In this CVERA e-zine, we provide a brief overview of some of the recent work conducted by CVERA staff in collaboration with a wide range of national and international institutions. More in-depth information can be found at http://www.ucd.ie/cvera/.

Integrating whole-genome sequencing and epidemiology to characterise *Mycobacterium bovis* transmission in Ireland: a proof of concept

In the Republic of Ireland, the herd-level incidence of bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, reached 6.4% by June 2025, highlighting bTB's risk to animal health, biosecurity and the economy. The complexity of bTB epidemiology, driven by multiple host species, undetected transmission and incomplete diagnostic sensitivity, makes surveillance and control challenging. Pathogen whole-genome sequencing (WGS) can clarify transmission dynamics but is constrained by the slow, variable mutation rate of *M. bovis*. This pilot case study integrates WGS with epidemiological data to elucidate transmission event pathways and could be a starting point for future automation. A decision-tree framework was developed to classify likely transmission event pathways by integrating *M. bovis* WGS sourced from the bTBGenie research project and epidemiological data. Transmission event pathways for this case herd were classified as "local area transmission", "within-herd transmission", and "cattle movement-associated transmission", divided into "between-herd" and "within-herd" transmission. Integrating WGS with detailed epidemiology enables identification of probable bTB transmission event pathways, revealing undetected infections and highlighting biosecurity concerns associated with undetected carriers. The decision-tree framework provides a scalable approach for retrospective outbreak investigation, targeted surveillance, and efficient resource allocation, particularly in high-risk systems such as Controlled Finishing Units. The findings in the study highlight the importance of transboundary collaboration in persistent bTB hotspots. Automating this approach could support validation of disease epidemiological models, guide targeted interventions, and optimise resource allocation, supporting Ireland's goal of bTB eradication. The study included researchers from UCD CVERA, the Department of Agriculture, Food and the Marine (DAFM), Agri-Food and Biosciences Institute NI (AFBI), DAFM Central Veterinary Research Laboratory (CVRL) & the UCD School of Veterinary Medicine. The paper by Harvey et al will be published in the *Irish Veterinary Journal* shortly.

Q fever in Ireland characterising zoonotic risk

Q fever is a bacterial infection found in many Irish cattle. It is also known as coxiellosis and is caused by the bacteria *Coxiella Burnetii*. Both animals and people can be infected without showing any signs. In cattle, it can cause abortions and fertility problems. In people, symptoms, if they appear, can include fever, headache, muscle aches, or cough. Most people recover fully, but it can be more serious for pregnant women, people with heart problems, or those with weak immune systems. Even though Q fever is common in Irish cattle, very few human cases are reported each year. People usually get infected through close contact with livestock, particularly during calving or lambing. This means that many farmers may be exposed without knowing it. A new study, led by Dr. Katie Corridan, funded by the Department of Agriculture, Food and the Marine, and based at the Centre for Veterinary Epidemiology and Risk Analysis (UCD School of Veterinary Medicine), in collaboration with colleagues from St Vincents University Hospital and Beaumont Hospital, is investigating this gap and is seeking farmers to take part. Volunteers fill out a short questionnaire and give a small blood sample, which is tested for Q fever antibodies. This free test can show if the volunteer has been exposed to Q fever in the past. The results from this study will help researchers understand who is at risk, raise awareness and support better protection for farmers' health. For more information, please visit Q fever study information.

Preparation for a potential outbreak of bluetongue virus in Ireland: surveillance design to estimate local prevalence after an initial case detection

Bluetongue virus serotype 3 emerged in northern Europe in 2023 and 2024. As of September 2025, Ireland is bluetongue free. However, to inform control decisions in the event of a possible incursion, a surveillance plan to detect cases and estimate prevalence is required. We created an active surveillance plan for 20 km radius temporary control zones (TCZs) after initial case detection. Potential TCZs (n = 1,062) covering Ireland were generated, and surveillance sample sizes were estimated based on cattle data in each TCZ. A two-stage (herd and animal level) design accounted for within-herd clustering. We simulated implementation of the surveillance plan in each TCZ to understand surveillance performance in the Irish cattle population. Within herd prevalence of 30% was used for all simulations, and we assumed the use of RT-PCR with perfect specificity and 99% sensitivity for diagnosis. Based on 100 simulations per TCZ, mean apparent animal level prevalence within tested infected herds ranged from 25 to 32%. With simulated between-herd prevalence of 5%, when between 39 and 61 herds per TCZ were sampled, apparent between-herd prevalence ranged between 3% and 6%. With simulated between-herd prevalence of 30%, and 10–11 herds per TCZ sampled, apparent between-herd prevalence ranged from 20 to 36%. Within herds, sampling 10–11 cattle was sufficient for prevalence estimation. We integrated Shiny and ArcGIS web applications to allow users to simulate scenarios under different settings. These include different test sensitivity and specificity, and different within- and between- herd prevalence contexts. This interface presents infected herds sampled, and true- and false- positives and negatives in a variety of conditions. Evidence from this scenario analysis can be integrated into a multi-pronged early warning and potential follow-up surveillance programme to facilitate decision making in the event of an incursion of BTV into Ireland. The web application associated with this paper is: https://www.arcgis.com/apps/dashboards/16722dde78d240f4a96303173bc6da2c. This paper by Casey-Bryars et al is available at *Irish Veterinary Journal 78, 30 (2025)*.

