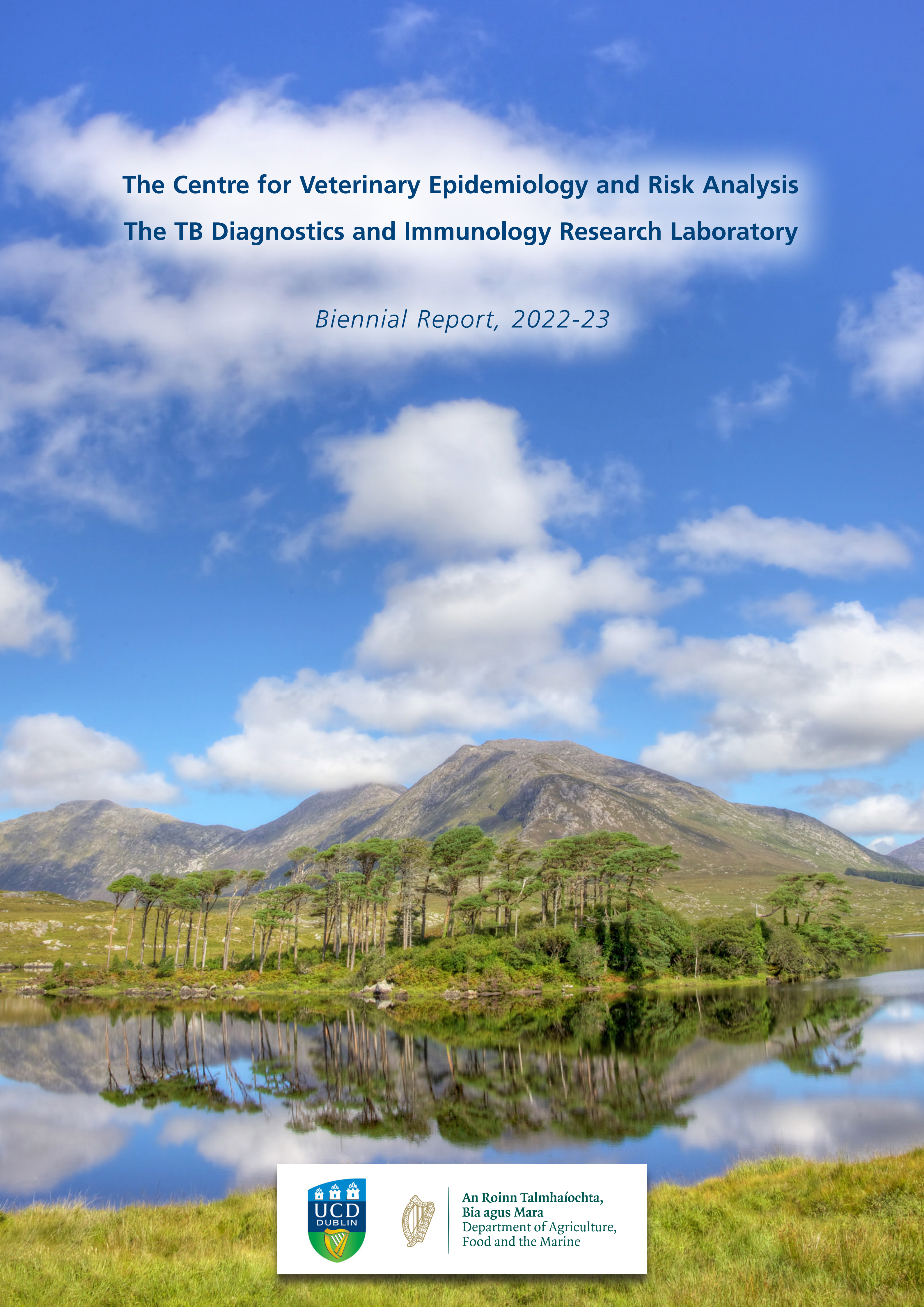

The Centre for Veterinary Epidemiology and Risk Analysis
The TB Diagnostics and Immunology Research Laboratory

Biennial Report, 2022-23

UCD
DUBLIN

An Roinn Talmhaíochta,
Bia agus Mara
Department of Agriculture,
Food and the Marine

The Centre for Veterinary Epidemiology and Risk Analysis

The TB Diagnostics and Immunology Research Laboratory

Biennial Report, 2022-23

S.J. More and D.M. Collins (editors)

H.K. Tin (illustrations)

ISBN: 978-1-910963-760

Preface

The Department of Agriculture, Food and the Marine (DAFM) provides ongoing financial support to two research units within the UCD School of Veterinary Medicine at University College Dublin:

- The UCD Centre for Veterinary Epidemiology and Risk Analysis (UCD CVERA); and
- The TB Diagnostics and Immunology Research Laboratory

These units each work to support DAFM policy, inspectorate and laboratory staff in the area of animal health. UCD CVERA is a national resource centre, providing policy advice, and conducting epidemiological research on a wide range of animal health issues. In addition, UCD CVERA provides general support to government, industry and the veterinary profession. The TB Diagnostics and Immunology Research Laboratory focuses on bovine and badger tuberculosis research.

This report documents work conducted by, or in association with, these UCD-based research units during 2022 and 2023.

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Acknowledgements

The Centre for Veterinary Epidemiology and Risk Analysis

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- UCD School of Veterinary Medicine
- UCD Laboratory of Wildlife Ecology & Behaviour
- UCD School of Public Health, Physiotherapy and Sports Science

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- Instituto Politécnico de Bragança, Bragança, Portugal
- IQinAbox ApS, Værløse, Denmark
- National Centre for Scientific Research, Paris, France
- National Veterinary Institute (SVA), Uppsala, Sweden
- Royal GD, Deventer, The Netherlands
- Swedish University of Agricultural Sciences, Skara, Sweden
- Technopole Agricole et Vétérinaire, Malzéville, France
- University Farm Animal Clinic, Harmelen, the Netherlands
- University of Coimbra, Coimbra, Portugal
- University of Turin, Turin, Italy
- Utrecht University, Utrecht, the Netherlands
- Wageningen University, Wageningen, The Netherlands

The TB Diagnostics and Immunology Research Laboratory

Gamma-interferon (IFN-γ) blood testing and research

Staff from the UCD laboratory acknowledge the help and support of Regional Veterinary Office (RVO) staff in providing samples for the IFN-γ test.

Badger Vaccine development

Staff working on the Badger Vaccine Project acknowledge the contribution and support of colleagues at the mycobacteriology laboratory (DAFM Veterinary Laboratory Service, Backweston, Celbridge, Co. Kildare, Ireland). We also acknowledge the staff at the Regional Veterinary Offices (RVOs) for their contribution of samples and expert knowledge to the "Local transmission risk" research project.

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TB Diagnostics and Immunology Research Laboratory

Gamma-interferon (IFN-γ) blood testing and research

- Eamonn Gormley
- Mairéad Doyle
- Tara Fitzsimons
- Kevina McGill

Badger Vaccine development

- Eamonn Gormley
- Tara Fitzsimons
- Kevina McGill

Overview

The Centre for Veterinary Epidemiology and Risk Analysis

The UCD Centre for Veterinary Epidemiology and Risk Analysis (UCD CVERA) is the national resource centre for veterinary epidemiology in Ireland, located within the UCD School of Veterinary Medicine at University College Dublin. The Centre was initially established as the Tuberculosis Investigation Unit, but has since broadened its remit to cover a wide range of international, national and local animal health matters, including:

- Epidemiological support for the control and eradication of regulatory animal diseases, including the national eradication programme for bovine tuberculosis, and for emergency animal disease preparedness and response;
- Work in support of Animal Health Ireland (www.animalhealthireland.ie), which is providing a proactive, coordinated and industry-led approach in Ireland to non-regulatory animal health concerns (such as mastitis, bovine viral diarrhoea, infectious bovine rhinotracheitis and Johne's disease);
- Epidemiological support for a broad range of other animal health and welfare issues relating to animal health surveillance, on-farm investigations, welfare of farmed livestock and horses, health of companion animals and farmed fish, and international collaboration; and
- In relation to COVID-19, since March 2020, several members of UCD CVERA have contributed to the work of the IEMAG (Irish Epidemiological Modelling Advisory Group) in support of the National Public Health Emergency Team (NPHET). IEMAG has provided advice and expertise to inform of national decision-making in the area of epidemiological data and modelling.

UCD CVERA staff work closely with national policy-makers, both in government and industry. Staff also contribute to training in veterinary medicine, both to undergraduates and postgraduates. A broad range of expertise is represented within the Centre, including database development and management, geographic information systems, biostatistics, veterinary medicine and epidemiology. The Centre is staffed by employees of University College Dublin and of the Department of Agriculture, Food and the Marine (DAFM).

As a result of a second strategic review conducted during 2023, UCD CVERA has clearly defined strategic goals, objectives and expected outcomes, and reports to a Board of Management which is comprised of an independent Chairperson and senior members of DAFM and UCD CVERA. The UCD CVERA Strategic Plan 2024-27 is available at **https://www.ucd.ie/cvera/reports/**

Minister McConalogue (Minister for Agriculture, Food and the Marine, centre) launched the UCD CVERA Strategic Plan 2024-27 during December 2023 with Professor Rory Breathnach (Dean and Head of the UCD School of Veterinary Medicine, right) and Professor Simon More (Director of UCD CVERA, left).

The TB Diagnostics and Immunology Research Laboratory

The Tuberculosis Diagnostics and Immunology Research Laboratory based at UCD engages in routine IFN-γ testing of blood samples submitted from Regional Veterinary Offices. Arising from the large number of samples tested each year, there is a focus, in collaboration with CVERA, on analysing the data to gauge the performance of the test under Irish conditions and searching for ways to improve the accuracy of testing. The laboratory also carries out basic research to improve the performance of the IFN-γ test and develop novel diagnostic tests for bovine TB. The laboratory staff liaises with colleagues working in institutions at home and abroad to share knowledge of the test and keep abreast of any new developments that may impact on its performance.

A second key area of work for the laboratory is the badger vaccine programme of research with the objective to use vaccination to control tuberculosis in badgers and to break the link of infection to cattle. With the implementation of a national vaccination programme underway, the UCD laboratory continues to provide key scientific support to vaccine research projects and the delivery of the strategy.

Further information

In this report, projects are either:

- Complete projects, which includes those projects where relevant peer-reviewed papers, or equivalent, have been published in 2022/23 and early 2024, or
- Current projects, which includes the balance of active projects covering the spectrum from an advanced research concept through to final write-up or manuscript in press.

