2026

All Things

BLV

July 14-17, 2026

East Lansing
Michigan

2026 All Things BLV

July 14-17, 2026 | East Lansing, Michigan

Welcome to the 2026 All Things BLV Conference!

This conference strives to provide a welcoming and collaborative gathering place for sharing ideas, successes, challenges, and needs regarding bovine leukosis while also providing career development, mentorship, and training to early career individuals and students.

The international gathering for discussion and learning among researchers, extension specialists, producers, veterinarians, and students is vital for progress in global bovine leukosis diagnosis, management, and control.

We are pleased that you could join us. We look forward to all future collaborations and advancements gained as a result of the 2026 All Things BLV conference.

The 2026 Planning Committee!

https://www.canr.msu.edu/blv/

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July 14, 2026

4:00 p.m. **Tour of new MSU Dairy Cattle Teaching and Research Center and ice cream social**

July 15, 2026

7:00 a.m. **Registration and Breakfast**

8:45 a.m. **Conference Welcome**
Dr. Tasia Kendrick, Michigan State University

9:00 a.m. **Opening Keynote:**
Bovine Leukemia Virus…There Is a Human Factor, and We Have to Deal with It.
Dr. Frank van der Meer, University of Calgary

10:00 a.m. **Deciphering Host-Virus Interactions for Control and Eradication Programs in Regions with High BLV Prevalence**
Dr. Stephen Valas, French Agency for Food, Environmental and Occupational Health and Safety (Anses)

10:20 a.m. **Genomic Signatures of Selection in Immune Regulatory and MHC Regions Provide Candidate Targets for Bovine Leukemia Virus Research**
Alix Booms, CentralStar Cooperative/Antelbio

10:40 a.m. **Break**

11:00 a.m. **Exhausted T Cells Drive CCL4-mediated Macrophage Accumulation and Reduced Antigen Presentation in Enzootic Bovine Leukosis**
Hayato Nakamura, Hokkaido University

11:20 a.m. **Single-cell RNA Sequencing Reveals Divergent B-cell Expansion States Associated with Distinct Immune Trajectories During Bovine Leukemia Virus Infection**
Tanner Scull, Texas Tech University

11:40 a.m. **Our Challenge in Clinical Application of Diagnosis and Prediction of Enzootic Bovine Leukemia By BLV Clonality Analysis**
Dr. Tomohiro Okagawa, Hokkaido University / FASMAC Co., Ltd.

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July 15, 2026 *(continued)*

12:00 p.m. **The Risk Assessment of EBL Onset by High-Throughput Clonality Analysis Of BLV-Infected Cells Using RAISING**
Maho Inoue, Hokkaido University

12:20 p.m. **Networking Lunch**

1:50 p.m. **First Evidence of BLV in Culicoides Biting Midges Collected on Cattle Farms in Poland**
Dr. Aneta Pluta, National Veterinary Research Institute

2:10 p.m. **Comparing Three BLV Control Strategies Using Proviral Load and Their Effects on Prevalence and Incidence in Dairy Herds**
Dr. Simon Bourassi, Atlantic Veterinary College, University of Prince Edward Island

2:40 p.m. **Break**

2:55 p.m. **Panel: Understanding the Host Response to BLV: Implications for Disease Control**

3:55 p.m. **A Small Polypeptide Encoded by Antisense Long Non-Coding Rnas Mediates Bovine Leukemia Virus Replication**
Dr. Luc Willems, National Fund For Scientific Research at University of Liege

4:15 p.m. **Direct LAMP Amplification from Whole Blood to Detect BLV DNA**
Dr. Scott Sherrill-Mix, Michigan State University

4:35 p.m. **A Novel Approach for Early Detection of Bovine Leukemia Virus Using Precision Technology to Monitor Biometric Signatures**
Ted Brooks, Michigan State University

4:55 p.m. **Break**

5:15 p.m. **Keynote Address:**
Genetic and Immunological Landscapes of Leukemogenesis in Enzootic Bovine Leukosis
Dr. Tomohiro Okagawa, Hokkaido University / FASMAC Co., Ltd.

6:15 p.m. **Networking Dinner**

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8:00 a.m.	**Registration and Breakfast**
9:00 a.m.	**Panel: Prospects and Challenges of Emerging Technologies in BLV Research and Control**
10:00 a.m.	**Break**
10:20 a.m.	**Decline of Maternally Derived Anti-Bovine Leukemia Virus Antibody Levels in Holstein Heifers on Commercial Dairy Farms** *Olivia Willoughby, University of Guelph*
10:40 a.m.	**Association of Bovine Leukemia Virus Infection on Health, Milk Production, Fertility, and Longevity in Dairy Cattle** *Modesto Elvir Hernandez, University of Florida*
11:00 a.m.	**Associations of Bovine Leukemia Virus Infection with Fertility, Disease, and Culling Risk** *Olivia Willoughby, University of Guelph*
11:20 a.m.	**Break**
11:40 a.m.	**Business Meeting**
12:00 p.m.	**Networking Lunch** **Graduate Student Career Development and Networking Session**
2:00 p.m.	**Keynote Address: Bovine Leukemia Virus Vaccine: Progress and Future Steps** *Dr. Karina Trono, INTA Argentina*
3:00 p.m.	**Break**
3:15 p.m.	**Epidemiological Trends During a BLV Eradication Program in French Reunion Island Herds** *Camille Demassieux, Agency for Food, Environmental and Occupational Health & Safety (ANSES), France*
3:35 p.m.	**Prevalence of Bovine Leukemia Virus Antibodies and Proviral Load on Front Range Dairy Farms in Colorado and Wyoming** *Marcie Bernard, Colorado State University*

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July 16, 20267 (*continued*)

3:55 p.m.	**Longitudinal Assessment of Proviral Load In BLV-Infected Dairy Cattle And Implications for Testing Frequency** *Dr. Simon Bourassi, Atlantic Veterinary College, University of Prince Edward Island*
4:15 p.m.	**Break**
4:30 p.m.	**Panel: Global Perspectives on BLV Control: Current Status and Future Challenges**
5:30 p.m.	**Conference Closing Discussion** *Dr. Tasia Kendrick, Michigan State University*
5:45 p.m.	**Offsite Networking Dinner at the Harrison Roadhouse**