Estimating sectoral livestock biomass and stock value using data from national diseases eradication programs: a case study based on the Irish cattle herd from 2011 to 2021

Livestock biomass is a denominator for a wide range of important production metrics, including productivity, environmental impact, greenhouse gas emissions, and antimicrobial usage. Accurate biomass estimates allow cross-sectoral and international comparisons for these important indices across a range of high-priority areas, which can then inform policy risk assessments and decision-making. Similarly, accurate estimates of the value of livestock are needed to monitor economic efficiency and productivity and understand the costs associated with animal health policy decisions. Previous methods to estimate biomass have relied on assigning an average liveweight for a given species and multiplying this by the number of individual animals of that species in a region. However, without taking into account the population's demographics and structure, these approaches cannot be relied upon to accurately represent the cattle population. Using data from the Irish cattle herd as a case study, this study developed liveweight and value models and applied these models to a cattle registration and movement database to estimate the biomass (kg) and economic stock value (€) of each animal and herd, aggregated by herd type based on a herd classification tree model, and explored trends in biomass and stock value over time. The Irish cattle sector biomass increased from 2,924,800 tonnes in 2011 to 3,317,100 tonnes in 2021, and the cattle sector stock value increased from €6,323.7 m in 2011 to €8,792.3 m in 2021. Furthermore, this study demonstrated the biomass and stock value within-year and between years. This study illustrate a novel approach using real-time movement data for dynamic estimates of biomass and stock value at animal-, herd- and national-level that can be applied in countries with existing animal registration and movement tracing systems. The paper was led by Emma-Jane Murray and included collaborators from the UCD School of Veterinary Medicine, the Roslin Institute at the University of Edinburgh, the Department of Agriculture, Food and the Marine, UCD CVERA, Animal Health Ireland, the Glenythan Vet Group and the Dunnydeer Veterinary Group in Aberdeenshire. Murray et al is available at *Frontiers in Veterinary Science* 12, 1648948 (2025).

Herd-level prevalence of high fat-to-protein ratio and associated factors during early lactation in Irish spring-calving dairy herds

This study used national milk data from over 11,051 Irish spring-calving dairy herds from 2014 to 2023 to assess herd-level prevalence of high fat-to-protein ratio (FPR) (>1.4), as a proxy measure for negative energy balance (NEB), and associated factors. NEB during early lactation increases the risk of metabolic disease, reduces fertility performance, and limits profitability in dairy systems. Median herd-level prevalence of high FPR (>1.4) <30 DIM had a 10-year mean of 14.57% (annual median ranged from 10.81 to 20%), decreasing to 8.10% (annual median ranged from 6.09 to 12.90%) from ≥30 to <60 DIM, with annual variation noted. Results highlighted seasonal and herd-level factors influencing herd-level prevalence of high FPR. The months of February and March, coinciding with housing, feeding of conserved forage, peak calving, and early grazing periods, were associated with the highest prevalence. Genetic traits and 305-day milk yield were linked to herd-level prevalence of high FPR. Higher-yielding herds were associated with reduced odds of increased herd-level prevalence of high FPR, i.e., reduced risk of NEB at herd level. These findings identify important factors associated with herd-level prevalence of high FPR during early lactation, which can help inform future preventative strategies aimed at improving herd health, productivity, and sustainability in Irish dairy herds. This paper was led by Raffaela Marian from the Section of Herd Health and Animal Husbandry in the UCD School of Veterinary Medicine. The paper by Marian et al is available at *Animals* 15, 3068 (2025).

DisplayTB

DisplayTB has been updated to include Bovine Tuberculosis (bTB) data for Q3/2025. Additional functionality including ability to select information by county and reginal veterinary office has been added. The DisplayTB mapping dashboard was created by CVERA as part of a research program into Bovine Tuberculosis (bTB) being conducted by the Centre for the Department of Agriculture, Food and the Marine (DAFM). The National TB Forum highlighted the need for DAFM to communicate area risk of bTB to farmers. As such, CVERA created an interface to allow stakeholders to view the current and recent bTB status of herds in their area of interest. Please note, this is an ongoing research project, and the content is likely to change over time. The values presented are compiled by CVERA from data snapshots provided by DAFM. This may result in some errors of interpretation and may not account for errors of corrections in the source data held by DAFM. For this reason, the dashboard is considered only a research prototype and should not be used for official reporting purposes. To protect the identity of individual farmers, a process was developed to aggregate farms into larger spatial units. To view the DisplayTB mapper, please visit https://tinyurl.com/mr38vkyp

One Health Centre Conference 2025 - One Health UCD

The UCD One Health Centre Conference "*From Priorities and Clusters to Real-World Impact: One Health in Action*" is being held on the 9th of December in O'Reilly Hall in University College Dublin. The conference will bring together internationally renowned speakers and will showcase the depth and breadth of UCD and Ireland's One Health expertise. From cutting-edge research and education to policy, public health, agriculture, and environmental action, contributors will span government, academia, civil society and international organisations. For more information and to register for the conference, please visit (https://www.ucd.ie/onehealth/newsandevents/onehealthcentreconference2025/). A special early bird rate is available until the 28th of November 2025.

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http://www.ucd.ie/cvera
+353 (0)1 716 6144
@ucd-cvera.bsky.social
@UCD_CVERA