (2021) [11] identified prevalences of 23.4% at the herd level and 10.8% at the individual level, while in Maranhão, Pereira and coauthors (2023) [10] reported 9.09% PCR positivity. In Minas Gerais, Morais and Nascimento (2024) observed 57% of reactive animals, reinforcing the importance of continuous serological monitoring. A recent study in Santa Catarina (2023) presented prevalence estimates associated with molecular characterization of BLV [12,13].

Countries and regions with advanced economies and high consumption of beef and dairy products have shown greater concern regarding BLV due to its impact on productivity and potential public health implications. Since the 1960s, nations such as the United Kingdom, Denmark, the Netherlands, New Zealand, and Australia have implemented rigorous eradication programs, successfully eliminating the virus from their herds [14]. In contrast, countries like the United States, Canada, Argentina, and Japan have not fully adopted comprehensive BLV control measures, maintaining infection rates that exceed 40%, underscoring the persistent global disparity in disease management [15].

Transmission Dynamics and Modeling

Transmission of bovine leukemia virus (BLV) occurs through both horizontal and vertical routes, with horizontal spread primarily associated with iatrogenic practices such as the reuse of needles, contaminated palpation gloves, castration tools, drug or vaccine applicators, and inadequately sanitized surgical instruments for rectal examination, these transmission routes are summarized in Figure 1. Vertical transmission, on the other hand, may take place transplacentally or through the ingestion of colostrum and milk from infected dams, allowing early-life infection of calves [13].

A newborn calf that consumes colostrum from an infected cow whether or not it is the dam passively receives maternal antibodies, which can lead to positive serological test results throughout the early months of life, typically up to approximately six months [15].

Recent investigations have reinforced that exposure to infected lymphocytes whether in blood, milk, or secretions is a major driver of viral dissemination within herds. In the study by Quadros and coauthors, it revealed that cows exhibiting persistent lymphocytosis are key contributors to BLV propagation, significantly influencing epidemiological modeling parameters such as the basic reproduction number and shaping containment strategies [15,16].

In Brazil, data published in 2024 indicated that milk and colostrum represent critical pathways for early-life transmission, underscoring the need for preventive measures in neonatal management. Collectively, these findings highlight that effective BLV control relies on disrupting transmission at the herd level through systematic testing, segregation of seropositive animals, rigorous hygiene of veterinary tools, and avoidance of high-risk handling practices [17].