In addition to scientific projects, UCD CVERA provides scientific support to a range of national organisations. Examples of epidemiological, statistical, geographical and database related scientific support provided by UCD CVERA staff are also included.

Manuscript preparation is conducted in accordance with Uniform Requirements for Manuscripts Submitted to Biomedical Journals of the International Committee of Medical Journal Editors (previously the Vancouver Group). For further information, see www.icmje.org. Guidelines for the transparent reporting of specific study types (for example, the CONSORT statement for transparent reporting of trials, www.consort-statement.org) are followed. An up-to-date list of all peer-review papers produced by, or in association with, the UCD Centre for Veterinary Epidemiology and Risk Analysis, and /or the TB Diagnostics and Immunology Research Laboratory is available at **www.ucd.ie/cvera**. Follow us on Twitter **@ucd_cvera**.

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Bovine tuberculosis

bTB in cattle

The role of wildlife in bovine TB

Supporting studies

bTB statistics

National maps

bTB surveillance

Gamma-interferon (IFN-γ) blood testing and research

The gamma-interferon (IFN-γ) assay is used as a tool by ERAD to assist in the eradication of bovine tuberculosis from the national herd. In addition to the UCD laboratory which primarily takes in samples from the Leinster area and neighbouring counties, the Cork Blood Testing Laboratory (BTL) and FarmsLab Diagnostics (Elphin, Co. Roscommon) provide full IFN-γ testing in infected herds from the southern and northern / western regions of the country respectively. The Sligo Regional Veterinary Laboratory carries out the first (stimulation) stage of the assay, with blood plasmas transported to UCD for the second stage ELISA step. In the period 2022-2023, 59,333 blood samples were submitted to the UCD laboratory for IFN-γ testing.

The samples submitted for IFN-γ test currently originate mainly from:

- bovine reactor re-test herds, where the IFN-γ test is used to diagnose infected animals that are missed by the SICTT (false negatives). Among all of the diagnostic tests carried out, approx. 10% were classified as positive.
- SICTT reactor animals where the IFN-γ test is used to confirm the exposure status of SICTT positive animals. Among all of these tests carried out, approx. 70% were classified as positive.

The laboratory continues to conduct research with a view to improving the performance of the assay under Irish conditions. It also carries out studies to identify additional cytokine biomarkers of bTB infection and to understand the complex interplay between the expression of cytokines that impact on the levels of IFN-γ produced in the assay. The studies have reached a stage where they are now being tested and evaluated in high-risk relapse herds. The laboratory, along with CVERA and DAFM has engaged in an analysis of the impact of changing the interpretation cut-off for the IFN-γ test on the disclosure of bTB infected animals in herds (published 2024). We also carry out research on estimating the potency of tuberculin using the IFN-γ assay. The lab is also engaged in active research with groups based at UCD and elsewhere to use advanced transcriptomic tests to better understand the specific immune responses to infection with tuberculosis.

High-resolution transcriptomics of bovine purified protein derivative-stimulated peripheral blood from cattle infected with *Mycobacterium bovis* across an experimental time course

Correia, C.N.[1], McHugo, G.P.[1], Browne, J.A.[1], McLoughlin, K.E.[1], Nalpas, N.C.[1], Magee, D.A.[1], Whelan, A.O.[2], Villarreal-Ramos, B.[2], Vordermeier, H.M.[2], Gormley, E.[3], Gordon, S.V.[3, 4], MacHugh, D.E.[1, 4]

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***Tuberculosis* 136, 102235 (2022)**

https://doi.org/10.1016/j.tube.2022.102235

Improved bovine tuberculosis (bTB) diagnostics with higher sensitivity and specificity are urgently required. A better understanding of the peripheral blood transcriptional response of *Mycobacterium bovis*-infected animals after bovine purified protein derivative (PPD-b) stimulation of whole blood—an important component of current bTB diagnostics– will provide new information for development of better diagnostics. RNA sequencing (RNA-seq) was used to study the peripheral blood transcriptome after stimulation with PPD-b across four time points (–1 wk pre-infection, and +1 wk, +2 wk, and +10 wk post-infection) from a 14-week M. bovis infection time course experiment with ten age-matched Holstein-Friesian cattle. In vitro PPD-b stimulation of peripheral blood from M. bovis-infected and non-infected cattle elicited a strong transcriptional response. Comparison of PPD-b stimulated, and unstimulated samples revealed higher expression of genes encoding cytokine receptors, transcription factors, and interferon-inducible proteins. Lower expression was seen for genes encoding proteins involved in antimicrobial activity, C-type lectin receptors, inhibition of signal transduction, and genes encoding metal ion transporters. A transcriptional signature associated with the peripheral blood response to PPD-b stimulation consisting of 170 genes was identified exclusively in the post-infection time points. Therefore, this represents a panel of potential biomarkers of *M. bovis* infection.

Investigation of the association between the Enferplex bovine tuberculosis antibody test and the future risk of bovine tuberculosis in Irish cattle in infected herds: a pilot field study

Madden, J.M.[1], Casey-Bryars, M.[1], More, S.J.[1, 2], Barrett, D.[3], Gormley, E.[2], Ryan, E.[3]

[1] UCD CVERA, [2] UCD School of Veterinary Medicine, [3] DAFM

***Veterinary Research Communications* 48, 555–561 (2024)**

https://doi.org/10.1007/s11259-023-10200-3

The Single Intradermal Comparative Tuberculin Test (SICTT) and the interferon-gamma (IFN-γ) assay are the approved diagnostic tests for bovine tuberculosis (bTB) in Ireland. The aim of this pilot study was to explore if there was any added diagnostic benefit from applying the Enferplex bTB test (an antibody test) in severe bTB herd breakdowns after the removal of cattle that had tested positive to the SICTT and the IFN-γ test. In addition to the normal bTB testing and management protocols, the animals in these herds that tested negative to SICTT and the IFN-γ test were followed forward for a period of two years. All animals were tested by Enferplex at enrolment. The time to subsequent bTB detection (diagnosed with SICTT/IFN-γ tests or detection of visible lesions at routine slaughter) for animals that tested positive or negative to the Enferplex bTB test at the start of the study was compared using Kaplan–Meier survival curves and Cox based survival models. Of the 484 enrolled animals (from 11 herds), 171 (35.3%) and 151 (31.1%) initially tested positive in the Enferplex assay under the high sensitivity and high specificity interpretation settings respectively. The results of the survival analysis showed that there was no difference in the survival time to a positive diagnosis with bTB during the follow-up period between animals initially classified as positive and negative by the Enferplex test. Further research is warranted to explore the potential benefit of using the Enferplex test in other scenarios.

The impact of changing the cut-off threshold of the interferon-gamma (IFN-γ) assay for diagnosing bovine tuberculosis in Ireland

Madden, J.M.[1], O'Donovan, J.[2], Casey-Bryars, M.[1], Sweeney, J.[3], Messam, L.L.[4], McAloon, C.G.[4], More, S.J.[1, 4], Kenny, K.[5], Ryan, E.[2], Gormley, E.[4]

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***Preventive Veterinary Medicine* 224, 106129 (2024)**

https://doi.org/10.1016/j.prevetmed.2024.106129

In Ireland, the interferon-gamma (IFN-γ) assay is routinely used as an ancillary test interpreted in parallel with the single intradermal comparative tuberculin test (SICTT) to maximize the detection of bovine tuberculosis (bTB) infected animals. Up until 2018, a positive test result was recorded in the IFN-γ ELISA assay following whole blood stimulation with purified protein derivative (PPD)-bovine (B), PPD-avian (A) and nil sample (N), using the interpretation criteria, B-N > 50 optical density units (OD), B > 100 and B-A > 0. Following a review of available data, the threshold of the B-A component changed to B-A > 80. As predicting the impact of changing the cut-off thresholds for the IFN-γ test *de novo* is challenging, the aims of this study were to follow animals that initially tested negative using the new IFN-γ assay interpretation criteria and investigate their future risk of disclosure with bTB, with a focus on animals that otherwise would have been removed when using the older interpretation criteria (0 < B-A ≤ 80). Enrolled animals (n = 28,669 cattle from 527 herds) were followed up for two years (2019–2021), or to point of bTB detection or death. At the end of follow-up, 1151 (4.0%) of enrolled animals were bTB cases. The majority of these cases were diagnosed using SICTT (80.5%). The cumulative number of positive animals that would have been removed if the old cut-off (0 < B-A ≤ 80) was used amounted to 1680 cattle (5.9% of the enrolled cohort). Of these, 127 (7.5%) were diagnosed with bTB during follow-up. In contrast, 1024 of the 1151 cattle which subsequently tested positive during the study period following a negative IFN-γ test would not have been identified with the old or new IFN-γ cut-off criteria. Survival analysis showed that animals that would have been removed under the old interpretation criteria were at increased risk of a positive diagnosis with bTB during follow-up compared to other test negative animals. A newly developed risk prediction model (using a Cox proportional hazard model) showed that age, animal number of SICTT tests, number of inconclusive SICTT tests, B-A (IFN-γ assay), B-N (IFN-γ assay), animals from store herds and the percentage of the rest of the herd that were positive during the breakdown were statistically significantly associated with bTB detection. However, inclusion of the IFN-γ OD variables did not show added value in terms of prediction performance of the model.

Spatial representation of the specificity of the SICCT test in cattle herds in Ireland

McGrath, G. et al.
UCD CVERA

There is a longstanding and commonly held belief amongst some veterinary practitioners and farmers that parts of Ireland experience higher rates of false positive Single Intradermal Comparative Cervical Tuberculin (SICCT) skin tests in cattle. This is thought to be caused by non-tuberculous environmental mycobacteria. This project will explore the spatial distribution of Irish SICCT reactors believed to be false positive singletons.

Near real-time spatio-temporal analysis of bovine tuberculosis in Irish cattle populations

Madden, J. et al.
UCD CVERA

The emergence of clustered outbreaks of bovine tuberculosis (bTB) poses a significant challenge to bTB eradication in Ireland. A bTB cluster or 'hotspot' is currently defined following the exceedance of a defined number of reactor herds within an electoral division. However, this approach is inadequate for describing the spatial and temporal aspects of clusters. Further, despite agreed national operating rules in the national eradication programme, there may be variations at administrative levels which alter the time to detection of potential bTB clusters. This study will explore methodologies to identify spatial regions with unusually elevated bTB risk. It will build on an existing spatio-temporal modelling framework but crucially, it will attempt to incorporate data in near real-time to monitor how bTB outbreaks may be developing.