July 17, 2026

7:00 a.m.	**Breakfast**
7:30 a.m.	**Meet in the Brody Hall Lobby for Group Transportation to the Tour**
9:30 a.m.	**Arrive at West Michigan Beef Co. LLC (Hudsonville, MI)** • **Discussion with USDA Inspector and Co-Founder Don Vander Boon** • **Tour Plant**
11:15 a.m.	**Depart Processing Facility**
Noon	**Lunch at Voogt Family Farm**
1:15 p.m.	**Voogt Family Farm Tour** • **Registered Angus Cow Calf Program** • **Rotational Grazing Program**
2:15 p.m.	**Depart for MSU**
4:00 p.m.	**Conference Concludes**

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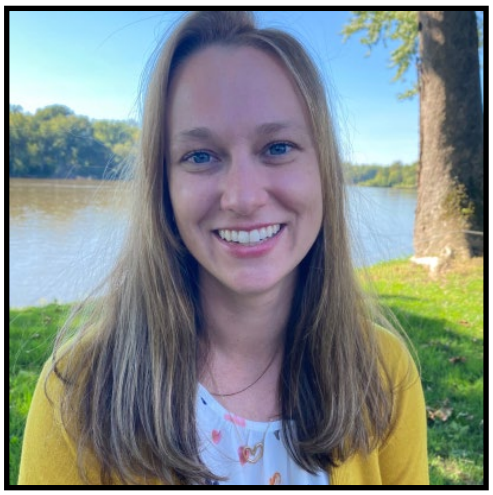
Conference Welcome



Tasia Kendrick

Associate Professor
Michigan State University

Tasia Kendrick is an Associate Professor in the Department of Animal Science at Michigan State University. She leads the Michigan State University Bovine Leukemia Virus Research and Extension Team and is a member of the 2026 All Things BLV Conference Planning committee. Currently, her team includes 1 technician, 1 PhD student, and 12 undergraduate students. She is a trained geneticist conducting research in both education and animal disease, specifically Bovine Leukemia Virus. Since 2017, her work in bovine leukosis has resulted in 20 publications, a host of invited workshops/presentations, and mentorship of both graduate (n=15) and undergraduate students (n=30).

She received her PhD from the University of Missouri and completed post-doctoral training at the USDA/ARS National Animal Disease Center in Ames, IA. Her primary teaching responsibilities include a junior-level genetics and animal breeding course (Genetic Improvement of Domestic Animals), an introductory animal science course (Introduction to Disciplines of Animal Science), and a graduate level teaching methods course (Methods of Teaching Animal Science).

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Opening Keynote Address:

Let’s Take: Bovine Leukemia Virus…There is a Human Factor, and We Have to Deal with It.

Bovine Leukemia Virus (BLV) is often discussed in terms of diagnostics, transmission pathways, prevalence, and control strategies. However, the success or failure of BLV management ultimately depends on people. This presentation will explore two of the most significant human dimensions influencing BLV research and control efforts.

First, we will examine why some researchers and consumers view BLV as a potential zoonotic agent. Although studies have reported associations between BLV and human tissues, substantial scientific questions remain regarding causality, biological plausibility, study design, and reproducibility. Understanding both the findings and limitations of this body of research is essential for communicating risk accurately and maintaining public trust.

Second, we will discuss why many producers remain reluctant to implement BLV control programs despite growing evidence of the virus's economic and animal health impacts. Factors such as cost, labor requirements, competing management priorities, uncertainty regarding return on investment, and differing perceptions of risk all influence decision-making on farms. Drawing on principles of behavior change, risk communication, and knowledge translation, this session will explore practical approaches for increasing producer engagement and overcoming barriers to adoption.

By focusing on the human factors that shape both scientific discourse and on-farm decision-making, this presentation will challenge participants to consider how communication, trust, perception, and leadership influence the future of BLV control. Because when it comes to Bovine Leukemia Virus, the biology is only part of the story—the human factor matters just as much.

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Frank van der Meer

Professor
University of Calgary

Dr. Frank van der Meer is a Professor of Global Health and Infectious Diseases at the University of Calgary Faculty of Veterinary Medicine in Calgary, Alberta, Canada. He earned his Doctor of Veterinary Medicine degree from Utrecht University in the Netherlands and completed a Ph.D. in Virology focused on antiviral therapies for coronaviruses and lentiviruses.

Dr. van der Meer's research and teaching span virology, vaccinology, diagnostics, molecular epidemiology, phylodynamics, and infectious disease evolution. His career has included positions at Utrecht University, Wageningen University, and the University of Calgary, where he has been a faculty member since 2010. His expertise extends beyond animal health to One Health approaches that integrate human, animal, and environmental health, with a particular interest in global health, intercultural collaboration, knowledge translation, and infectious diseases in low- and middle-income countries.

Recognized internationally for his work in veterinary and comparative virology, Dr. van der Meer brings extensive experience in research, education, and disease surveillance across a range of emerging and endemic infectious diseases.

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Deciphering Host-Virus Interactions for Control and Eradication Programs in Regions with High BLV Prevalence

Dr. Stephen Valas, French Agency for Food, Environmental and Occupational Health and Safety (ANSES)

Authors:
Stephen Valas[1], Camille Demassieux[1], Nicolas Leoville[2], Marc Tabouret[1]
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[2]Field Veterinary Laboratory (LDA974), Reunion Island

Segregating or culling all seropositive cattle from herds is considered the most effective eradication strategy against BLV, but this costly approach cannot be thoroughly implemented in herds or regions with high BLV prevalence. In the past few years, field trials showed that proviral load (PVL) in blood and polymorphism within the bovine DRB3 gene could be used as biomarkers to reduce the transmission rate and prevalence of BLV in highly affected herds. PVL, which represents the amount of infected cells, is strongly correlated with infectiousness of BLV-infected animals and disease progression. Furthermore, PVL is influenced by DRB3 gene polymorphism, with specific alleles being associated with low (resistant alleles) or high (susceptible alleles) PVL. However, knowledge on the association between PVL and DRB3 alleles remains scarce. In this study, the relationships between PVL and DRB3 alleles were determined in 215 seropositive cows from the French Department Reunion, a Southwestern Indian Ocean island. PVL was measured by digital PCR and DRB3 alleles were determined by multiplex next-generation sequencing. Concomitantly, BLV isolates from 26 herds were genetically characterized. A total of 25 DRB3 alleles were identified. Four DRB3 alleles, including one novel allele, were classified as resistant (002:01, 009:02, 014:01:01 and 007:01). In contrast, two DRB3 alleles were classified as susceptible (012:01 and 015:01). The relationship between PVL and DRB3 polymorphism was unrelated with viral diversity since all gag and env BLV sequences belonged to genotype G2. These results confirmed that analysis of DRB3 alleles could predict the risk of BLV transmission, offering new insights in management of animals to improve the efficiency of eradication programs. They also contributed to the broader knowledge of the global BLV epidemiology, showing for the first time that BLV strains prevalent in Reunion Island were genetically conserved and closely related to those circulating in South America.

