

Centre for Veterinary Epidemiology and Risk Analysis (CVERA)



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/>, noting the role of CVERA to provide high quality independent scientific research and advice to support national evidence-based policy-making in animal health & welfare and public health and related matters.

The new Veterinary Medicines Regulation: rising to the challenge

This article by More et al focuses on the new Veterinary Medicines Regulation, which is applicable across all Member States of the European Union, including Ireland, from 28 January 2022. From this date, prophylactic use of antimicrobials (AMs) in groups of animals is banned, metaphylactic use in groups of animals is restricted, and certain AMs are reserved for humans only. For private veterinary practitioners (PVPs), the Regulation will lead to specific prescribing changes, including the requirement to shift from blanket to selective dry cow therapy and for prescribing choices to be guided by the categorisation for AMs developed by the European Medicines Agency (EMA). More broadly, the Regulation requires a fundamental shift in thinking both in terms of AM usage and of the role of the PVP. Given the close association between mastitis control and intramammary AM stewardship, it is imperative that prescribing and mastitis control decisions are made concurrently. On those farms with sub-optimal mastitis control, mastitis issues will need to be sustainably resolved. A detailed farm investigation by the PVP, in

partnership with the farmer and other milk quality professionals, is essential, to understand the epidemiology and on-farm drivers of mastitis, to develop farm-specific action plans, and to facilitate ongoing monitoring of progress. It is vital that PVPs provide leadership, with the provision of a holistic, herd health approach to inform both prescribing and mastitis control decisions in herds under their care. The study was conducted by members of the UCD School of Veterinary Medicine, Animal Health Ireland and UCD CVERA. [[Irish Veterinary Journal 75, 2 \(2022\)](#)].

Future risk assessment of *M. bovis* in raw cheese milk
Specialty cheeses, which are often produced using raw milk, present challenges to risk managers in countries where *Mycobacterium bovis* is endemic or (re-) emerging. A key concern is the potential risk of zoonotic transmission of *M. bovis* via the consumption of dairy products produced using raw milk originating from herds infected with *M. bovis* (bovine tuberculosis, bTB). Two studies by Collins et al have now been published in support of future risk assessment of *M. bovis* in raw cheese milk:

Prevalence of *Mycobacterium bovis* in milk on dairy cattle farms: an international systematic literature review and meta-analysis

This study systematically reviewed published studies to estimate the prevalence of *M. bovis* in on-farm bulk-tank milk (BTM) and individual cow's milk (IM) by meta-analysis. For IM, the overall prevalence was summarised at 5% (95%CI: 3%–7%). In TST positive cows, prevalence was summarised at 8% (95%CI: 4%–13%). For BTM, the overall prevalence independent of individual herd TST infection status was summarised at 5% (95%CI: 0%–21%). There was considerable heterogeneity evident among the included studies, while PIs were also wide. Despite international efforts to control tuberculosis, this study by Collins et al highlights the risk of zoonotic transmission of *M. bovis* via unpasteurised milk and dairy products made using raw milk. [[Tuberculosis 132, 102166 \(2022\)](#)].

Parameter estimates to support future risk assessment of *Mycobacterium bovis* in raw milk cheese

The aim of this study was to determine parameter estimates to support the future risk assessment of *Mycobacterium bovis* in raw milk cheese. In this study, the hazard was identified as viable *M. bovis* organisms in raw milk cheese. Parameters of interest in this study related to exposure assessment (the estimated extent of human exposure to viable *M. bovis* organisms) and hazard characterisation (the risk posed to human health following exposure to viable *M. bovis* organisms). The pathway for exposure assessment was visualised using a conceptual framework, which describes the steps through which *M. bovis* may be transferred from an infected animal(s) through manufacturing to the final cheese product. Estimation of most parameters for exposure assessment and hazard characterisation was undertaken using systematic literature review and meta-

analysis. Estimates could be derived for many parameters, but not all. In particular, the number of *M. bovis* organisms excreted in the milk and present in the faeces of infected cattle are unknown. There is zero-tolerance for *M. bovis* in foods of animal origin destined for human consumption in European legislation. [[Microbial Risk Analysis \(in press\) \(2022\)](#)].

