

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 policymaking in animal health & welfare and public health and related matters.

Stewardship of intramammary antimicrobials

The Veterinary Medicines Regulation (2019/6) will apply in Ireland from 22 January 2022, with an emphasis on prudent and responsible antimicrobial usage. Relevant to this Regulation, the Veterinary Council of Ireland (VCI) approached the CellCheck technical working group (TWG) for technical perspectives on key definitions and prescribing guidelines for dry-cow and intramammary antimicrobials. The TWG, chaired by Simon More, includes a group of 18 technical experts drawn from all relevant fields and a broad range of organisations. In its submission to the VCI, the TWG focused on prescribing guidelines for veterinarians, animal- and herd-level information to inform prudent prescribing, and accompanying national actions to address suboptimal mastitis and support prudent prescribing. The TWG submission has been presented at several public fora, including the Oireachtas Joint Committee for Agriculture and the Marine (on 23 March), a meeting of iNAP (Ireland's National Action Plan on Antimicrobial Resistance; on 29 March) and the CellCheck Implementation Group (on 07 April).

Future risk of bovine tuberculosis (*Mycobacterium bovis*) breakdown in cattle herds 2013-2018: a dominance analysis approach

A paper on the future risk of bovine tuberculosis, led by Byrne et al from the DAFM One Health Scientific Support Unit, has been published. In this study, the future risk of herd breakdowns (BD) were estimated, for the cohort of herds that were derestricted during 2013 in Ireland using multivariable logit regression models, with a dominance analysis approach. BD length was a significant predictor of future risk, primarily driven by long BDs > 230 days relative to short BDs < 130 days (OR 95%CI: 1.157–1.851), as was having had a previous BD (OR 95%CI: 1.012–1.366). Herd-size was the dominant predictor of future risk (accounted for 46% of predicted variance), suggesting significant increase in risk of future breakdown with increasing (log) herd-size (OR 95%CI: 1.378–1.609). There was significant spatial variation in future risk across counties, and it was the second most dominant predictor of future risk (25% of predicted variance). In contrast, the size of index breakdowns was not a strong predictor of future risk over a 5-year period. [Byrne et al. Microorganisms 9, 1004].

Epidemiological parameters for COVID-19 modelling

Since the start of the pandemic, CVERA have contributed to national efforts in epidemiological COVID-19 modelling (IEMAG; the Irish Epidemiological Modelling Advisory Group to NPHET). As part of this work, there has been a need for a detailed understanding of a range of epidemiological parameters based on all available published information. Previously, CVERA contributed to published papers on the serial interval and generation time, the incubation period, and the duration of the infectious period of COVID-19. Recently, there have been further publications, on the relative infectiousness of symptomatic and asymptomatic individuals [McElroy et al. BMJ Open 11, e042354], on pre-symptomatic transmission of SARS-CoV-2 infection [Casey-Bryars et al. BMJ Open (in press)], and on serial interval and the proportion of transmission events that can be attributed to pre-symptomatic transmission, based on contact tracing data from Ireland [McAloon et al. BMC Public Health 21, 805]. In addition, CVERA has produced weekly outputs to IEMAG through the analysis of anonymised mobile phone records and high-resolution geocoded case data, to monitor population movement and the spatial spread of the disease. In addition, a spatio-temporal model has been developed to explore the association between deprivation index and COVID-19 incidence [Madden et al. submitted]. Results suggest that prioritising densely populated, deprived areas (that are at increased risk of comorbidities) during vaccination rollout may capture people that are at risk of infection and, potentially, also those at increased risk of hospitalisation.

A systematic framework of modelling epidemics on temporal networks

A paper by Humphries et al the UCC School of Mathematical Sciences presents a modelling framework for the spread of epidemics on temporal networks. The proposed temporal pair-based model that is systematically derived from this framework offers an improvement over existing pair-based models by moving away from edge-centric descriptions while keeping the description concise and relatively simple. We show that the shift in perspective from individualbased to pair-based quantities enables exact modelling of Markovian epidemic processes on temporal tree networks. On arbitrary networks, the proposed pairbased model provides a substantial increase in accuracy at a low computational and conceptual cost compared to the individual-based model. From the pair-based model, we analytically find the condition necessary for an epidemic to occur, otherwise known as the epidemic threshold. [Humphries et al. Applied Network Science 6, 23].

A large-scale epidemiological model of BoHV-1 spread in the Irish cattle population to support decision-making in conformity with the European Animal Health Law

Infectious bovine rhinotracheitis (IBR), caused by the virus BoHV-1, is currently endemic in Ireland. This is in contrast to many countries in continental Europe where there has been a rapid move towards BoHV-1 freedom. Building on earlier work in support of the bovine viral diarrhoea (BVD) eradication programme, Jonas Brock of Animal Health Ireland (AHI) has developed a largescale epidemiological model of BoHV-1 in the Irish cattle population, which has offered the opportunity to evaluate a range of eradication options for Ireland, both in terms of effectiveness and cost-effectiveness, whilst ensuring compliance with key principles as outlined in the EU Animal Health Law. This work is being undertaken in collaboration with colleagues from the Helmholtz Centre for Environmental Research GmbH -UFZ in Leipzig (Germany), AHI and CVERA. As part of his work, Jonas has made some important methodological advances. In particular, animal movement is now an emergent property of this model, which allows BoHV-1 control scenarios to be modelled into the future, beyond the period when animal movement data are available. [Brock et al. Preventive Veterinary Medicine 192, 105375].