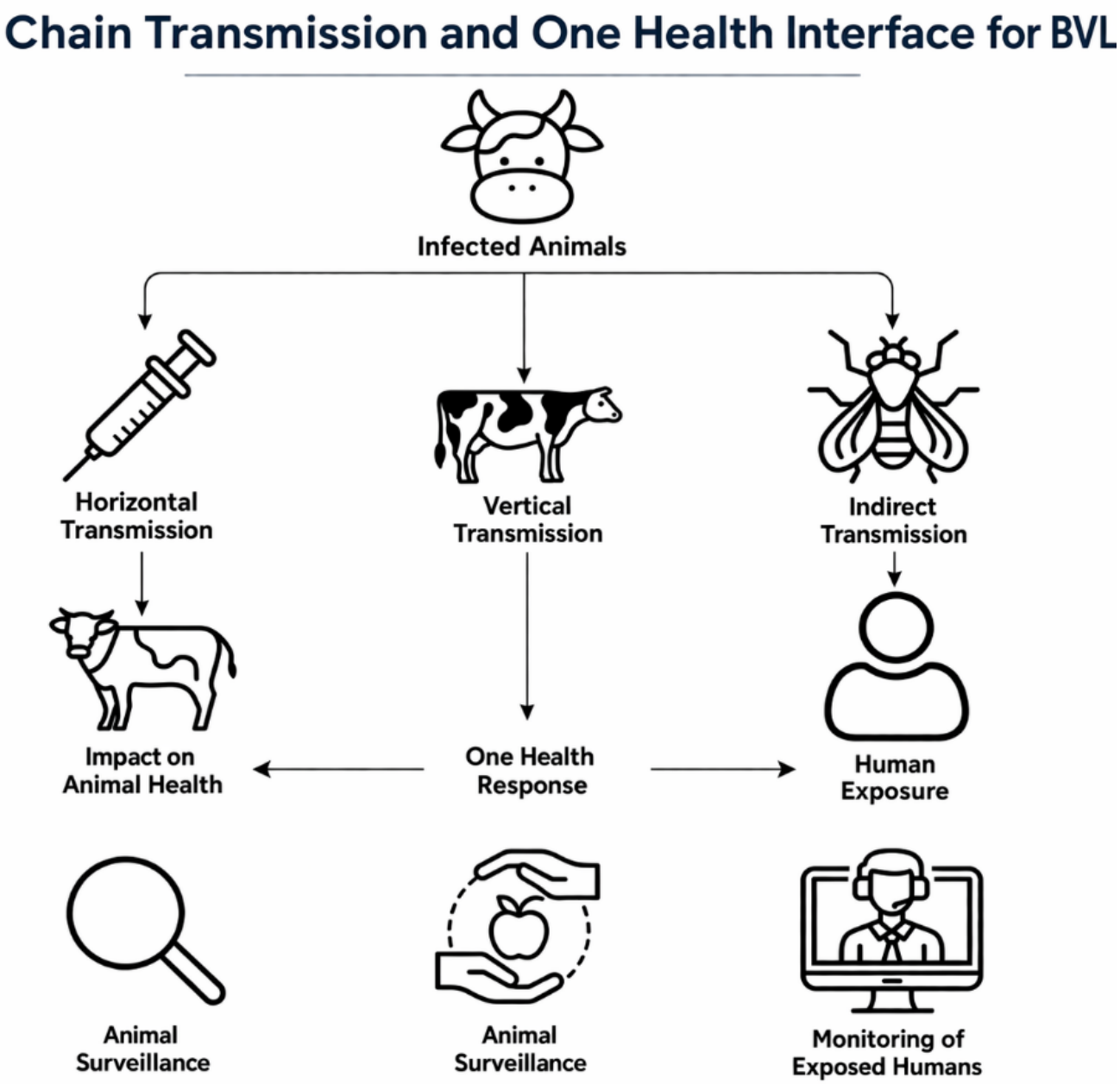

Figure 1. Schematic chain of BLV transmission routes, their impacts on animal production, and potential human exposure interfaces in the One Health context.

Diagnosis and molecular advances

In Brazil, bovine leukosis is not included among the diseases routinely screened in official animal health programs, although the World Organisation for Animal Health (WOAH) establishes that its detection must be formally reported. For the international trade of live cattle, several importing countries demand proof that animals are free of infection, typically through serological assays such as AGID (Agar Gel Immunodiffusion) or ELISA (Enzyme-Linked Immunosorbent Assay). These methods, endorsed by the WOAH, identify infection by detecting antibodies directed against the viral envelope protein gp51 and the capsid protein p24. [17]. Recent advances in molecular diagnostic technologies have greatly enhanced the detection and genetic characterization of bovine leukemia virus (BLV). A 2024 multicenter evaluation comparing 11 different qPCR (real-time quantitative) and ddPCR (droplet digital PCR) protocols revealed substantial methodological variability among laboratories, underscoring the urgent need for standardization to ensure diagnostic reliability and data comparability [18].

Furthermore, genotypic diversity analyses have provided valuable insights into viral evolution and transmission dynamics, enabling the reconstruction of outbreak origins and epidemiological linkages. For

instance, a study conducted by Ramalho and coauthors, in northeastern Brazil identified multiple circulating genotypes among dairy herds, contributing to the growing molecular surveillance framework for BLV [18,19].

As summarized in Table 1, the application of high-sensitivity molecular diagnostic methods including qPCR and ddPCR has proven essential for detecting animals with low proviral loads, thereby enhancing early identification of infected cattle. This molecular precision provides a strategic advantage for herd-level management, enabling the implementation of targeted and cost-efficient control programs that can significantly reduce BLV persistence and transmission within populations.

Table 1. Summary of diagnostic methods, host species, frequency of detection, potential vectors, and epidemiological distribution of bovine leukemia virus (BLV) reported in the last five years (2020–2025).

Species	Diagnostic Method	Frequency	Vector/Route	Geographic Distribution
Cattle (Brazil)	Serology (ELISA), PCR	23–40% prevalence	Iatrogenic, colostrum, milk	All states; SE region ~40%
Cattle (USA)	ELISA, qPCR, ddPCR	Variable by herd	Iatrogenic, colostrum	>40% in many regions
Cattle (Europe)	ELISA, PCR surveillance	Near zero (eradicated)	Strict controls	BLV-free or sporadic reintroduction
Humans	PCR on breast tissue, blood	~27% pooled detection	Hypothetical (food, contact)	Multiple countries; heterogeneous studies
Diagnostics (inter-lab)	qPCR/ddPCR comparison	74–100% sensitivity range	N/A	Highlights need for standardization
Vectors/ Mechanical	Epidemiological observation	Context dependent	Biting flies, ticks, iatrogenic	Field contribution still being quantified

Impact on animal health, productivity, and the economy

Although most BLV-infected cattle remain asymptomatic, persistent infection is increasingly recognized as a hidden driver of economic loss in dairy production. Affected herds often experience reduced milk yield, higher culling rates, shortened productive lifespan, and signs of immunological impairment that predispose animals to secondary infections [20,21,22].