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Genomic Signatures of Selection in Immune Regulatory and MHC Regions Provide Candidate Targets for Bovine Leukemia Virus Research

Alix Booms, CentralStar Cooperative/Antelbio

Authors:

A. Booms[1,2], C. Lohr[2], G. A. Coetzee[1], S.J. Wells[3], B.A. Crooker[4], and C. Droscha[2]

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The objective of this study was to develop a hybrid capture tool for targeted sequencing of immune regulatory elements and MHC BoLA (Bovine Leukocyte Antigen) genes in Holstein cattle and to assess how six decades of breeding may have shaped these regions. Using published epigenetic datasets, we identified 70 regulatory regions of interest (ROIs) that become more accessible in response to infection. With the addition of whole-genome low-pass sequencing (Skim-seq) we also characterized genome-wide diversity across unselected Holstein cows, contemporary Holstein cows, and contemporary elite Holstein bulls.

Runs of homozygosity (ROH) analyses revealed a genome-wide loss of diversity in contemporary Holsteins, while F_{ST} analyses identified variants that 1) differentiate contemporary and unselected animals within immune-related regulatory and MHC coding regions and 2) are predicted to have allele-specific effects on gene expression. Together, these findings highlight candidate MHC coding and regulatory regions that may contribute to variation in immune responses and provide a foundation for future studies investigating genetic susceptibility and resilience to Bovine Leukemia Virus (BLV) infection in Holstein cattle.

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Exhausted T cells drive CCL4-mediated Macrophage Accumulation and Reduced Antigen Presentation in Enzootic Bovine Leukosis

Hayato Nakamura, Hokkaido University

Authors:
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Bovine Leukemia Virus (BLV) induces enzootic bovine leukosis (EBL), in which immune dysfunction is thought to contribute to disease progression. Previous studies have shown that T cells expressing multiple immune checkpoint molecules, particularly PD-1 and TIM-3, exhibit features of functional exhaustion in EBL cattle. In addition, our preliminary transcriptomic analyses suggested that these exhausted T cells may exhibit increased expression of chemokine-related genes, including CCL4. However, the functional significance of this observation and its contribution to the tumor microenvironment remain unclear.

In this study, we performed comprehensive flow cytometric and functional analyses to elucidate the role of PD-1$^+$TIM-3$^+$ exhausted T cells in CCL4-mediated macrophage recruitment in EBL tumors.

Elevated CCL4 production was confirmed in tumor-derived cell cultures, and intracellular staining identified PD-1$^+$TIM-3$^+$CD4$^+$ T cells as a major source. Functional migration assays demonstrated that CCL4 preferentially induces the recruitment of monocytes/macrophages compared to other immune cell subsets. Further analysis of the tumor microenvironment revealed that macrophages accumulating in EBL tumor-draining lymph nodes exhibit phenotypic alterations, including reduced expression of MHC class I/II molecules, suggesting impaired antigen-presenting capacity. In addition, these macrophages displayed features consistent with an immunoregulatory phenotype.

Collectively, our findings indicate that exhausted T cells in EBL tumors are not merely dysfunctional but actively shape the tumor microenvironment through CCL4 production, promoting the recruitment of macrophages with reduced antigen-presenting capacity. This CCL4-driven axis provides a mechanistic link between T cell exhaustion and macrophage-mediated immune suppression in BLV-associated tumors.

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Single-Cell RNA Sequencing Reveals Divergent B-Cell Expansion States Associated with Distinct Immune Trajectories During Bovine Leukemia Virus Infection

Tanner Scull, Texas Tech University

Authors:
T. F. Scull[1,2], C. Strieder-Barboza[1,2], O.J. Benitez[1,2]
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[2]*School of Veterinary Medicine, Texas Tech University, Amarillo, Texas, USA*

This study aimed to identify transcriptional pathways associated with immune dysfunction during Bovine Leukemia Virus (BLV) infection using single-cell RNA sequencing (scRNA-seq) of peripheral blood mononuclear cells (PBMCs). Early- to mid-lactation Holstein cows were screened for BLV antibodies and proviral load (PVL) by ELISA and PCR. Animals were classified as BLV-negative (n = 4) or BLV-positive (n = 16), with positive animals stratified into low-, moderate-, and high-PVL groups. PBMCs were processed for scRNA-seq using the Parse Evercode™ platform. Analyses included unsupervised clustering, cell-type annotation, comparison of immune-cell proportions, sample-level differential gene expression analysis, functional enrichment, and ligand-target signaling inference. Differentially expressed genes were defined by an adjusted $P < 0.05$ and $|\log2 \text{ fold change}| > 1$. Relative immune composition shifted with increasing PVL, characterized by expansion of the B-cell compartment and decreased relative abundance of T cells (Kruskal–Wallis, $P < 0.01$ for both). Two infection-associated B-cell states were enriched primarily in moderate- and high-PVL animals. Based on marker and pathway-expression profiles, these populations were characterized as BCR-signaling-associated B cells and TGFβ-remodeling B cells. However, differential expression analysis by PVL identified significant transcriptional changes primarily within the B-cell compartment, with no significant differentially expressed genes detected in T-cell or myeloid compartments. Sample-level analysis revealed substantial heterogeneity among moderate- and high-PVL animals, which were dominated by either BCR-signaling-associated or TGFβ-remodeling B cells. Animals were therefore grouped as BLV-negative, infected non-TGFβ-B-cell-dominant, or infected TGFβ-B-cell-dominant. This grouping revealed extensive differential expression across B-cell, T-cell, and myeloid compartments in TGFβ-B-cell-dominant animals compared with both BLV-negative and infected non-TGFβ-B-cell-dominant animals. Functional enrichment identified downregulation of broad immune pathways in T cells and antiviral-defense pathways in monocytes. Ligand-target analysis further predicted broad TGFB1-associated signaling from TGFβ B cells to multiple immune compartments. These findings suggest that BLV infection is associated with divergent B-cell state dominance and that the phenotype of the expanded B-cell population may better explain downstream immune dysfunction than PVL alone. This supports a cell-state-divergent model of BLV pathogenesis in which infected animals may follow distinct cellular immune trajectories. More broadly, these findings raise the possibility that the cellular identity of the expanding B-cell population not PVL alone may influence clinical trajectory and help explain variation in immune dysfunction, persistent lymphocytosis, and progression toward enzootic bovine leukosis.