Is there an association between road building and bovine tuberculosis herd risk? A three time-points study in Ireland, 2011-2020

In this study, we investigated whether (motorway) road construction was associated with an increased risk of bTB in associated cattle herds. For this study, we considered three observation periods relating to road building, including pre-construction (2011–2014), construction (2015–2017) and post-construction (2018–2019). Herds located at a distance of >3 km from the roadworks were found to be at reduced risk of a bTB breakdown over the construction period compared with those situated within 1 km of the roadworks for ≥ 1 reactor/s (>3 km and construction vs. <1 km: OR: 0.595, 95 % Confidence Interval (CI): 0.354–0.999) or ≥ 3 reactors (>3 km and construction vs. <1 km: OR: 0.431, 95 % CI: 0.174–1.067). Other previously reported risk factors such as inward movements, herd-size and herd-type were also associated with bTB risk in the final models (≥ 1 reactor/s and ≥ 3 reactors). These findings by Barroso et al appear to be consistent with bTB breakdowns being a consequence as opposed to coincident to road construction, given the temporal and spatial consistency of the evidence. Further research is warranted to verify this pattern occurs elsewhere, and the underlying biological mechanism. Until further data are available, we recommend that badgers are vaccinated, as a precautionary measure, in advance of the commencement of major roadworks. The study was conducted by members of the Instituto de Investigación

en Recursos Cinegéticos (UCLM-CSIC) in Spain, the DAFM Ruminant Animal Health Division, the DAFM One Health Scientific Support Unit & UCD CVERA. [[Preventive Veterinary Medicine 198, 105542 \(2022\)](#)].

Numbers of close contacts of individuals infected with SARS-CoV-2 and their association with government intervention strategies

Contact tracing is conducted with the primary purpose of interrupting transmission from individuals who are likely to be infectious to others. Secondary analyses of data on the numbers of close contacts of confirmed cases could also provide an early signal of increases in contact patterns that might precede larger than expected case numbers; evaluate the impact of government interventions on the number of contacts of confirmed cases; or provide data information on contact rates between age cohorts for the purpose of epidemiological modelling. We analysed data from 140,204 close contacts of 39,861 cases in Ireland from 1st May to 1st December 2020. Negative binomial regression models highlighted greater numbers of contacts within specific population demographics, after correcting for temporal associations. Separate segmented regression models of the number of cases over time and the average number of contacts per case indicated that a breakpoint indicating a rapid decrease in the number of contacts per case in October 2020 preceded a breakpoint indicating a reduction in the number of cases by 11 days. We found that the number of contacts per infected case was overdispersed, the mean varied considerable over time and was temporally associated with government interventions. Analysis of the reported number of contacts per individual in contact tracing data may be a useful early indicator of changes in behaviour in response to, or indeed despite, government restrictions. This study, led by McAloon et al, provides useful information for triangulating assumptions regarding the

contact mixing rates between different age cohorts for epidemiological modelling. [[BMC Public Health 21, 2238 \(2021\)](#)].

Seroprevalence of *Mycoplasma bovis* in bulk milk samples in Irish dairy herds and risk factors associated with herd infection status

This study by McAloon et al is the first to describe herd apparent prevalence for *Mycoplasma bovis* exposure in Irish dairy herds. There is high herd apparent prevalence among dairy herds in Ireland, with evidence from 45% of tested herds of at least past exposure to *M. bovis*. Risk factors associated with herd-level seropositivity included increasing herd size, the number of contiguous neighbouring farms, the buying in behaviour (reflected as an increased risk associated with those herds who bought from more than 2 sources) and region (as identified by county). [[Journal of Dairy Science \(in press\) \(2022\)](#)]. This paper will be available shortly.