A recent economic assessment in the United States estimated that each infected cow may result in financial losses of several hundred dollars annually, highlighting the broader impact on herd profitability. Complementarily, a 2025 study analyzing cows with high proviral loads revealed strong correlations with decreased milk output and increased frequency of subclinical disorders, further supporting the biological basis of these losses [23]. Collectively, these findings emphasize that BLV should not be regarded as a merely “silent infection,” but rather as a significant health and management concern requiring integrated monitoring and control strategies in modern dairy systems.

Zoonotic risk and interface with human health

The possible zoonotic role of bovine leukemia virus (BLV) has emerged as a contentious and increasingly scrutinized issue. Accumulating systematic reviews describe the detection of BLV nucleic acids or antibodies in human samples, especially in breast tissue and peripheral blood, thereby fueling speculation about interspecies transmission events. In a large synthesis, Mendoza and coauthors reported an estimated prevalence of roughly 27% (17–37%) across 10,398 human samples, albeit with pronounced between-study heterogeneity [24].

Building on these observations, a meta-analysis published in 2024 identified a statistical association between BLV detection and breast cancer risk, pointing to a putative link that merits rigorous evaluation. Yet, in the absence of mechanistic evidence, causality remains unproven. The mere detection of BLV DNA in human tissues does not, at present, equate to productive infection or clinically relevant disease, and no consistent signal of pathogenicity has been demonstrated. Consequently, findings based solely on viral sequences must be interpreted with considerable caution [25].

Taking together, the current evidence suggests that humans may meet BLV or BLV-derived antigens, but it falls short of demonstrating active replication or pathogenic infection in people. The literature is dominated by cross-sectional and case control designs, frequently deploying non-standardized assays in diverse tissue matrices and populations, which complicates cross-study comparisons and constrains robust causal inference, particularly with respect to breast cancer. Notably, BLV is not formally recognized as a zoonotic pathogen, and no BLV-specific human clinical phenotype or human-to-human transmission pathway has been delineated. As a result, any appraisal of zoonotic risk must remain guarded and explicitly reflect these uncertainties [26]. Critical gaps persist at multiple levels, including poorly characterized transmission routes at the cattle–human interface, the lack of harmonized diagnostic frameworks, and the paucity of longitudinal or experimental investigations.

From a One Health perspective, these fragmented findings underscore the need for an integrated interpretative lens that concurrently considers infection dynamics in cattle, patterns and contexts of human exposure, and relevant food-chain and environmental interfaces. Table 2 captures this integrative view by mapping current BLV evidence onto gradations of zoonotic risk and outlining the corresponding implications for surveillance architecture and control policies [26,27]. Recent studies from the last five years reinforce the complexity of BLV's potential zoonotic interface while highlighting persistent methodological challenges.

A 2024 scoping review emphasized genetic similarities between BLV strains in humans, cattle, and food products like raw milk, suggesting plausible dietary transmission routes yet underscoring the need for One Health surveillance to track phylogenetic patterns. Similarly, Brazilian investigations during this period detected no BLV DNA in human breast cancer samples despite high regional milk consumption, contrasting with positive findings elsewhere and illustrating geographic variability in exposure risks. These divergent results, coupled with ongoing calls for standardized diagnostics and longitudinal cohorts, affirm that while interspecies contact occurs, definitive evidence of zoonotic pathogenicity remains elusive, prioritizing enhanced veterinary controls and human biomonitoring [28].

Table 2. One Health Overview of BLV Evidence, Zoonotic Risk Level, and Implications for Surveillance and Control

Evidence Domain	Main Findings	Zoonotic Evidence Level	Surveillance Implications	Control and One Health Implications
Animal infection and productivity	High BLV prevalence in dairy and beef herds; reduced milk yield, Shortened productive lifespan, increased culling	Defines large animal reservoir only; no direct zoonotic implication	Routine serological and molecular testing at herd level; prioritization of high-prevalence regions	Test and remove/segregate; biosecurity; improved neonatal management
Detection in human samples	BLV DNA and/or antibodies detected in breast tissue and blood; pooled detection ~27% with high heterogeneity	Suggestive exposure but not proof of active infection or disease causation	Targeted surveillance in high exposure groups (farmers, veterinarians, dairy workers) within research protocols	Emphasis on cautious interpretation, risk communication, and further research rather than reclassification as zoonotic
Food-chain exposure	BLV genetic material and proteins in raw milk and meat; impact of pasteurization unclears	Potential exposure route: clinical relevance remains unknown	Inclusion in selected food safety monitoring; assessment of processing steps and hygiene practices	Strengthening pasteurization, good manufacturing practices, consumer education. risk-based policy decisions
Integrated One Health surveillance	Few examples of combined animal–food–human monitoring; limited assay harmonization across sectors	Current evidence does not support broad human surveillance; justifies pilot initiatives	Development of harmonized protocols and shared data platforms across sectors	Design and evaluation of integrated control packages balancing animal health, public health, and economic feasibility

Food safety and route of exposure (meat, milk, processing)

Another emerging concern involves human exposure through the consumption of bovine-derived products, such as raw milk and undercooked meat, as well as direct contact with infected cattle. Recent reviews have reported the detection of BLV genetic material and proviral load in milk samples, prompting discussions about the need to consider this pathogen within the broader context of food safety monitoring [23].