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Our Challenge In Clinical Application of Diagnosis and Prediction of Enzootic Bovine Leukemia by BLV Clonality Analysis

Dr. Tomohiro Okagawa, Hokkaido University / FASMAC Co., Ltd.

Authors:
Tomohiro Okagawa, Maho Inoue, Naomi Nojiri, Kazuha Yoshida-Furihata, Naganori Nao, Hayato Nakamura, Naoya Maekawa, Shiro Murata, Kazuhiko Ohashi, Takahiro Matsudaira, Masumichi Saito, Satoru Konnai

Bovine Leukemia Virus (BLV) infects bovine B cells and integrates into the genome of infected cells as a provirus. While most infected cattle show no clinical signs, 1%–5% develop B-cell lymphoma, known as enzootic bovine leukosis (EBL). In Japan, BLV infection is widespread and EBL cases have been increasing for several decades. We propose that identifying high-risk infected cattle before EBL onset could prevent significant economic losses. Since clonal proliferation of BLV-infected cells is essential for EBL development, we hypothesized that the clonality of proviral integration sites could serve as a molecular marker for EBL diagnosis and prediction. Therefore, we developed a novel high-throughput amplification method of proviral integration sites (RAISING) and evaluated its utility for EBL diagnosis and prediction.

RAISING enabled rapid and sensitive amplification of proviral integration sites using DNA samples of BLV-infected cells, allowing highly accurate clonality analysis. Clonality analysis of blood samples from BLV-infected cattle showed that clonality value (Cv) was higher in EBL cattle than in non-EBL cattle. Diagnosis using Cv as a marker successfully distinguished EBL specimens from non-EBL specimens with high sensitivity and specificity. Longitudinal clonality analyses in BLV-infected sheep and cattle revealed that Cv increased 2 to 12 months before lymphoma onset. Thus, BLV clonality analysis using RAISING is a promising tool for EBL diagnosis and prediction. We are currently conducting EBL risk assessments based on the clonality analysis at model farms in Japan. This “bovine cancer screening” strategy will contribute to reducing livestock losses from EBL onset and improving productivity. In this presentation, we will discuss our approach and challenges toward EBL cleanliness through BLV clonality analysis.

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The Risk Assessment of EBL Onset by High-Throughput Clonality Analysis of BLV-Infected Cells Using RAISING

Maho Inoue, Hokkaido University

Authors:
Maho Inoue, Tomohiro Okagawa, Hayato Nakamura, Naomi Nojiri, Hazuka Yoshida-Furihata, Naganori Nao, Naoya Maekawa, Shiro Murata, Kazuhiko Ohashi, Takahiro Matsudaira, Masumichi Saito, Satoru Konnai

Bovine Leukemia Virus (BLV) infects bovine B cells and integrates into the host genome as provirus. After a long latent period, few infected cattle develop enzootic bovine leukosis (EBL), a B-cell lymphoma. A previous nationwide survey reported that the prevalence of BLV infection in Japan is 41% in dairy cattle and 29% in beef cattle. The incidence of bovine leukemia has been increasing over decades, with more than 4,000 tumor cases reported annually in recent years. Under these endemic conditions, it is extremely difficult to eradicate BLV infection in Japan through a test-and-cull strategy alone. Therefore, an approach for assessing the risk of EBL onset in BLV-infected cattle is needed.

In our previous study, we developed a molecular amplification method of proviral integration sites, Rapid Amplification of Integration Site without Interference by Genomic DNA Contamination (RAISING) and focused on the clonality of BLV-infected cells. We longitudinally analyzed the clonality of BLV-infected cells by RAISING in a sheep model of experimental BLV infection and confirmed the effectiveness of clonality value (Cv) for early detection of lymphoma development.

In this study, we evaluate whether BLV clonality analysis by RAISING is useful for EBL risk assessment in cattle. Since last year, we have conducted a follow-up study of more than 1,000 BLV-infected cattle in beef farms of Japan, analyzing the kinetics of Cv in peripheral blood and disease prognosis at six-month intervals. We found that some of the cattle with high Cv developed EBL within six months after being classified as a high-risk group. These findings indicate that BLV clonality analysis by RAISING is a useful method for EBL risk assessment. The ongoing follow-up study will further clarify how this strategy can be effectively implemented to achieve EBL-free status on BLV-endemic farms.

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First Evidence of BLV in Culicoides Biting Midges Collected on Cattle Farms in Poland

Dr. Aneta Pluta, Department of Virology and Viral Animal Diseases, National Veterinary Research Institute, Puławy, Poland

Bovine Leukemia Virus (BLV) is a cell-associated retrovirus of cattle transmitted mainly through the transfer of infected lymphocytes, but the possible role of hematophagous insects in its epidemiology remains incompletely understood. This study investigated BLV DNA in field-collected *Culicoides* biting midges and *Stomoxys calcitrans* from cattle farms in Poland. Insects were collected on four farms in northeastern Poland. *Culicoides sp.* were identified morphologically, classified by gonotrophic status, and pooled by species and status, whereas *S. calcitrans* were analysed individually. DNA quality was verified by PCR targeting insect markers. Bovine host DNA was detected by PCR targeting mitochondrial cytochrome *b* in *Culicoides* and prepronociceptin (*PNOC*) in *S. calcitrans*. BLV proviral DNA was detected by TaqMan real-time PCR targeting the *pol* gene, followed by nested PCR and sequencing of a 400 bp fragment of the *env* gene. BLV DNA was detected in 20 of 138 *Culicoides* pools (14.5%). BLV copy numbers ranged from 2 to 19,000 copies per 500 ng of total DNA. All BLV-positive *Culicoides* pools were also positive for bovine cytochrome *b* DNA. Among the *pol*-positive pools, 18 were positive in nested *env* PCR and 15 yielded high-quality sequences. One *S. calcitrans* specimen was also positive in both BLV assays. Sequences obtained from insects were identical to those from infected cattle, and phylogenetic analysis assigned them to genotype G4 and G7, the predominant BLV genotypes circulating in Poland. These findings provide field-based molecular evidence that *Culicoides* biting midges and *S. calcitrans* can carry bovine blood and BLV DNA under natural farm conditions, supporting their possible role in the mechanical transfer of BLV between cattle.