Quantifying the age-specific risk of bovine tuberculosis in cattle in Ireland

Madden, J.M. et al.
UCD CVERA

Most infectious diseases are age dependent. However, for bTB in Ireland, age-dependent risks have not yet been quantified. This project will focus on an extensive investigation of animal-level data (as opposed to herd-level) where the overall aim is to determine if there is an association between the age of an animal and bTB diagnosis (or more precisely, reaction to skin test or lesions etc.) and if so, to determine if this association varies by breed and herd type. We will conduct a comprehensive analysis of the association between age and several bTB-related outcomes.

bTB control

bTB eradication in Ireland: where to from here?

More, S.J.[1, 2]
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***Irish Veterinary Journal* 76, 11 (2023)**

https://doi.org/10.1186/s13620-023-00239-8

In an earlier paper from 2019 (*Irish Veterinary Journal* 72, 3 (2019)) **https://doi.org/10.1186/s13620-019-0140-x**), this author concluded that successful eradication of bovine tuberculosis (bTB) from Ireland by 2030 would be unlikely, given control strategies in place at that time plus the addition of badger vaccination. He argued that additional measures will be needed, broadly focusing on bTB risks from wildlife, risk-based cattle controls, and industry commitment. This paper considers these points in further detail. Ongoing monitoring of the badger vaccination programme (which is progressively being rolled out nationally) and associated research will be critical, with a focus both on programme inputs and outcomes. The direct contribution of cattle movements to bTB restrictions in Ireland has been evaluated. However, it is the indirect role of cattle movements in bTB restrictions that is likely of greater importance, particularly towards the latter phase of the eradication programme. In other national programmes, a range of risk-based approaches have been used to address the challenge of residual infection in cattle (that is, the presence of animals with persistent but undetected infection), and similar approaches are needed in Ireland. A number of authors have highlighted the critical importance of industry commitment to programme success, and the key role of programme governance to achieving this. In this commentary, the author briefly considers experiences from Australia and New Zealand in this regard. The author also reflects on the challenge of uncertainty in decision-making, the relevance to Ireland of lessons from other countries, and the potential contribution of new methodologies in support of the national programme. 'The tragedy of the horizon' was a term first used in the context of climate change, referring to the costs imposed on future generations that the current generation has no direct incentives to fix. This concept is equally relevant to bTB eradication in Ireland, where current decisions will have long-term consequences for future generations, including both the general public (through the Exchequer) and future Irish farmers.

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

Barroso, P.[1], Breslin, P.[2], McGrath, G.[3], Madden, J.M.[3], Tratalos, J.A.[3], More, S.J.[3, 4], Ryan, E.[2], Byrne, A.W.[5], Barrett, D.[5]

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***Preventive Veterinary Medicine* 198, 105542 (2022)**

https://doi.org/10.1016/j.prevetmed.2021.105542

Bovine tuberculosis (bTB) is a chronic infectious disease caused by *Mycobacterium bovis* which results in a significant economic cost to cattle industries and governments where it is endemic. In Ireland, the European badger is the main wildlife reservoir of infection. 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: pre-construction (2011–2014), construction (2015–2017) and post-construction (2018–2019). We selected 1543 herds situated, based on proximity, between >50 m and <5 km of the roadworks, and extracted information about their herd-size, herd-type, inward animal movements, bTB history, and distance to the roadworks. Generalized linear mixed models were performed, whose outcome were whether a herd experienced a bTB breakdown with ≥1 or ≥3 standard reactor/s, respectively. 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 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. The potential for badger social group disturbance leading to the spatial spread of infection to cattle herds, as previously described in the United Kingdom, could be a hypothetical mechanism to explain these findings. However, our findings are not consistent with previous Irish studies, including recent work from another road construction project, albeit running alongside and cross over an existing road rather than construction of a new road as in this case, or experiences from national targeted badger removal. 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.

Reprinted from Preventive Veterinary Medicine *198, Barroso et al, Is there an association between road building and bovine tuberculosis herd risk? A three time-points study in Ireland, 2011-2020, 105542, Copyright 2022, with permission from Elsevier.*

Bovine tuberculosis in youngstock cattle: A narrative review

Byrne, A.W.[1], **Barrett, D.**[1, 2], **Breslin, P.**[2], **Fanning, J.**[1], **Casey, M.**[3], **Madden, J.M.**[3], **Lesellier, S.**[4], **Gormley, E.**[5]

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***Frontiers in Veterinary Science* 9, 1000124 (2022)**

https://doi.org/10.3389/fvets.2022.1000124

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, remains a high-priority global pathogen of concern. The role of youngstock animals in the epidemiology of bTB has not been a focus of contemporary research. Here we have aimed to collate and summarize what is known about the susceptibility, diagnosis, transmission (infectiousness), and epidemiology to *M. bovis* in youngstock (up to 1-year of age). Youngstock are susceptible to *M. bovis* infection when exposed, with the capacity to develop typical bTB lesions. Calves can be exposed through similar routes as adults, via residual infection, contiguous neighborhood spread, wildlife spillback infection, and the buying-in of infected but undetected cattle. Dairy systems may lead to greater exposure risk to calves relative to other production systems, for example, via pooled milk. Given their young age, calves tend to have shorter bTB at-risk exposure periods than older cohorts. The detection of bTB varies with age when using a wide range of ante-mortem diagnostics, also with post-mortem examination and confirmation (histological and bacteriological) of infection. When recorded as positive by ante-mortem test, youngstock appear to have the highest probabilities of any age cohort for confirmation of infection post-mortem. They also appear to have the lowest false negative bTB detection risk. In some countries, many calves are moved to other herds for rearing, potentially increasing inter-herd transmission risk. Mathematical models suggest that calves may also experience lower force of infection (the rate that susceptible animals become infected). There are few modeling studies investigating the role of calves in the spread and maintenance of infection across herd networks. One study found that calves, without operating testing and control measures, can help to maintain infection and lengthen the time to outbreak eradication. Policies to reduce testing for youngstock could lead to infected calves remaining undetected and increasing onwards transmission. Further studies are required to assess the risk associated with changes to testing policy for youngstock in terms of the impact for within-herd disease control, and how this may affect the transmission and persistence of infection across a network of linked herds.

Estimating the hidden burden of bovine tuberculosis in Ireland

Casey, M. et al.

UCD CVERA

Effective control of bovine tuberculosis (bTB) in cattle is vital for Ireland's agri-food industry. Yet, despite expenditure of almost €100 million per annum on bTB surveillance and control, progress towards eradication has plateaued since 2015. Progress is inhibited by: imperfect diagnostic tests, gaps in our understanding of transmission and detection patterns of bTB, and barriers to stakeholder support for potential control measures. In this study, we aim to utilize a dynamic model of bTB transmission and detection in Irish cattle herds to better understand these processes and investigate the impact of potential interventions on the burden of bTB in cattle. The authors aim to provide a tool to stakeholders with which to better understand bTB transmission and diagnosis, and to explore the potential impact of interventions.

Post-quota effects on TB risk in dairy herds in Ireland?

Byrne, A.W. et al.

DAFM One-Health and Welfare Scientific Support Unit

Bovine tuberculosis remains a priority endemic disease in Ireland. There have been recent increasing trends in breakdown risk, and the average number of reactors disclosed per breakdown. Costs to the state are increasing due to compensation costs. Given the complex epidemiology of bTB in Ireland, there are several potential factors that may be impacting these changing dynamics, including the potential for residual infection causing recurrence, changes in the force of infection from wildlife or environmental sources, or demographic and industry structural changes that could increase spread and dissemination of infection within and across herds. The latter could be attributed to factors like increasing herd sizes or the movement of animals, which are known risk factors for bTB breakdown risk. In the dairy industry, there has been a rapid increase in average herd size over the last decade, related to changes in the milk production regulatory environment (the abolition of quotas). Despite the known epidemiology of bTB in Ireland, there is still uncertainty regarding the drivers of the recent increase. Furthermore, there has also been scepticism that increasing herd size, related to changes in policy relating to quotas, is an actual explanatory factor for the recent increases. This study will examine the risk of breakdown associated with an increase in herd size.

Estimating the burden of cattle disease in Ireland to inform private and public sector animal health investment policy considerations: A project contributing to the Global Burden of Animal Disease programme

Murray, E.-J. et al.

UCD School of Veterinary Medicine

For this project, estimates were generated of the livestock biomass and its associated stock value of the Irish cattle population across ten years, using monthly and annual data from the animal health systems in Ireland. Two animal-level linear models were created using the bTB-positive reactor slaughter records, including age, breed type, sex, liveweight, and value, and adjusted for month and year. The models were run via the national movement data, giving each animal a biomass (kg) and stock value (€) figure. The estimates were then aggregated at herd level. The herd types were classified based on the Brock et al. (2021) herd classification tree model. This study demonstrates the biomass and stock value at sector level and at herd level within year and between years. The estimates will be particularly informative to policymakers when planning new agricultural programmes, animal health surveillance, economic assessments, antimicrobial usage estimates, and analysing the structure of GHG emissions across production systems.

Creating a surveillance methodology to optimise the national phylogenetic baseline of *Mycobacterium bovis* in Ireland using a multidisciplinary team approach

O'Shaughnessy, J. et al

DAFM Central Veterinary Research Laboratory

The DAFM Central Veterinary Research Laboratory maintains a bionumerics database comprising of approximately 2,000+ genome sequenced *Mycobacterium bovis* isolates, derived mostly from cattle, fewer badgers and a small number of other species. The genome data for the cattle were obtained from a geographical spread of isolates focussing on 'home born' bovines. Additional isolates were acquired for specific projects relating to areas of counties Wicklow, Monaghan and Clare, as well as isolates arising from specific epidemiological queries from Regional Veterinary Offices (RVOs). Having a comprehensive sample of national *M. bovis* genetic diversity is essential to using Whole Genome Sequencing (WGS) as a reliable field tool in helping to determine putative source of infection. Several considerations must be given to ensure there is sufficient depth of resolution in such a sample of *M. bovis* diversity including an adequate spatial and temporal distributions of samples, a clear distinction between homebred and purchased in animals, a complete record of badger removal and vaccination in the relevant areas, and an ability to collect additional samples to identify gaps in phylogenetic clades. By examining the samples currently sequenced, we aim to create an optimised surveillance strategy to avail of retrospectively collected and banked tissue from cattle and badgers and prospective identification of priority areas to sample. This will provide a national 'baseline' of *M. bovis* genetic diversity, within a spatial and temporal framework, in an efficient manner which will in turn support practical decision making for epidemiological investigations.