Freedom from infection studies

Freedom from infection is an important concept underpinning the safe trade of cattle. However, control programmes (CPs) can vary between countries, and it can be difficult to compare freedom claims under different programmes. An EU project, STOC free, has been considering this issue in detail, evaluating methods that could be used to allow these comparisons. Two studies in support this work were recently published by Mercat et al and by Madouasse et al:

Capacity of a Bayesian model to detect infected herds using disease dynamics and risk factor information from surveillance programmes: A simulation study

Our objective was to evaluate the capacity of a Bayesian Hidden Markov Model, which computes a herd-level probability of being infected, to detect infected herds compared to using test results only. Herd-level risk

factors, infection dynamics and associated test results were simulated in a population of herds, for a wide range of realistic infection contexts and test characteristics. The model was used to predict the infection status of each herd from longitudinal data: a simulated risk factor and a simulated test result. The model predictive performances were evaluated using the simulated herd status as the gold standard. The model detected more infected herds than a single final test in 85 % of the scenarios which converged. The proportion of infected herds additionally detected by the model, compared to test results alone, varied depending on the context. It was higher in a context of a low herd test sensitivity. On average, around 20 %, for high test sensitivity scenarios, and 40 %, for low test sensitivity scenarios, of infected herds that were undetected by the test were accurately classified as infected by the model. Detection of additional newly infected herds was always associated with an increased number of false positive herds (except for one scenario). The number of false positive herds was lower for scenarios with low herd test sensitivity and moderate to high incidence and prevalence. These results by Mercat et al highlight the benefit of the model, in particular for control programmes with infection present at an endemic level in a population and reliance on test(s) of low sensitivity. [[Preventive Veterinary Medicine 200, 105582 \(2022\)](#)].

A modelling framework for the prediction of the herd-level probability of infection from longitudinal data

In this paper, we describe a statistical model for the prediction of herd-level probabilities of infection from longitudinal data collected as part of CPs against infectious diseases of cattle. The model was applied to data collected as part of a CP against bovine viral diarrhoea virus (BVDV) infection in Loire-Atlantique, France. The model represents infection as a herd latent

status with a monthly dynamics. This latent status determines test results through test sensitivity and test specificity. The probability of becoming status positive between consecutive months is modelled as a function of risk factors (when available) using logistic regression. Modelling is performed in a Bayesian framework. Prior distributions need to be provided for the sensitivities and specificities of the different tests used, for the probability of remaining status positive between months as well as for the probability of becoming positive between months. The impact of using different prior distributions and model implementations on parameter estimation was evaluated. The main advantage of this model is its ability to predict a probability of being status positive in a month from inputs that can vary in terms of nature of test, frequency of testing and risk factor availability/presence. The main challenge in applying the model to the BVDV CP data was in identifying prior distributions, especially for test characteristics, that corresponded to the latent status of interest, i.e. herds with at least one persistently infected (PI) animal. The model is available on Github as an R package (<https://github.com/AurMad/STOCfree>) and can be used to carry out output-based evaluation of disease CPs. The study was conducted by Madouasse et al. [[Peer Community Journal 2, e4 \(2022\)](#)].

***M. bovis* 2022**

The Seventh International Conference on *Mycobacterium bovis* (*M. bovis* 2022) will take place in Galway from 7-10 June 2022. The conference was originally due to take place in 2020. The Committee would like to thank our speakers, delegates, organisers, and sponsors for their continued support of the conference. The conference has attracted a high number of delegates from a wide range of countries. Building on the success of Cardiff 2014, *M. bovis* 2022 will gather together scientists, policy makers, veterinarians and

industry stakeholders from around the world with the aim of identifying constraints and providing practical solutions for the control and eradication of the *M. bovis*. To maintain the health and safety of all involved, the conference will abide by all public health measures applicable at the time of the conference. We would ask that all those intending to come to *M. bovis* 2022 familiarise themselves with travel and public health measures that are in place. The *M. bovis* 2022

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Organising Committee will continue to monitor the situation in Ireland and tailor our plans accordingly for a safe in-person conference in June 2022. Please visit www.mbovis2022.com for more information.

Previous news items, can be found at:
<http://www.ucd.ie/cvera/news/>