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Comparing Three BLV Control Strategies Using Proviral Load and Their Effects on Prevalence and Incidence in Dairy Herds

Dr. Simon Bourassi, Atlantic Veterinary College, University of Prince Edward Island

Coauthors:
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[1]Department of Health Management, Atlantic Veterinary College[2]Department of Pathology/Microbiology University of Prince Edward Island, Charlottetown, PE, Canada

Bovine Leukemia Virus (BLV) is an oncogenic retrovirus that integrates into the host genome as proviral DNA. Proviral load (PVL) is a reliable indicator of a cow's potential to transmit BLV. The objective of this study was to compare three control strategies targeting high-PVL cows: (1) culling all high-PVL cows, (2) culling some and segregating the remaining high-PVL cows, and (3) culling only some high-PVL cows without segregation, for reducing BLV prevalence and incidence in dairy herds in the Canadian Maritime provinces.

Twenty-one herds of an initial thirty enrolled completed a 3-year prospective study. Individual BLV antibody testing was conducted annually using milk ELISA for most lactating cows and serum ELISA for dry cows, bred heifers, and cows from robotic-milking herds. BLV-positive cows underwent PVL quantification by qPCR, with moderate- and low-PVL cows retested annually if retained in the herd. Herd-level BLV prevalence was calculated yearly, and incidence rates were calculated for the second and third years. Trends in prevalence and incidence were compared across years for each herd relative to the implemented control strategy.

Median within-herd prevalence decreased from 36% (IQR, 24–50%) in year 1 to 29% (IQR, 19–40%) in year 2 and 24% (IQR, 17–36%) in year 3. Median incidence rate declined from 1.26 cases/cow-year (IQR, 0.5–2.8) to 1.18 cases/cow-year (IQR, 0.4–2.8). Herds that culled all high-PVL cows or culled some with segregation of the remainder experienced significant reductions in prevalence and incidence over the study period. Herds that culled some high-PVL cows without segregation showed no meaningful decrease in prevalence or incidence rate. Among herds that culled all high-PVL cows, one herd was BLV-free, and two herds had no remaining high-PVL cows by year 3.

Conclusion: Targeted culling of high-PVL cows, particularly when combined with segregation of remaining high-PVL animals, can effectively reduce BLV prevalence and incidence in high-prevalence dairy herds and may represent a practical, feasible control strategy.

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A Small Polypeptide Encoded by Antisense Long Non-Coding Rnas Mediates Bovine Leukemia Virus Replication

Dr. Luc Willems, National Fund For Scientific Research at University of Liege

Authors:
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Bovine Leukemia Virus (BLV) induces a lymphoproliferative disease in ruminant species. The provirus transcribes antisense RNAs (AS1-S/L and AS2) from a promoter located in the 3′ LTR. Reduction of antisense transcription impairs viral replication and oncogenesis (*Joris et al., PLoS Pathog.* 20, e1012659). Although these antisense RNAs are predicted to be non-coding, AS1 contains a 264 bp open reading frame (AS-ORF). We investigated whether this ORF encodes a polypeptide and assessed its role in viral replication and pathogenesis.

A Nano-Glo/AS-ORF fusion protein was immunoprecipitated using sera from BLV-infected animals, followed by quantification of luciferase activity. The effect of the AS-ORF on transcription was analyzed using luciferase-based reporter assays in cell culture and RNA sequencing of primary peripheral blood mononuclear cells (PBMCs). Subcellular localization of the AS-ORF protein was examined by confocal microscopy. Replication of a BLV molecular clone carrying a mutation in the AS-ORF initiation codon was evaluated in sheep.

Antibodies recognizing the AS-ORF were detected in sera from BLV-infected sheep, supporting in vivo expression of the corresponding protein. The AS1-ORF protein enhanced basal transcription from the viral promoter and modulated the AP-1 signaling pathway. Mutation of the AS-ORF reduced viral infectivity in cell culture and resulted in lower proviral loads in experimentally infected sheep.

Although BLV antisense transcripts are predicted to be non-coding, the detection of anti-AS-ORF antibodies and the reduced replication of a BLV mutant unable to express the AS-ORF protein demonstrate the biological relevance of this previously unrecognized open reading frame.

This study examines a hidden genetic element of Bovine Leukemia Virus (BLV), a virus that causes leukemia in ruminants. BLV produces antisense RNAs thought to be non-coding, but one of them contains a small genetic region that might make a protein (AS1). BLV-infected animals produce antibodies against the AS1 protein, proving that it is made during infection. The AS1 protein affects gene expression in the infected cell. When AS1 is not produced, the virus replicated less efficiently in animals. These findings reveal an unexpected viral protein that contributes to BLV infection and disease development.

2026 All Things BLV

July 14-17, 2026 | East Lansing, Michigan

Direct LAMP Amplification from Whole Blood to Detect BLV DNA

Dr. Scott, Sherrill-Mix, Michigan State University

Authors:

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Millions of US dairy cows are infected with Bovine Leukemia Virus (BLV) compromising animal health and reducing yields. Effective control depends on the efficient detection of infection. The presence of BLV proviral DNA is usually detected by quantitative PCR which requires labor intensive DNA purification and expensive real-time thermocyclers. Loop-mediated isothermal amplification (LAMP) is an alternative to PCR that requires only minimal equipment and is often robust to inhibitors in biological samples but more prone to false positives than PCR. We developed molecular beacons for previously published BLV LAMP primer sets that greatly increased specificity and reduced problematic false positives. We tested the ability of these molecular beacon LAMP assays to detect BLV DNA by the direct addition of whole blood to amplification reactions without purification and found that BLV could be consistently detected. These results lay the groundwork for cheaper and easier BLV detection to enable more frequent screening and better control.

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A Novel Approach for Early Detection of Bovine Leukemia Virus Using Precision Technology to Monitor Biometric Signatures

Ted Brooks, Michigan State University

Bovine leukemia virus (BLV) infection poses significant challenges to the dairy industry by decreasing animal health, longevity, and reducing profits. In the United States 94% of herds contain one BLV-positive cow and ~42% of all cows are BLV infected. Infection with BLV is lifelong, and widespread prevalence precludes mass culling. Preventing BLV remains challenging due to the lack of methods to identify onset of infection. This study aims to identify BLV infection onset by: 1) optimizing molecular assays for early BLV infection and 2) exploring real-time biometric signatures from SmaxTec. Rumen boluses were placed in qPCR BLV-negative heifers (n=156) prior to first calving. Blood samples were collected from all animals monthly. Animals with a bolus-detected fever (0.66 - 2.25°C above baseline) had additional samples collected every two weeks for eight weeks. Samples were centrifuged, plasma and whole blood were aliquoted in 1.5 mL tubes and stored at -80°F. Seventeen infected animals were ELISA-positive and confirmed by proviral qPCR (gold standard AntelBio Strata-G kit). Blood samples from infected animals will be used for plasma IgM, RNA extractions, and DNA extractions. Fluorometric assay for presence of reverse transcriptase (RT) activity (ThermoFisher EnzChek) and RT-qPCR assay of RT activity level will evaluate potential of RT isolation for early BLV detection. Linear regression and machine learning will evaluate bolus data to identify abnormal body temperature events indicative of infection. Associating biometric events with onset of BLV infection, disease management strategies may be introduced to maintain health, longevity and improve economic stability of the dairy industry.