Bayesian modelling of bTB transmission factors in Irish cattle herds

Sweeney, J. et al.

University of Limerick

This study will investigate the drivers and transmission routes for bTB for the first time at a herd level using a spatiotemporal Bayesian modelling framework. The modelling framework employed allows us to include transfers of cattle between farms from the previous year, spatial risk associated for every farm, and additional covariates (herd type, herd size, imports, etc.). While the current project looks at annual level data, the model will work on finer time scales, say quarterly, though the computation cost associated with this finer scale has yet to be investigated.

Irish cattle movements

Can Ingoing Contact Chains and other cattle movement network metrics help predict herd-level bovine tuberculosis in Irish cattle herds?

Tratalos, J.A.[1], Fielding, H.R.[2], Madden, J.M.[1], Casey, M.[1], More, S.J.[1, 3]

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Preventive Veterinary Medicine **211, 105816 (2023)**

https://doi.org/10.1016/j.prevetmed.2022.105816

We used logistic regression to investigate whether the risk of an Irish cattle herd undergoing a bovine tuberculosis (bTB) breakdown increased with the size of the Ingoing Contact Chain (ICC) of previous herd to herd cattle movements, in a sequence up to eight moves back from the most recent, direct, movement into the herd. We further examined whether taking into account the bTB test history of each herd in the chain would improve model fit. We found that measures of cattle movements directly into the herd were risk factors for subsequent bTB restrictions, and the number of herds that animals were coming from was the most important of these. However, in contrast to a previous study in Great Britain, the ICC herd count at steps more remote than direct movements into the herd did not result in better fitting models than restricting the count to direct movements. Restricting the ICC counts to herds which had previously or would in the future test positive for bTB resulted in improved model fits, but this was not the case if only the previous test status was considered. This suggests that in many cases bTB infected animals are moving out of herds before being identified through testing, and that risk-based trading approaches should not rely solely on the previous test history of source herds as a proxy for future risk. Model fit was also improved by the inclusion of variables measuring bTB history of the herd, bTB in neighbouring herds, herd size, herd type, the movement network measures "in strength" and "betweenness", altitude, modelled badger abundance and county. Rainfall was not a good predictor. The most influential measures of bTB in nearby herds (a proxy for neighbourhood infection) were the proportion of herds with a history of bTB whose centroids were within 6 km, or whose boundaries were within 4 km, of the index herd. As well as informing national control and surveillance measures, our models can be used to identify areas where bTB rates are anomalously high, to prompt further investigation in these areas.

Regionalisation

Development and application of criteria that could be used to guide regional selection as part of an area-based approach to bTB eradication in Ireland

Tratalos, J. et al.

UCD CVERA

Regionalisation is a well-recognised approach to the control and eradication of animal diseases. It refers to the establishment and maintenance of distinct subpopulations of animals with specific health status within a territory, either through geographic separation (zoning) or management and husbandry practices related to biosecurity (compartmentalisation). Typically, regionalisation leads to the establishment of geographical boundaries around subpopulation of farms with similar disease status to which targeted control measures are imposed, such as movement restrictions, testing and/or vaccination, to minimise the risk of infection/disease spreading from higher to lower risk regions. Collectively this approach ensures forward momentum towards an improving national disease situation. Regionalisation has been a central strategy in many national control and eradication programmes for bovine tuberculosis (bTB), including Australia, Mexico, New Zealand, Spain, the United Kingdom, and the USA. As with other animal health issues, regionalisation is being used to create ‘risk boundaries’, thereby allowing disease control and surveillance to be differentiated on the basis of risk, to prioritise resource allocation, and to protect lower risk areas. In contrast to the international experience, the Irish bTB eradication programme does not differ by region. Rather, controls vary at a more granular level on the basis of the infection history of herds and localities. Given this context, the TB Forum has considered a number of policy options, including the potential of regionalisation in bTB eradication. The aim of this study is to calculate metrics which show the likely impact on herds of such an approach, specifically the number and type of cattle trades which would be prevented by risk-based trading.

A spatial epidemiological analysis of bovine tuberculosis in cattle herds in The Burren, County Clare, Ireland

Tratalos, J. et al.

UCD CVERA

Bovine tuberculosis (bTB) is endemic amongst the cattle population of Ireland, and mechanisms of transmission of infection include contact between cattle, within the same herd and from other herds (the latter both across farm boundaries and through trade between herds), contact with infected wildlife populations, especially badgers *(Meles meles)*, and, possibly, exposure to the causative organism, *Mycobacterium bovis*, residing in the wider environment. However, the relative contribution of each of these factors is poorly understood and is likely to vary from location to location. The Burren, which is located in County Clare on the west coast of Ireland is known for its uplands which are characterized by glaciated karst geology and the associated floral communities. Known locally as ‘winterage’, pastures are left ungrazed during the summer and cattle are moved onto them for the winter, typically from lower lying summer pastures. At the time that this study was conceived (in 2020), bTB prevalence in Burren cattle was believed to be unusually high relative to the rest of Ireland. The reasons for this have not been determined but a number of contributing localised factors have been suggested including: a poor diet, limited winter housing, a narrower genetic profile, cattle movement, wildlife patterns, and parasites leading to suppressed immune systems. This study documented the characteristics of Burren herds of relevance to bTB transmission and to investigate the possible causes of high rates of bTB there.

Farm fragmentation

Spatial structure of farms in Ireland (fragmentation)

McGrath, G.
UCD CVERA

Farm fragmentation refers to spatial disaggregation of a farm into smaller, often highly separated parcels of land. Ireland has a high proportion of fragmented farms; an issue not unique to Ireland. Spatial analysis of farms depends on assigning a location to livestock. Where a farm is heavily fragmented, this becomes problematic and introduces uncertainty. With increasingly sophisticated analytical techniques, reducing this uncertainty is imperative. This study explores techniques to quantify the extent and regional variation in fragmentation and the between-fragment distances of fragmented farms in Ireland. We will explore methodologies to help account for farm fragmentation in geospatial analysis and to assist in surveillance and field epidemiology. Having an understanding of the extent of fragmentation in Ireland will help inform policy makers across a number of areas from disease control to environmental policies.

The epidemiology of *Mycobacterium bovis* in badgers

The use of contact tracing and WGS to identify epidemiological links between identical isolates of *M. bovis* from cattle and badgers in Co. Monaghan

Harvey, N. et al.

UCD CVERA & DAFM

The identification (in time, in space, and at an animal level) of transmission events in bTB is difficult to establish due to the biology of the pathogen *(M. bovis)*, diagnostic tests available, and the heterogeneity of transmission pathways that occur in highly endemic populations. Consequently, the time from infection to identification can be difficult to quantify. Currently, contact tracing is the main epidemiological tool used to investigate bTB breakdowns at herd and individual animal level. Whole genome sequencing analysis technology has been developed as part of the bTB Genie project. Technology developed in that project, namely SNiP Genie, can sequence bTB isolates and identify the single nucleotide polymorphisms (SNP) that exists in an isolate. Isolates that are 5-10 SNP variations of each other are considered evidence of recent transmission. Data from the bTB Genie project have highlighted clades of isolates that exhibit 5 SNP variations of each other. These clades have been identified in geographically diverse locations. This project aims to construct an automated decision tree to explore the epidemiological links between these recent transmissions and to use data from the Irish cattle population as a proof of concept.

BCG vaccination in badgers

The badger vaccine development programme

The national programme of BCG vaccination of badger populations against tuberculosis is ongoing. Over many years leading to the implementation of the vaccine strategy the team at UCD has published much research on development of the BCG vaccine for use in badgers in experimental and field settings. In the most recently published study, we investigated the risk of vaccinated but non-infected badgers testing positive in the field-test for tuberculosis in badgers. The study can be summarised as follows:

Seroconversion against antigen MPB83 in badgers* (Meles meles) *vaccinated with multiple doses of BCG strain Sofia
Until recently the BCG Danish strain 1331, manufactured in Denmark, was the only commercially licensed BCG vaccine for use in the European Union and the vaccine of choice for delivery to badgers in Ireland. However, due to a shortage of supply of this vaccine strain, the BCG Sofia SL222 vaccine strain, derived from the Russian BCG master stock strain has been used as an alternative vaccine strain in Ireland. With commencement of badger vaccination in Ireland with the BCG Sofia strain, a question was raised as to whether vaccination would result in detectable serological responses against the MPB83 antigen (produced by BCG Sofia), thus compromising the test performance of the DPP VetTB assay (MPB83 is used to diagnose TB in badgers in the field). The principle objective of this study was to vaccinate and boost a group of captive TB-free badgers by the intra- muscular route with BCG Sofia strain to measure serological and cell- mediated immune responses over the course of 18 months post- vaccination. The results showed that primary vaccination with a single dose of BCG Sofia did not generate any test positive responses in the DPP VetTB assay when serum or whole blood was tested. Following booster vaccination, more animals tested positive in serum than with whole blood and the duration of positive responses was also longer when measured in serum. These results helped to inform policy decisions on booster vaccinations and when vaccinated badgers could be tested for evidence of TB infection.

Other badger vaccine projects
The laboratory provides scientific support for the DAFM national badger vaccination programme. Staff are actively involved in the "Local transmission risk" research project by assisting to process field blood samples for antibody testing.