Although the actual zoonotic risk remains uncertain, the presence of documented transmission routes in animals including colostrum ingestion and contaminated instruments suggests that viral particles may persist in certain animal-derived products. This highlights the importance of integrating molecular surveillance data with hygiene protocols, processing standards, and pasteurization efficacy assessments to minimize potential exposure risks [24]. In developing livestock systems, such as those in Brazil, where biosecurity measures and control programs vary widely, this issue demands particular attention. Strengthening preventive actions is essential not only for animal health management but also for ensuring consumer safety and public confidence in the dairy and meat supply chains.

Control strategies and policies from a One Health perspective

Countries that have successfully eradicated bovine leukemia virus (BLV), particularly several in Europe, implemented rigorous test-and-slaughter programs combined with mandatory culling policies and strict restrictions on the movement of infected animals. These coordinated measures proved highly effective in achieving national-level elimination [16–25]. In contrast, in high-prevalence regions—such as the United States and several developing countries such intensive eradication strategies are often economically impractical. The commentary “Why It’s Time to Control BLV” highlights the need to adapt control strategies to modern commercial production systems, balancing economic feasibility with epidemiological effectiveness [26].

Under the One Health framework, effective BLV management requires an integrated and multidisciplinary approach that encompasses active herd surveillance, continuous monitoring along the food production chain, and evaluation of potential human exposure pathways among farmers, veterinarians, and consumers. Equally important is the establishment of coordinated risk-communication strategies among stakeholders, ensuring that animal health policies, food safety measures, and public health initiatives operate in a harmonized and evidence-based manner [27]. Control programs must also consider economic impacts, public health implications, and production sustainability. In countries such as Brazil where cattle farming is characterized by small and medium-scale producers, diverse breeds, and heterogeneous management practices the contextual adaptation of international guidelines is essential to ensure both practicality and long-term success.

Although BLV is not classified as a zoonotic pathogen, its relevance has expanded beyond the confines of veterinary medicine. Increasingly, its control is being approached through a One Health framework, recognizing the interconnected implications for animal health, food production chains, and potential occupational exposure.

Knowledge Gaps and Research Priorities

Despite substantial advances in understanding BLV epidemiology and improving diagnostic tools, key questions remain unanswered regarding how frequently and under which conditions humans are exposed to BLV, whether detected viral sequences in human tissues represent transient exposure or persistent infection, and what the true clinical significance of these findings might be.

Existing systematic reviews and meta-analyses reporting BLV detection in humans and potential associations with breast cancer are limited by heterogeneity in study design, sample size, tissue selection and laboratory methods, as well as by incomplete control for confounding factors.

From a One Health perspective, priority research areas include:

- Standardization and external quality assessment of BLV assays for both animal and human samples to ensure comparability across laboratories and regions.
- Longitudinal cohort or nested case–control studies that can address temporality and dose–response relationships between BLV exposure and potential health outcomes.
- Integrated surveillance pilots that jointly monitor BLV in herds, food products and selected human risk groups (farmers, veterinarians, dairy workers) in high prevalence settings.

- Implementation of research to identify economically feasible, context-adapted control packages for high-prevalence countries, particularly in Latin America.

As a narrative mini-review, this work is inherently limited by its non-systematic literature selection and the possibility of publication bias. Despite these constraints, it offers a concise overview of recent evidence on BLV within the One Health context.

CONCLUSION

Bovine leukemia virus (BLV) remains a relevant pathogen with significant impact on cattle health and productivity at the global level. Although recent studies have reported BLV DNA or antibodies in human specimens, the available evidence does not support active infection or a causal role in human disease. At present, BLV cannot be regarded as a confirmed zoonotic agent. Even so, the growing body of molecular and epidemiological data underscores the need for continued interdisciplinary investigation within a One Health framework. Future work combining robust veterinary surveillance, harmonized diagnostic methodologies, and well-designed epidemiological studies will be crucial to clarify the biological relevance of BLV exposure in humans and to inform evidence-based public health and livestock management policies.

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Use of Generative Artificial Intelligence

The authors declare that large language models and other generative artificial intelligence (AI) or AI-assisted technologies cannot be credited as authors and have not been listed as authors of this paper.

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