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July 14-17, 2026 | East Lansing, Michigan

Keynote Address:

Genetic and Immunological Landscapes of Leukemogenesis in Enzootic Bovine Leukosis

Authors: Tomohiro Okagawa, Maho Inoue, Hayato Nakamura, Honami Shimakura, Misono Tominaga, Koume Matsubara, Naomi Nojiri, Kazuha Yoshida-Furihata, Naganori Nao, Naoya Maekawa, Shiro Murata, Kazuhiko Ohashi, Takahiro Matsudaira, Masumichi Saito, Satoru Konnai

Bovine Leukemia Virus (BLV) establishes persistent infection in cattle by integrating into the B-cell genome as a provirus. While most infected cattle show no clinical signs, few infected cattle develop enzootic bovine leukosis (EBL), whose leukemogenic mechanisms remain poorly defined.

In this study, we applied RAISING, a rapid, sensitive, accurate, and high-throughput method for proviral integration analysis, to comprehensively examine BLV proviral integration sites and patterns in tumor cells from 230 EBL cattle. In 18.7% of EBL cases, the gene loci of proviral integration were shared with other EBL cases. Totally, 21 such “hotspot” loci were identified, with cancer driver genes located their upstream. The BLV provirus functioned as a cis-regulatory element, and chimeric transcripts consisting of the BLV antisense gene and driver genes were detected in EBL tumors, supporting a model in which hotspot integration promotes tumorigenesis through transcriptional activation of cancer drivers.

Although EBL tumor cells have long been assumed to harbor a single proviral copy, our analysis revealed that most tumors contained multiple proviral copies per cell, with two copies in 57% and three copies in 11% of cases, whereas 32% harbored a single copy. B-cell receptor repertoire analysis demonstrated predominant expression of a single clonotype in most tumors, confirming monoclonal B-cell expansion and suggesting that accumulation of multiple proviral integrations contributes to malignant transformation.

Furthermore, single-cell RNA sequencing of tumorized lymph nodes from EBL revealed an increased population of exhausted $CD8^+$ T cells and infiltration of regulatory T cells and tumor-associated macrophages. These findings suggest that an immunosuppressive tumor microenvironment supports tumor proliferation and maintenance in EBL.

Collectively, this study provides an integrated genetic and immunological framework for BLV-induced leukemogenesis. Ongoing analyses linking proviral integration patterns with longitudinal immune responses in BLV-infected carriers will further refine this model and advance understanding of EBL tumorigenesis.

Tomohiro Okagawa

Assistant Professor
One Health Research Center at Hokkaido University

Tomohiro Okagawa, D.V.M., Ph.D., is a researcher in veterinary immunology and molecular diagnostics, currently affiliated with the One Health Research Center at Hokkaido University and the Business Development Unit at FASMAC Co., Ltd., Japan. He received his Ph.D. in Veterinary Medicine from Hokkaido University in 2016, where he has continued his research career as a postdoctoral researcher and specially appointed assistant professor. He has authored 113 peer-reviewed publications, filed 12 patent applications, and received 7 academic awards. His research is characterized by an integrated bench-to-field approach, spanning fundamental studies of disease mechanisms, the development of molecular diagnostic platforms and therapeutic strategies, and their implementation in real-world livestock settings through close academia–industry collaboration. His work on Bovine Leukemia Virus infection focuses on elucidating leukemogenesis, host–virus interactions, immune responses, and the clonal dynamics of BLV-infected cells to improve disease control and management strategies on farms.

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July 14-17, 2026 | East Lansing, Michigan

Decline of Maternally Derived Anti-Bovine Leukemia Virus Antibody Levels in Holstein Heifers on Commercial Dairy Farms

Olivia Willoughby, University of Guelph

Authors:

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The objective was to examine changes in Bovine Leukemia Virus (BLV) seropositivity in dairy heifers. Heifers were enrolled on 8 dairy farms in Ontario, Canada (adult BLV seroprevalence: 11–44%) from Mar–Aug 2024. Calves enrolled between 0–180 d were sampled every 21 d until 181 d old; older animals were sampled quarterly until May 2025. Seropositivity (> 45% inhibition) was assessed using a commercial ELISA kit (Biovet, St. Hyacinthe, QC). The dataset contained 10,989 ELISA results from 2,431 heifers sampled between 0 and 365 d old. Samples were assigned to 30-day age windows (0–12 months). Raw seroprevalence was 59%, 42%, 19%, 6%, 4%, 3%, and 4% at 0, 2, 4, 6, 8, 10, and 12 months, respectively. Associations between age and seropositivity were assessed using a mixed effects logistic regression model with age (months) as a scaled continuous fixed effect and farm as a random effect. Seropositivity declined with age (AOR = 0.17 per month, CI: 0.15–0.20, P<0.01). The intraclass correlation coefficient (9.6%) indicated that some variation in seropositivity was due to farm-level clustering. For 530 calves enrolled between 0-21 d of age, the association between dam and calf seropositivity was evaluated using mixed-effects regression models. Time-to-seronegativity among initially seropositive calves was assessed using a Cox proportional hazards model. Although not all calves received their dam's colostrum, calves from seropositive dams had higher odds of being seropositive (LSM 88±5% vs. 51±8%; AOR = 6.81, 95% CI: 3.56–13.02, P<0.01), higher mean ELISA inhibition (55.1±3.53 vs. 23.5±2.92, P<0.01), and longer median time to seronegativity (157 vs. 88 d; HR = 0.32, 95% CI: 0.23–0.44, P<0.01). Maternal antibodies appear to be the primary driver of early-life BLV seropositivity in calves. Almost all calves were seronegative by 6 months old, suggesting that true infection is uncommon in calves

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Association of Bovine Leukemia Virus Infection on Health, Milk Production, Fertility, and Longevity in Dairy Cattle