Epidemiological drivers of Bovine Viral Diarrhoea Virus once herd prevalence is low

An eradication programme for bovine viral diarrhoea (BVD) has been in place since 2013, leading to a yearon-year reduction in BVD herd incidence. This study was undertaken to understand the risk of herd infection towards the latter stages of eradication, when herd prevalence is low. In particular, we were interested in the drivers of BVD infection in those herds that were positive for the first time in 2019. A generalised linear mixed model, including a county level random effect, was used to investigate the impact of herd size, management system, measures of proximity to infected herds, and measurements of inward movement. The best-fit model explaining the probability of being a case retained herd size, a network measurement of spatial proximity to BVD infected herds and potential Trojan dams (pregnant animals brought into the herd that could potentially be carrying infected calves in utero). These findings may help target both the end-stages of Ireland's BVD eradication programme and post-eradication surveillance. Miriam Casey, Jamie Tratalos and Simon More of CVERA collaborated with colleagues from Animal Health Ireland and the Department of Agriculture, Food and the Marine to deliver this project

which is currently being prepared for submission to a peer-reviewed journal.

EuFMDiS national foot-and-mouth disease transmission model for Ireland

CVERA worked with the National Disease Control Centre (NDCC) of the Department of Agriculture, Food and the Marine (DAFM) and with the European Commission for the Control of Foot and Mouth Disease (EuFMD) to parameterise the EuFMDis model for Ireland. This model can be used to evaluate various control options to eradicate the foot-and-mouth disease (FMD). It can also evaluate available resource and vaccine supply issues. CVERA collated cattle, pig, sheep and goat population, movement and management system data from Ireland and provided measures of indirect contacts. We collaborated with EuFMDiS modellers and DAFM stakeholders to parameterise a national FMD transmission model for Ireland. The Irish model is used by the NDCC as part of a Europe wide project using FMD transmission simulations to explore various control options and resource usage. A project entitled "Impact of on-farm biosecurity level in pig herds on the spread and control of foot-and-mouth disease" based upon the Irish FMD model was recently presented by EuFMD collaborators at the Open Session of EuFMD.

Livestock disease resilience: from individual to herd level

In the context of animal disease control, vaccination and animal breeding each has the potential to protect the individual, allowing animals to maintain performance in the face of a pathogen challenge. These can be considered 'direct vaccine effects' in veterinary epidemiology, and 'individual disease resilience' in animal breeding. Vaccination and animal breeding also have the potential to protect the herd through 'indirect effects' that impact on the pathogen load in the environment (by reducing susceptibility to infection, reducing the magnitude of infectiousness, and reducing the duration of the infectious period). In animal breeding, this is known as 'herd disease resilience'. As a collaboration between the Roslin Institute in Scotland, Genus-PIC in Germany and CVERA, this paper highlights the shared goals of animal breeding and veterinary epidemiology in animal disease control and seeks to clarify differences in terminology to facilitate further collaborative approaches to sustainable control of infectious diseases in livestock. [Doeschl-Wilson et al. <u>Animal (in press)</u>] will be available shortly.

Protecting bees: a new way forward for risk assessment

A new scientific opinion from the European Food Safety Authority has just been published, to coincide with World Bee Day (20 May), setting out an integrated, holistic framework to assess the combined effects of multiple stressors on honey bees. This work was requested by the European Parliament's Committee for the Environment, Public Health and Food Safety (ENVI), and is a major step forward in efforts to help reverse the decline of insect pollinators in Europe by proposing a new approach to the environmental risk assessment of honey bees. Simon More chaired the working group that developed this opinion. For more information, please visit <u>here</u>.

Key learnings during the development of a generic data collection tool to support assessment of freedom of infection in cattle herds

Many EU Member States have implemented control or eradication programmes for endemic infectious diseases in cattle. However, the design of these programmes varies between countries and comparison is complex. Although output-based methods (to estimate the confidence of freedom) are under development, there is as yet no practical framework that could be applied to a variety of infectious diseases. A data collection tool to address this issue was developed by experts from two international projects, including STOC free (Surveillance Tool for Outcome-based Comparison of FREEdom from infection, www.stocfree.eu) and SOUND control (Standardizing OUtput-based surveillance to control Non-regulated Diseases of cattle in the EU, www.sound-control.eu). This paper outlines the lessons that were learned during the development of this data collection tool, which was used both for the evaluation of data availability and during actual data collection. These lessons will assist with the development of any generic data collection tool for animal disease control purposes, and will also facilitate development of output-based modelling frameworks that aim to calculate confidence of freedom from infection. van Roon et al. Frontiers in Veterinary Science 8, 656336].

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

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