Protective immunity against tuberculosis in a free-living badger population vaccinated orally with *Mycobacterium bovis* Bacille Calmette–Guérin

Gormley, E.[1], Ní Bhuachalla, D.[1, 2], Fitzsimons, T.[1], O'Keeffe, J.[2], McGrath, G.[3], Madden, J.M.[3], Fogarty, N.[4], Kenny, K.[4], Messam, L.L.McV.[1], Murphy, D.[1, 2], Corner, L.[1]

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***Transboundary and Emerging Diseases* 69, e10–e19 (2022)**

https://doi.org/10.1111/tbed.14254

Vaccination of badgers with *Mycobacterium bovis* Bacille Calmette–Guérin (BCG) has been shown to protect badgers against tuberculosis in experimental trials. During the 3-year County Kilkenny BCG vaccine field study, badgers were treated orally with placebo (100% in Zone A), BCG (100% in Zone C) or randomly assigned 50%: 50% treatment with BCG or placebo (Zone B). At the end of the study, 275 badgers were removed from the trial area and subjected to detailed post-mortem examination followed by histology and culture for *M. bovis*. Among these badgers, 83 (30.2%) were captured for the first time across the three zones, representing a non-treated proportion of the population. Analysis of the data based on the infection status of treated animals showed a prevalence of 52% (95% CI: 40%–63%) infection in Zone A (placebo), 39% (95% CI: 17%–64%) in Zone B (placebo) and 44% (95% CI: 20%–70%) in Zone B (BCG vaccinated) and 24% (95% CI: 14%–36%) in Zone C (BCG vaccinated). There were no statistically significant differences in the proportion of animals with infection involving the lung and thoracic lymph nodes, extra-thoracic infection or in the distribution and severity scores of histological lesions. Among the 83 non-treated badgers removed at the end of the study, the infection prevalence of animals in Zone A (prevalence = 46%, 95% CI: 32%–61%) and Zone B (prevalence = 44%, 95% CI: 23%–67%) was similar to the treated animals in these zones. However, in Zone C, no evidence of infection was found in any of the untreated badgers (prevalence = 0%, 95% CI: 0%–14%). This is consistent with an indirect protective effect in the non-vaccinated badgers leading to a high level of population immunity.
The results suggest that BCG vaccination of badgers could be a highly effective means of reducing the incidence of tuberculosis in badger populations.

Seroconversion against antigen MPB83 in badgers *(Meles meles)* vaccinated with multiple doses of BCG strain Sofia

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***Research in Veterinary Science* 149, 119–124 (2022)**

https://doi.org/10.1016/j.rvsc.2022.06.011

Serological diagnosis of *Mycobacterium bovis* infection in badgers *(Meles meles)* has relied primarily on antibody recognition of MPB83, a sero-dominant antigen of *M. bovis*. Most vaccine studies in badgers to date have used the Bacille Calmette-Guerin (BCG) Danish strain, a low producer of MPB83. Due to a supply shortage of the BCG Danish strain, the BCG Sofia SL222 strain has been considered as an alternative vaccine. This strain is a high producer of MPB83 raising the possibility that vaccinated animals will test sero-positive in diagnostic assays that use this antigen. In this study we vaccinated a group of eleven badgers with BCG Sofia SL222 by injection via the intramuscular route and a booster vaccine dose was similarly delivered at 12 weeks and 64 weeks. Primary vaccination did not result in measured detection of antibodies against MPB83 in any badger during the first twelve weeks using serum or whole blood tested by the Dual Path Platform (DPP) VetTB, however, MPB83 antibodies were detected in a semi-quantitative ELISA assay. Following delivery of booster BCG at 12 weeks and 64 weeks, antibody responses against MPB83 were recorded in badgers using whole blood and serum on DPP VetTB and by ELISA. At all time points, vaccination was also associated with the in vitro production of gamma interferon (IFN-γ) following stimulation of lymphocytes with bovine and avian tuberculin (PPD) but not with MPB83 or *M. bovis* specific antigen CFP-10. The results indicate that serological diagnosis of tuberculosis using tests that target MPB83 may be compromised if badgers are repeatedly vaccinated with BCG Sofia.

Simulating partial vaccine protection: BCG in badgers

Smith, G.C.[1], Barber, A.[2, 3], Breslin, P.[4], Birch, C.[5], Chambers, M.[6], Dave, D.[5], Hogarth, P.[5], Gormley, E.[7], Lesellier, S.[5, 8], Balseiro, A.[9, 10], Budgey, R.[1]

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***Preventive Veterinary* Medicine 204, 105635 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105635

In wildlife disease management there are few diseases for which vaccination is a viable option. The human vaccine BCG has been used for the control of bovine tuberculosis in badgers since 2010 and is expected to increase. Understanding the long-term effects of repeated vaccination campaigns on disease prevalence is vital, but modelling thus far has generally assumed that a vaccine provides perfect protection to a proportion of the population, and that animals exposed to a repeated vaccination have a second independent chance of becoming protected. We held a workshop with experts in the field to obtain consensus over the main pathways for partial protection in the badger, and then simulated these using an established model. The available data supported the possibility that some individuals receive no benefit from the BCG vaccine, others may result in a delayed disease progression and in the remaining animals, vaccine protected the individual from any onward transmission. Simulating these pathways using different levels of overall efficacy demonstrated that partial protection leads to a reduced effect of vaccination, but in all of the identified scenarios it was still possible to eradicate disease in an isolated population with no disease introduction. We also identify those potential vaccination failures that require further investigation to determine which of our proposed pathways is the more likely.

Infection control strategies in a multi-host system

Inferring bovine tuberculosis transmission between cattle and badgers via the environment and risk mapping

Chang, Y.[1], Hartemink, N.[1, 2], Byrne, A.W.[3], Gormley, E.[4], McGrath, G.[5], Tratalos, J.A.[5], Breslin, P.[6], More, S.J.[4, 5], de Jong, M.C.M.[1]

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Frontiers in Veterinary Science 10, 1233173 (2023)

https://doi.org/10.3389/fvets.2023.1233173

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, is one of the most challenging and persistent health issues in many countries worldwide. In several countries, bTB control is complicated due to the presence of wildlife reservoirs of infection, i.e. European badger *(Meles meles)* in Ireland and the UK, which can transmit infection to cattle. However, a quantitative understanding of the role of cattle and badgers in bTB transmission is elusive, especially where there is spatial variation in relative density between badgers and cattle. Moreover, as these two species have infrequent direct contact, environmental transmission is likely to play a role, but the quantitative importance of the environment has not been assessed. Therefore, the objective of this study is to better understand bTB transmission between cattle and badgers via the environment in a spatially explicit context and to identify high-risk areas. We developed an environmental transmission model that incorporates both within-herd/territory transmission and between-species transmission, with the latter facilitated by badger territories overlapping with herd areas. Model parameters such as transmission rate parameters and the decay rate parameter of *M. bovis* were estimated by maximum likelihood estimation using infection data from badgers and cattle collected during a 4-year badger vaccination trial. Our estimation showed that the environment can play an important role in the transmission of bTB, with a half-life of *M. bovis* in the environment of around 177 days. Based on the estimated transmission rate parameters, we calculate the basic reproduction ratio (R) within a herd, which reveals how relative badger density dictates transmission. In addition, we simulated transmission in each small local area to generate a first between-herd R map that identifies high-risk areas.

Quantification of local bovine tuberculosis (bTB) transmission in badgers and cattle with and without vaccination of badgers *(Meles meles)* in the Republic of Ireland (RoI)

Chang, Y., de Jong, M.C.M. et al.
Wageningen University and Research Centre, Wageningen, The Netherlands

As yet, methodology has not yet been available to assess the impact of badger vaccination at a local level. In this project, the spatio-temporal heterogeneity of bTB transmission in a multi-host system (badgers and cattle) will be quantified across areas with vaccinated and unvaccinated badger populations, and factors involved in limiting the success of badger vaccination will be identified. Further, a risk-map of local reproduction ratios (R-map) will be generated, including for different control scenarios, in combination with existing cattle control measures, including vaccination of badgers.

Is badger vaccination, in combination with existing cattle-based controls, sufficient to eradicate bovine tuberculosis from Ireland? Insights based on a two-host and multi-route transmission model

Chang, Y., de Jong, M.C.M. et al.
Wageningen University and Research Centre, Wageningen, The Netherlands

Bovine tuberculosis (bTB) has a complex infection ecology, and it has not yet been possible to quantify the relative contribution of different infection sources in Ireland. Further, these estimates are likely to vary spatially. Using a metapopulation model, this study aims to disentangle the relative contribution of different infection sources and to assess whether measures that target different routes of infection can eliminate bTB from a region.

Ecological impact on badger populations of bovine TB vaccination

Tratalos J. et al.
UCD CVERA

In recent years, vaccination of badgers *(Meles meles)* has been used in many areas of Ireland as an alternative to culling, as a mechanism to reduce, and eventually eliminate, bovine tuberculosis (bTB) transmission to cattle. There is a need to evaluate how this vaccination programme is performing, and its likely contribution to bTB control in Ireland. To this end, a subset of the vaccine areas were chosen for analysis. Data relating to each badger caught in these areas were recorded. Colleagues in Wageningen will examine the degree to which the vaccination programme is likely to achieve its aim of reducing bTB transmission, and how this might vary spatially. Concurrently, data collected will be used to illuminate the ecology of the vaccinated badger population in Ireland, through the effect on changes in life expectancy and survivorship of badgers brought about by vaccination itself and through the concomitant reduction in culling. Comparisons of badgers captured in the vaccine zones when compared to those caught at non-vaccine zones may provide insights into the likely long-term effects of vaccination on badger behaviour and population dynamics, and how this might affect inter and intra-species bTB transmission.

Clear TB 2

Murphy, K. et al.
UCD Laboratory of Wildlife Ecology & Behaviour

This project seeks to use spatial data to build a simulation environment to test the link between clearfell forestry and herd breakdown through bovine tuberculosis (bTB), caused by *Mycobacterium bovis* which remains an endemic pathogen of significant socio-economic impact within the Republic of Ireland. The control of the pathogen is complex due to the chronic nature of infection, the characteristics and performance of available tests, and the presence of wildlife hosts. In Ireland, the primary wildlife host known to be involved in the epidemiology of bTB in cattle is the European badger, *Meles meles*. However, deer has also been hypothesized to be involved in high density areas where forest cover is abundant. Murphy et al. found a significant effect of the interaction between the extent of clearfell forestry removed and the extent of natural grassland and mixed forestry present on relative bTB risk. This interaction was dynamic, leading to an increase or decrease of the relative bTB risk depending on where (between 2 and 6 km from the farm) and when (between 0 and 36 months prior to the bTB outbreak) the clearfell operations occurred. This study provides empirical evidence of the link between mechanised forestry operations and fluctuating relative bTB risk in cattle farms, although the mechanism behind it is yet to be elucidated. Given our data, we hypothesise that wildlife hosts may abandon the area subjected to clearfell when disturbance is highest (during active operations and shortly afterward) but are subsequently attracted back to the site as they regenerate, potentially affecting the contact rates with livestock and thus, relative bTB risk. In this project we seek to simulate and disentangle that mechanism.