Modesto Elvir Hernandez, University of Florida

Authors:

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The study aimed to evaluate whether infection with Bovine Leukemia Virus (BLV) in heifers is associated with the development of economically important diseases such as metritis and clinical mastitis, as well as its association with milk yield, reproductive performance, and herd removal in dairy cattle. Holstein heifers (n = 8,334) were BLV tested at 382 ± 16 days of age and were followed through lactations 1, 2, and to the end of lactation 3. Individual electronic farm records were retrieved for metritis, clinical mastitis, milk production, reproductive performance, herd removal (culling or death), and calving-related problems events. Analyses were performed using logistic regression for metritis, Poisson regression for clinical mastitis, and an ANOVA model for milk yield. Reproductive performance and herd removal (culling and dead) were analyzed using the Cox proportional hazard model. Being BLV-positive as a heifer was associated with an overall clinical mastitis development, mostly because of increased clinical mastitis development in lactation 2, and associated with an overall increased hazard of removal from the herd because of death, mostly because of increased hazard of death in lactations 1 and 3. Moreover, being BLV-positive as a heifer was associated with reduced milk yield in lactations 1 and 3, but not in lactation 2. However, being BLV-positive as a heifer was not associated with metritis development and reproductive performance. We conclude that being BLV-infected as a heifer was associated with clinical mastitis development, reduced milk yield, and an increased hazard of herd removal in dairy cows.

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Associations of Bovine Leukemia Virus Infection with Fertility, Disease, and Culling Risk

Olivia Willoughby, University of Guelph

Authors:

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The objective was to investigate the associations of Bovine Leukemia Virus (BLV) infection with health, fertility, and culling. Cows were enrolled from -21 to 50 DIM from Jan 2024 – Sept 2024 on 9 farms. (BLV prevalence 11%-44%). Animals at risk of seroconversion were re-sampled quarterly until May 2025. Samples were considered positive with ≥ 45% inhibition on ELISA and negative with < 35% inhibition; samples between 35 – 44% inhibition were considered suspect. Cows were classified as seropositive if they had a positive ELISA result pre-calving and seronegative if they had negative ELISA results pre-and post-calving. Data from farm software included parity, milk fever, retained placenta, metritis, mastitis, and calving, breeding, and culling dates. The final dataset contained 1360 animals; 24% were BLV-seropositive and 13% had at least one recorded disease. Logistic regression was used to evaluate the association between seropositivity and the occurrence of ≥ 1 recorded disease before 250 DIM, conception risk at first service, pregnancy by 120 DIM and risk of culling to 250 DIM. Survival analyses were used to assess time to pregnancy. Seropositive cows had greater odds of ≥ 1 disease (LSM = 8% ± 3% vs 5% ± 2% *P*=0.05, AOR = 1.76, CI: 1.19–2.62), and lower odds of pregnancy at first service (LSM = 42% ± 4% vs 50% ± 3%, *P*=0.05, AOR = 0.73, CI: 0.53-1.01) and of pregnancy by 120 DIM (LSM = 72% ± 5% vs 80% ± 3%, *P*=0.03, AOR = 0.66, CI: 0.45-0.97). No difference in the hazard of pregnancy by 250 DIM was observed (HR = 0.89, CI: 0.76-1.05, P=0.16). Seropositive cows had higher odds of culling by 250 DIM (LSM = 32% ± 6% vs 9% ± 2%, AOR = 4.62, *P*<0.01). BLV seropositivity is associated with greater disease and culling risk and reduced reproductive performance.

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July 14-17, 2026 | East Lansing, Michigan

Keynote Address:

Bovine Leukemia Virus Vaccine: Progress and Future Steps

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Bovine leukosis is a widespread disease with no available vaccine or treatment. In Argentina, each cow that dies from lymphosarcoma results in an estimated economic loss of $5,000 USD. Additionally, trade restrictions on infected animal genetic material indirectly impact cattle producers.

In 2008, the University of Liège, Belgium, and INTA, Argentina, developed a genetically modified, attenuated Bovine Leukemia Virus strain for use as a vaccine against bovine leukosis. The strain was patented in several countries and, after regulatory approval in Argentina, was authorized for commercial purposes in 2022, becoming the first and only genetically modified virus approved for commercial use in a vaccine against bovine leukosis.

Safety and efficacy were demonstrated in four *in vivo* bovine trials during the regulatory process. The strain fulfilled the objectives of provoking a protective immune response with attenuated capacity for in vivo replication and lack of transmission to newborn calves and milk, showing a dramatically reduced phenotype compared to the wild-type circulating strain.

In 2023, we analyzed the economic feasibility of a gene-based vaccine. The vaccine's main active ingredient, a candidate plasmid construct containing the complete proviral DNA of the attenuated strain, was produced and characterized in 2024. In 2025, the transfection efficacy of the plasmid DNA was confirmed in ovine and bovine models.

Future steps include:

1. Large-scale plasmid manufacturing process development
2. Optimization of bacterial culture yield and plasmid production
3. Minimization of plasmid mass per dose using a delivery system
4. Validation of vaccine efficacy in a pilot field trial

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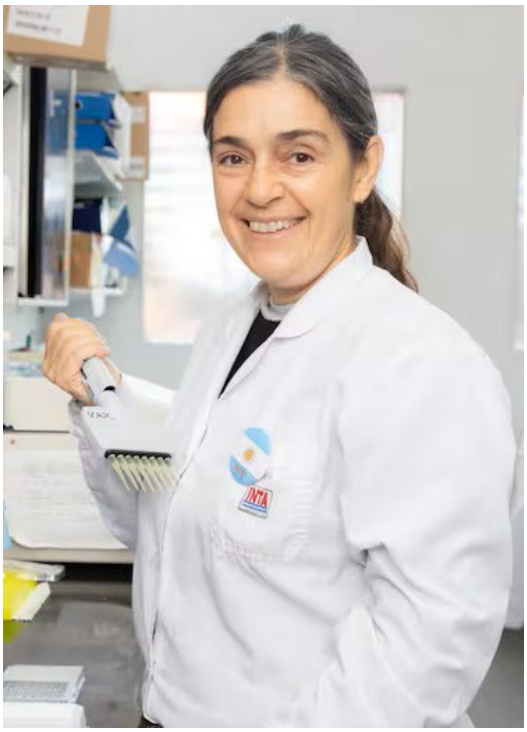

Karina Trono

Researcher

CONICET

Director IVIT

Dr. Karina Trono is an Independent Researcher with CONICET and Director of the Institute of Virology and Technological Innovations (IVIT), a joint INTA-CONICET research institute in Argentina. She earned her Doctor of Veterinary Sciences degree from the University of Buenos Aires and has dedicated her career to veterinary virology, immunology, infectious disease epidemiology, and the development of vaccines and diagnostic tools for animal diseases.