Seventh International Conference on Mycobacterium bovis

The Seventh International Conference on *Mycobacterium bovis* (*M. bovis* 2022) was held in NUI Galway during June 2022 after a two year postponement due to Covid-19. More than 430 delegates from 29 countries attended the conference.

As with previous conferences in the series, *M. bovis* 2022 gathered together scientists, post-graduates, policy makers, veterinarians and industry stakeholders from around the world with the aim of sharing information that would help to provide practical solutions for the control and eradication of *M. bovis*. The seven conferences in the series have taken place in:

Year	Location	Journal edition
1991	Dublin, Ireland	*Veterinary Microbiology* 40, 1-2 **https://sciencedirect.com/journal/veterinary-microbiology/vol/40/issue/1**
1995	Dunedin, New Zealand	-
2000	Cambridge, England, UK	*Tuberculosis* 81, Issues 1–2 **https://sciencedirect.com/journal/tuberculosis/vol/81/issue/1**
2005	Dublin, Ireland	*Veterinary Microbiology* 112, Issues 2–4 **https://sciencedirect.com/journal/veterinary-microbiology/vol/112/issue/2**
2009	Wellington, New Zealand	*Veterinary Microbiology* 151, Issues 1–2 **https://sciencedirect.com/journal/veterinary-microbiology/vol/151/issue/1**
2014	Cardiff, Wales, UK	-
2022	Galway, Ireland	*Irish Veterinary Journal* 76, (Suppl. 1) **https://irishvetjournal.biomedcentral.com/articles/supplements/volume-76-supplement-1**

A concerted effort was made to include a wide range of topics related to *Mycobacterium bovis* in the programme including: One Health, national control strategies, immunology, diagnostics, social science, wildlife, cattle vaccination, and epidemiology. The conference consisted of 17 plenary talks, more than 50 stream presentations, and over 130 posters.

The conference was organised by staff from UCD CVERA, the UCD School of Veterinary Medicine, the Department of Agriculture, Food and the Marine, and Abbey Conference & Events.

A selection of papers based on presentations by the plenary speakers were published in *The Irish Veterinary Journal*. The special collection, edited by Prof. Eamonn Gormley, is available at: ***https://irishvetjournal.biomedcentral.com/articles/supplements/volume-76-supplement-1***

Building a breakdown database

Building a bovine tuberculosis (bTB) breakdown dataset

Madden, J.M. et al.
UCD CVERA

The Irish bovine tuberculosis (bTB) eradication scheme collates detailed information on all aspects of the programme including results from herd level skin tests, animal level laboratory tests (from animals with suspect lesions) and gamma interferon (IFN-γ) testing. Data is stored across multiple databases within separate systems (e.g., Animal Health Computer System (AHCS), Animal Identification and Movement System (AIM), Laboratory Information Management System (LIMS)). To answer basic bTB epidemiology questions regarding herd breakdowns (BDs), number of reactors per BD, etc., we must have a dataset that incorporates all these sources of information. Unfortunately, the various datasets do not seamlessly merge. Thus, the aim of this ongoing essential data manipulation project is to collate and merge the various bTB datasets into a manageable dataset which can be used to explore pertinent bTB research hypotheses.

The Irish cattle population

The Irish cattle population structured by enterprise type: overview, trade & trends

Brock, J.[1, 2], Lange, M.[1], Tratalos, J.A.[3], Meunier, N.[2], Guelbenzu-Gonzalo, M.[2], More, S.J.[3, 4], Thulke, H.-H.[1], Graham, D.A.[2]

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***Irish Veterinary Journal* 75, 6 (2022)**

https://doi.org/10.1186/s13620-022-00212-x

The cattle sector is the most important economic production unit of the Irish farming and agri-food sector. Despite its relevance, there has been limited quantitative information about the structure of differing cattle production types and of the connections between them. This paper addresses this gap by providing, for the first time, an overview of the Irish cattle population structured by enterprise type. We collected data from the cattle register for the period 2015 to 2019 and assigned registered herds to one of 18 different herd types using a recently published herd type classification approach. This allows, for the first time, to exploring changes in enterprise types and subtypes over time, and describing the movements between these subtypes and from these subtypes to slaughter. The overview and associated classification presented in this study will form the basis for a number of future comparative studies, including cross-sectoral assessments of profitability, estimation of the extent of animal health losses on Irish cattle farms or structural analysis of Greenhouse Gas (GHG) emissions across production systems.

Risk assessment of *Mycobacterium bovis* in raw milk cheese

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

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***Tuberculosis* 132, 102166 (2022)**

https://doi.org/10.1016/j.tube.2022.102166

Bovine tuberculosis, caused by *Mycobacterium bovis (M. bovis)*, is a globally distributed chronic disease of animals. The bacteria can be transmitted to humans via the consumption of unpasteurised (raw) milk, thus representing an important public health risk. To investigate the risk of zoonotic transmission of *M. bovis* via raw milk, 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. In total, 1,339 articles were identified through seven electronic databases and initially screened using titles and abstracts. The quality of 108 potentially relevant articles was assessed using full texts, and 67 articles comprising 83 studies (76 IM and 7 BTM), were included in the meta-analysis. The prevalence of *M. bovis* in IM and BTM was summarised according to the diagnostic test used, and the tuberculin skin test (TST) infection status of the individual cows (for IM) or herds (for BTM). Heterogeneity was quantified using the I-squared statistic. Prediction intervals (95% PIs) were also estimated. 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. Inconsistency in the quality of reporting was also observed resulting in missing information, such as the TST infection status of the individual animal/herd. No study reported the number of *M. bovis* bacteria in test-positive milk samples. Several studies reported the detection of *M. tuberculosis* and *M. africanum* in milk. Despite international efforts to control tuberculosis, this study highlights the risk of zoonotic transmission of *M. bovis* via unpasteurised milk and dairy products made using raw milk.

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

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***Microbial Risk Analysis* 21, 100204 (2022)**

https://doi.org/10.1016/j.mran.2022.100204

Zoonotic tuberculosis, caused by *Mycobacterium bovis*, is mainly linked to the consumption of raw milk from infected cows. In many countries, cases are rare, due to pasteurisation of milk and national programmes to control *M. bovis* infection in cattle. Speciality cheeses, which are often produced using raw milk, present challenges to risk managers in countries where *M. 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). The aim of this study was to determine parameter estimates to support the future risk assessment of *M. 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 reviews. 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. This work has highlighted important gaps in knowledge, and areas for further research. For each of the parameters for which estimates are available, we outline the types/sources of uncertainty as reflected in relevant published papers. In any future application of these parameter estimates, care will be needed to reflect the uncertainties associated with these elements of exposure assessment.

Zoonotic tuberculosis

Immunosuppressed pets as a conduit for zoonotic tuberculosis

Ottewill, C.[1], Dolan, L.[1], Bailén, E.L[2, 3], Roycroft, E.[4, 5], Fitzgibbon, M.[4, 5], Donohue, E.O.[6], McLaughlin, A.M.[1], McGrath, G.[2], Keane, J.[1, 7]

[1] Department of Respiratory Medicine, National Tuberculosis Centre, [2] Irish Mycobacteria Reference Laboratory, St. James Hospital, [3] Department of Public Health, Health Service Executive, [4] UCD CVERA, [5] Langford Vets, Small Animal Referral Hospital, University of Bristol, Langford, United Kingdom, [6] Department of Medicine, [7] TCD Department of Clinical Microbiology

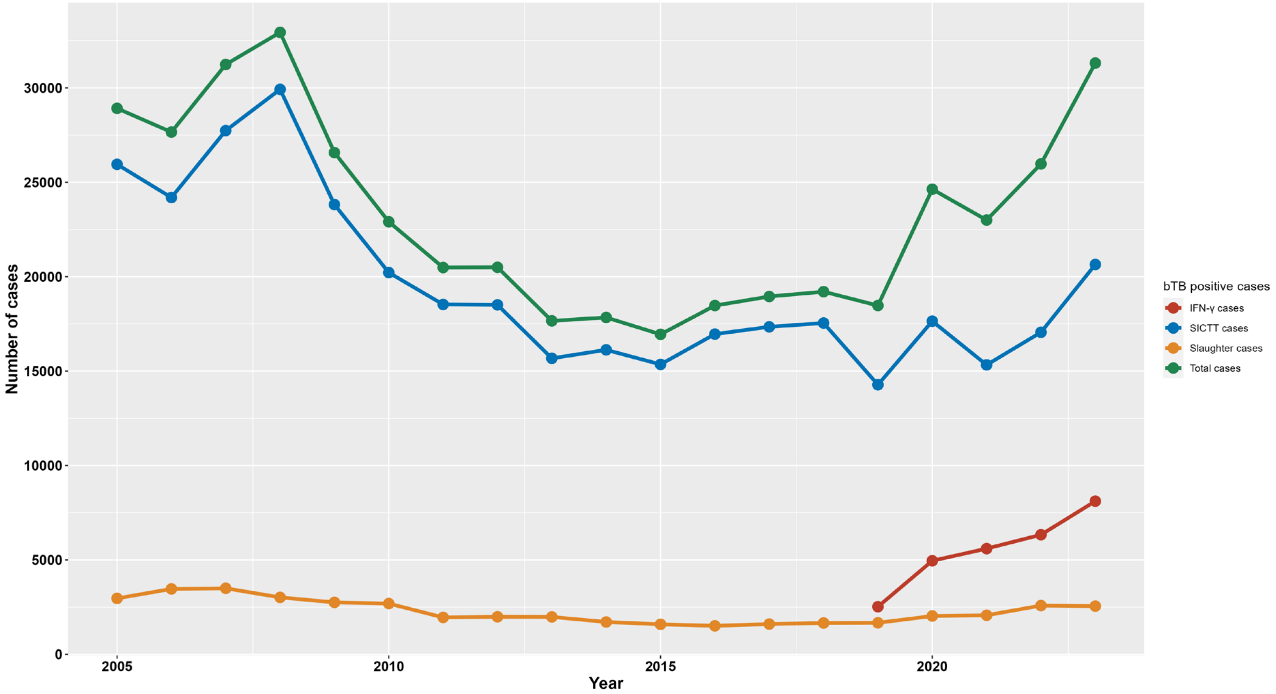
***American Journal of Respiratory and Critical Care Medicine* 208, 732–733 (2023)**

https://doi.org/10.1164/rccm.202304-0734LE

This correspondence to the Editor of The American Journal of Respiratory and Critical Care Medicine demonstrates a case of zoonotic transmission of M. bovis from incidental wild animal hosts to the environment, to an immunosuppressed household pet (canine), to another pet (feline), to human (as confirmed with WGS), to another human. This outbreak shows how an immunocompromised pet can be the conduit for a zoonotic infection in cohabiting humans. It raises the issue that immunocompromised pets may potentially pose a risk to the health of their owners, and other close contacts.