Dr. Trono is internationally recognized for her pioneering work on Bovine Leukosis, including the development of a vaccine that has received patent protection in the European Union, Canada, the United States, Brazil, Colombia, Mexico, India, and Argentina. She has authored more than 70 scientific publications, directed numerous graduate students, and contributed to the development of diagnostic technologies for diseases such as Equine Infectious Anemia. Her research achievements have earned multiple national and international awards recognizing her contributions to veterinary science, innovation, and rural development.

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Epidemiological Trends During a BLV Eradication Program in French Reunion Island Herds

Camille Demassieux, Agency for Food, Environmental and Occupational Health & Safety (ANSES), France

Authors:
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Several European countries, including France, eradicated Bovine Leukemia Virus (BLV) in the 90's. However, the French overseas territory of La Réunion, a southwestern Indian Ocean Island, combines a significant cattle industry with a long-lasting enzootic circulation of BLV. A seroprevalence survey conducted in 2018 revealed a herd prevalence of 55% and 100% in cow–calf (n= 220) and dairy (n= 66) herds, respectively. In 2020, a mandatory control program has been launched by the government and professional associations.

The plan initially targeted herds with prevalence up to 50%, and was then gradually expanded to all herds. All cattle older than 12 months were subject to mandatory testing by ELISA. Different control strategies were applied, including testing and culling or segregating seropositive animals. The selective removal of super-shedders detected by quantitative PCR test was used in some highly infected dairy herds. Concomitantly, several measures were implemented to prevent viral spread, including hygienic practices targeting iatrogenic transmission, the control of insect vectors (Stomoxys) and movement restrictions between herds. The program received financial support from local and national authorities to cover the costs of veterinary inspections, blood sampling and diagnosis, and compensation for premature culling and renewal of animals.

The aim of this study was to describe the evolution of the enzootic, by a longitudinal analysis of the course of prevalence and incidence at the herd and the population levels. For this purpose, data from birth to death of 103,310 animals were collected from the national cattle database, associated with corresponding screening tests results. We gathered the control measures that have been implemented, including the different approaches of dealing with infected animals. The funding allocated by the authorities to support this management plan was also estimated.

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Prevalence of Bovine Leukemia Virus Antibodies and Proviral Load on Front Range Dairy Farms in Colorado and Wyoming

Marcie Bernard, Colorado State University

Authors:

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Bovine Leukemia Virus (BLV) is a retrovirus infecting cattle lymphocytes, leading to lymphosarcoma in about 10% of infected cattle. BLV is present on over 94% of U.S. dairies and infection results in reduced milk production, reduced longevity, and economic losses. BLV transmission is thought to occur primarily through transfer of infected lymphocytes via multiple routes. One way to assess transmission risk is comparing management practices across farms with different BLV prevalence. The objective of this study was to evaluate whole-blood BLV antibody and proviral load (PVL) prevalence across multiple cattle classes on Front Range dairies. On 16 dairies, approximately 10 cattle from each of 8 cattle classes were sampled: preweaned calves, weaned calves, yearling heifers, 18-month-old heifers, and 1st, 2nd, 3rd, and 4th and greater lactation cows. Among 1,361 whole-blood samples, antibody was detected in 25.3% and provirus was detected in 15.9% (3.4% high; 3.0% moderate; and 9.5% low). Preweaned calves had the highest antibody prevalence (58.5%) likely due to colostral immunoglobin transfer from dams, while yearling heifers had no detectable BLV antibodies. Antibody and PVL prevalence increased with lactation. Cows in 4th and greater lactation exhibited the highest antibody (49.5%) prevalence among lactating cows, consistent with cumulative lifetime exposure. They also exhibited the highest overall PVL (43.8%) prevalence, including 11.3% high PVL, suggesting older cows are the most infectious. We observed substantial variation in prevalence among dairies, suggesting management practices influence transmission dynamics.

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Longitudinal Assessment of Proviral Load in BLV-infected Dairy Cattle and Implications for Testing Frequency

Dr. Simon Bourassi, Atlantic Veterinary College, University of Prince Edward Island

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Proviral load (PVL), expressed as proviral copies of Bovine Leukemia Virus (BLV) per WBC (1 WBC =2 bos actin gene copies), is a key indicator of transmission risk and disease progression and is increasingly used to guide control programs. However, longitudinal data on PVL dynamics at the individual cow level remain limited.

This prospective study quantified temporal changes in PVL over three years and evaluated implications for PVL testing frequency. A total of 716 BLV-positive cows from 25 dairy herds in Atlantic Canada were enrolled. Cows underwent annual PVL quantification by qPCR (2–3 PVL tests/cow at ~12-month intervals). PVL was analyzed using a repeated-measures linear mixed-effects model with herd and cow as random effects and lactation number as a confounder. PVL values were cube root–transformed to meet model assumptions.

Median PVL increased over time from 0.54 (IQR: 0.11–1.39) at first testing to 0.63 (0.12–1.71) and 0.97 (0.22–1.87) copies per cell at subsequent tests. The mixed model demonstrated a significant upward PVL trend, increasing by 0.11 and 0.16 units (cube root scale) at the second and third tests, respectively ($P < 0.001$). Most PVL variation occurred at the cow level (84.4%), compared to low herd-level variation (3.2%).

Category transitions showed that 12% and 53% of low-PVL (<0.5) and moderate-PVL (0.5-1.0) cows progressed to high PVL (>1.0) over two years, respectively. Within one year, 34% and 19% of moderate-PVL cows developed high PVLs during the first and second intervals, respectively. All cows initially classified as high PVL remained high. Twenty (2.8%) cows maintained undetectable PVLs over the study period despite confirmed seropositivity.

These findings demonstrate that PVL increases over time, especially moderate-PVL cows. Biennial and annual testing of low-PVL and moderate-PVL cows, respectively, may enhance the cost efficiency of using PVL as part of BLV control programs.

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Thank You

Planning Committee

Phil Durst
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Jason Lombard
Frank Van der Meer
Aneta Pluta
Tomohiro Okagawa
Tasia Kendrick

Future Collaboration Opportunities

Join the Google Group and request to be added by emailing: blv-connect@googlegroups.com

You may also email Tasia Kendrick at taxistas@msu.edu

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