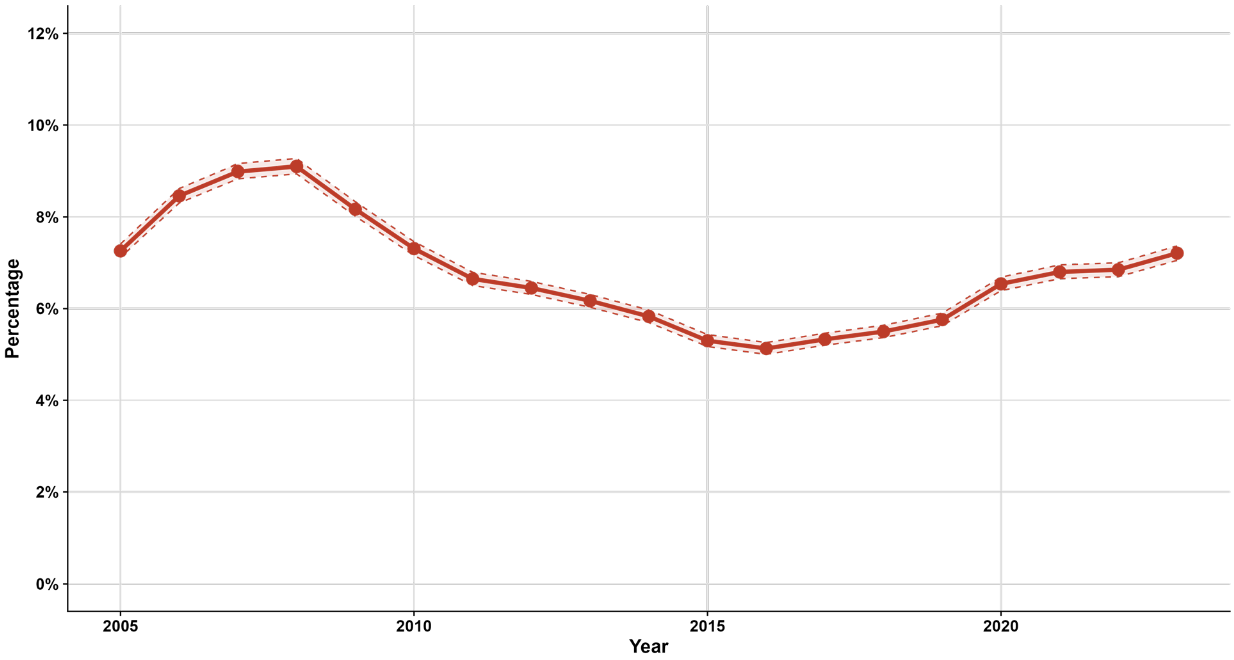
Ottewill, C., Dolan, L., Bailén, E.L., Roycroft, E., Fitzgibbon, M., Donohue, E.O., McLaughlin, A.M., McGrath, G., Keane, J., 2023. Immunosuppressed Pets as a Conduit for Zoonotic Tuberculosis. American Journal of Respiratory and Critical Care Medicine *208, 6, 732–733.*
Readers are encouraged to read the entire article for the correct context at ***https://doi.org/10.1164/rccm.202304-0734LE***

bTB cases by year (2005 - 2023)

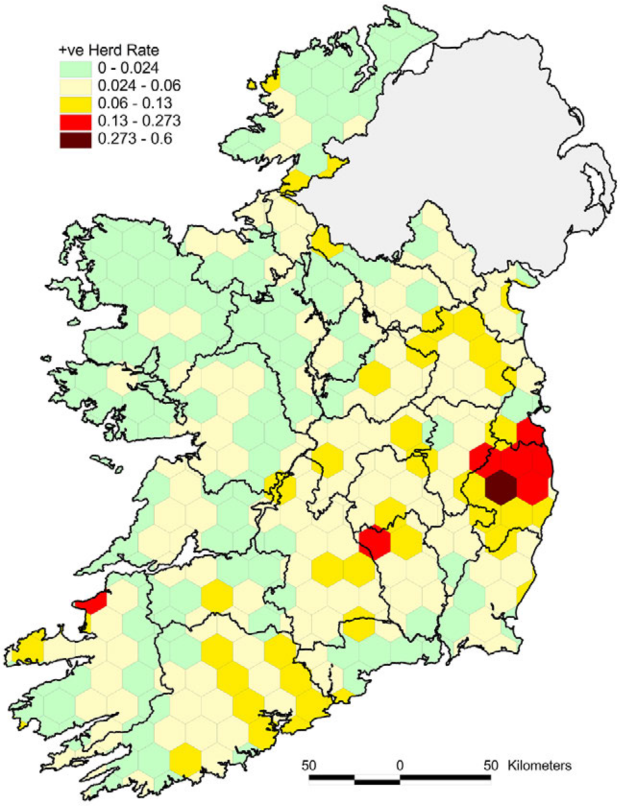


Plot developed from various AHCS data sources supplied to CVERA.
SICTT: Single Intradermal Comparative Tuberculin Test; IFN-γ: interferon-gamma assay
Total cases = IFN-γ + SICTT + slaughter.
Figures are an approximation to DAFM figures and there may be minor discrepancies (e.g. date of detection if diagnosed by more than one method).
IFN-γ cases prior to May 2019 were interpreted as SICTT cases.
Slaughter cases are clear animals that were sent for slaughter and lesion(s) found which were laboratory confirmed as m.bovis. From May 2022, this included PCR testing.

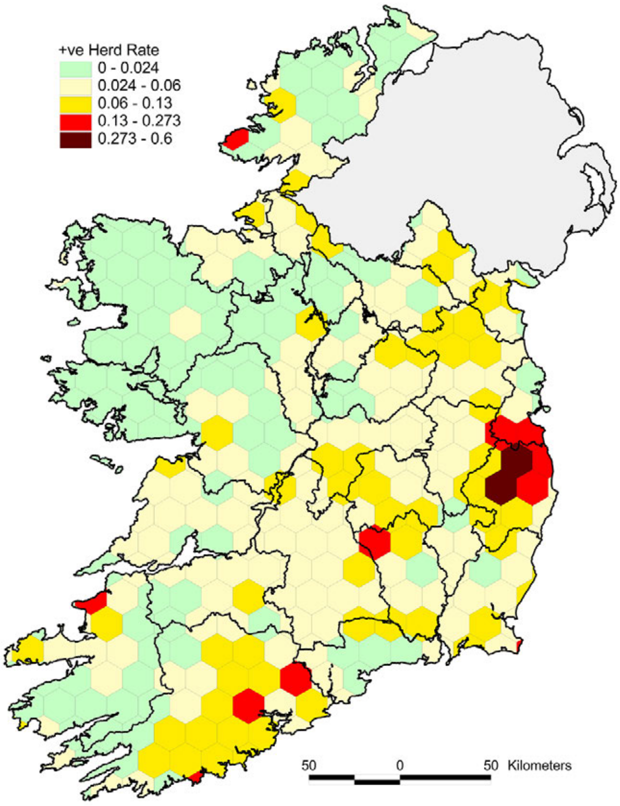
Percentage of overall herds per year in a breakdown



Plot developed from various AHCS data sources supplied to CVERA.
Numerator = number of herds with a BD during that year (herds with multiple BDs in a year only counted once).
Denominator = number of unique herds that had a skin test record in that year.
95% confidence intervals included (Wilson score interval method)



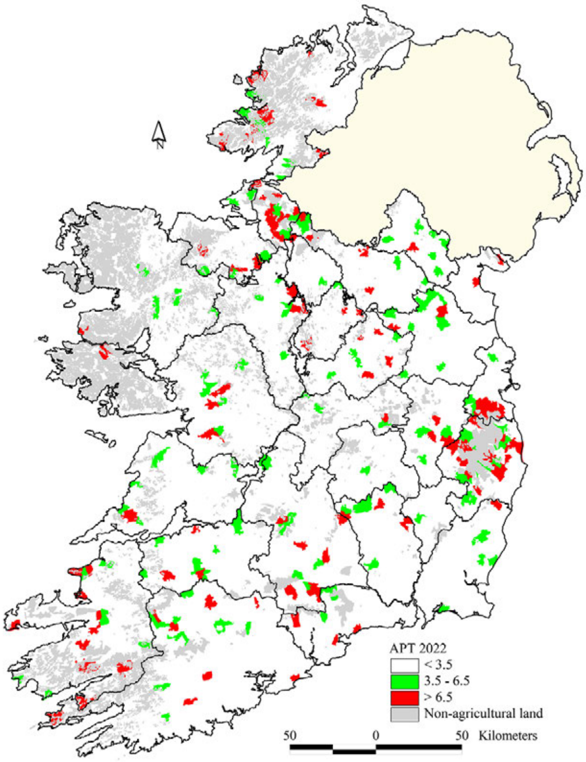
2022



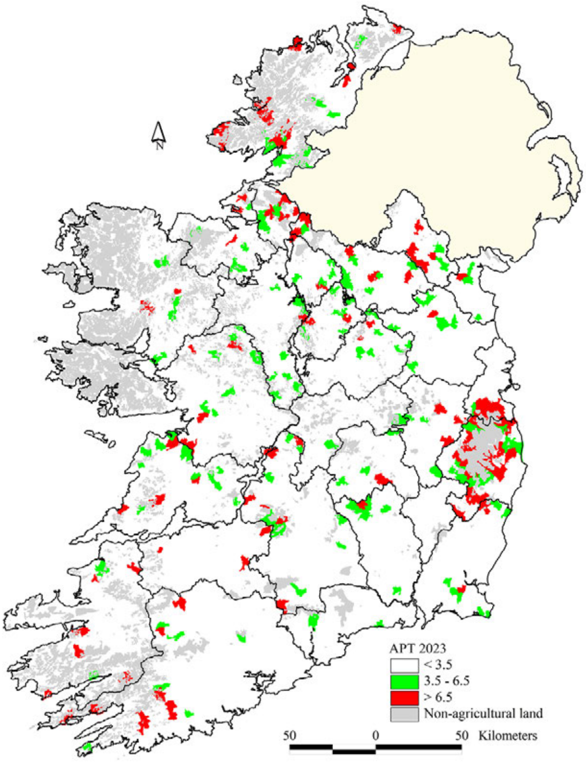
2023

Proportion of positive herds to all active herds per hexagon per year (a positive herd being defined as having 1 or more animals testing positive to the Single Intradermal Comparative Tuberculin Test "skin test positive" in that calendar year)

APT per DED (standard reactors)

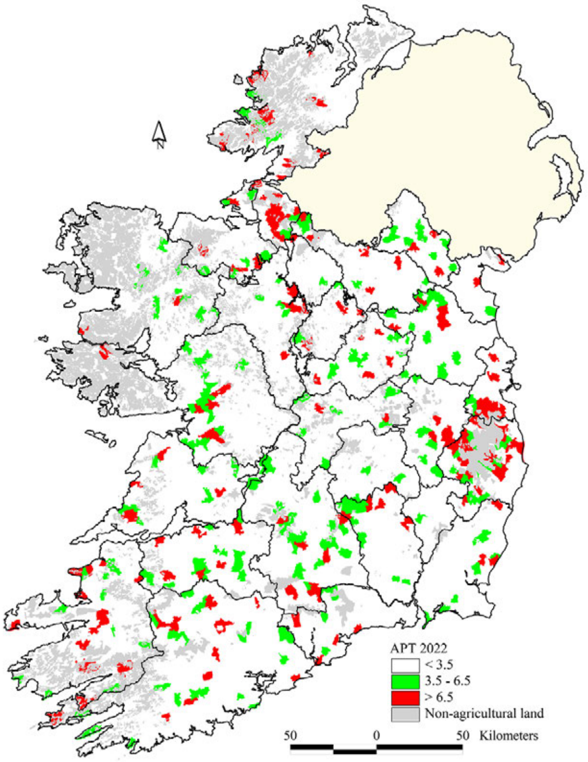


The total number of standard reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2022

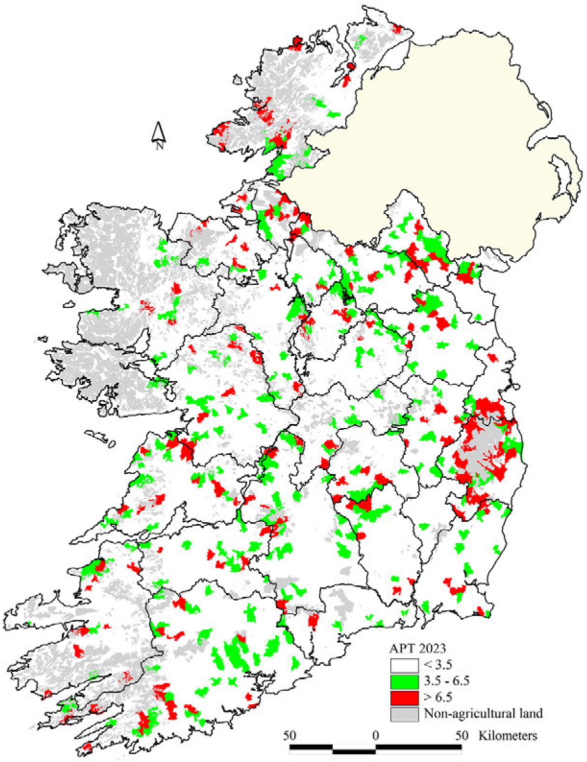


The total number of standard reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2023

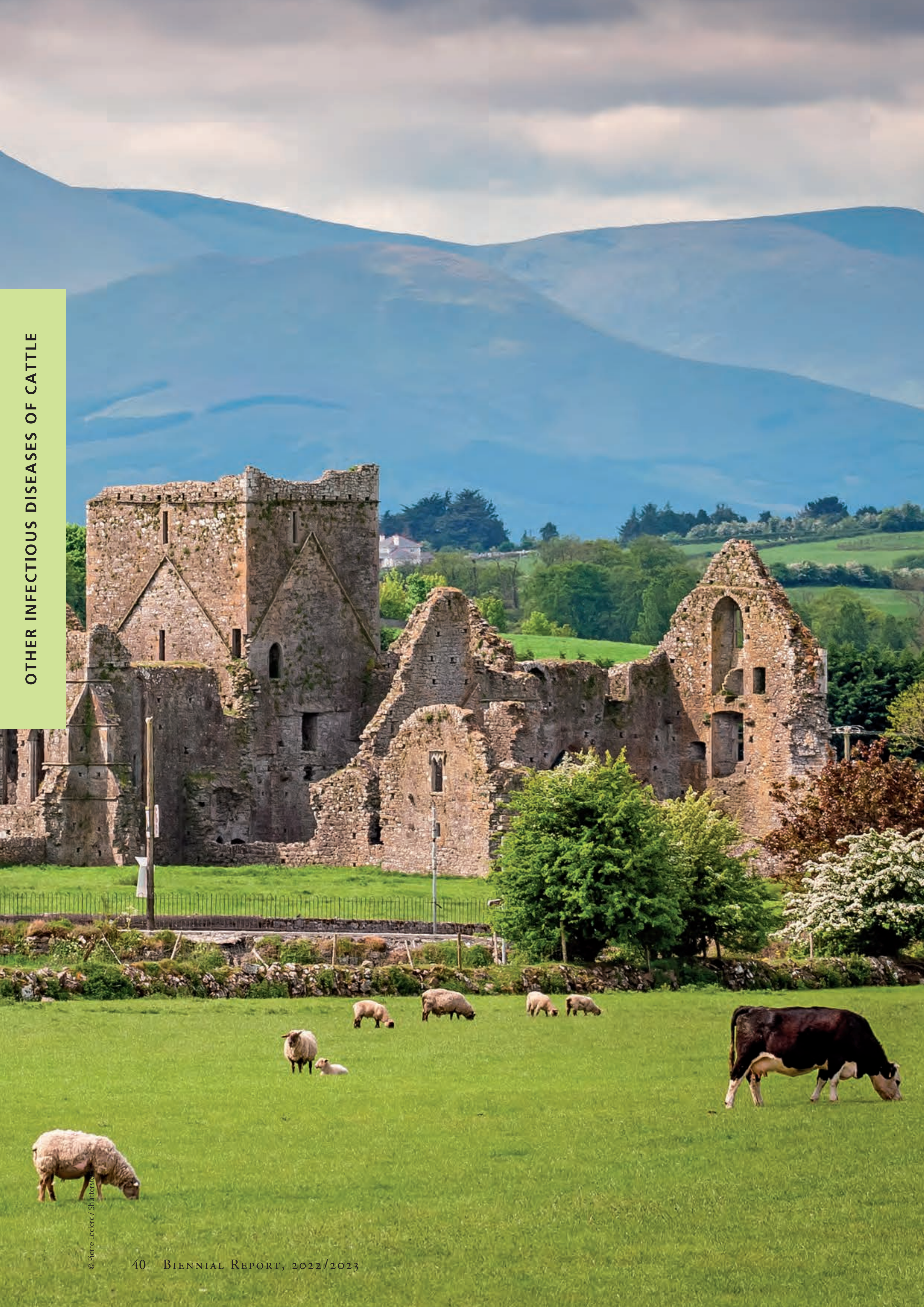
APT per DED (total reactors)



The total number of reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2022



The total number of reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2023



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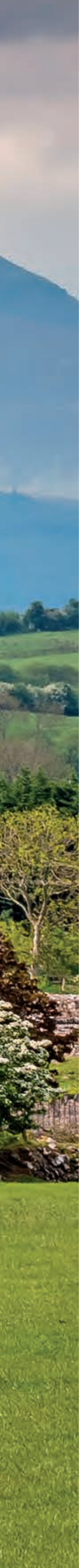

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Other infectious diseases of cattle

Infectious bovine diseases in general

Bovine viral diarrhoea (BVD)

Risk factors for detection of bovine viral diarrhoea virus in low-risk herds during the latter stages of Ireland's eradication programme

Casey-Bryars, M.[1], Tratalos, J.A.[1], Graham, D.A.[2], Guelbenzu-Gonzalo, M.P.[2], Barrett, D.[3], O'Grady, L.[4, 5], Madden, J.M.[1], McGrath, G.[1], More, S.J.[1, 4]

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***Preventive Veterinary Medicine* 201, 105607 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105607

A national programme to eradicate bovine viral diarrhoea (BVD) has been in place in Ireland since 2013. To inform decision making in the end stages of eradication, and support the development of post-eradication surveillance strategies, an understanding of risks of infection in a low prevalence system is required. A case-control study design was implemented. The study population comprised bovine herds that had calves born and tested negative for BVD virus (BVDV) every year from 2013 to 2019 (n = 46,219 herds). We defined cases as herds which had one or more test positive calves for the first time in 2019 (n = 204). Controls (n = 816) were randomly sampled from the herds which remained test negative in 2019. The effects of herd size, management system, inward movements, including those of potential trojan dams (pregnant animals brought into the herd that could potentially be carrying infected calves in utero), and proximity to herds testing positive in the preceding year, were investigated. Network analysis approaches were used to generate variables measuring connections with test positive herds through inward cattle movements. A generalised linear mixed model, including a county-level random effect, was used to explore these risk factors. Our final model retained ln (herd size) (Odds Ratio (95% CI): 1.72 (1.40, 2.12)), distance from test positive herds (0.54 (0.44, 0.66) for each extra land-parcel boundary crossed to reach the closest herd which tested positive the preceding year), and ln (potential trojan dams + 1) (1.29 (1.05, 1.60)). The same variables were retained in the model where herds with confirmed transient infections only (n = 25) were excluded. Our findings suggest that care with biosecurity at farm boundaries and visitors and equipment entering the farm, and avoidance or careful risk assessment of purchasing potentially pregnant animals, may help prevent introduction of BVDV to low-risk herds. At policy level, consideration of herd size, proximity to test positive herds and purchasing patterns of potentially pregnant cattle may help target surveillance measures towards the end of the eradication programme.

Bulk tank milk and abattoir surveillance, analysis of antibody testing for BVD, IBR and JD and integration into control and eradication programmes

Brock, J. et al.

Animal Health Ireland

The ongoing testing of bulk tank milk and abattoir samples is an important contributor to national animal health surveillance. These data provide ongoing insights into the prevalence (both at animal- and herd-level) and distribution of three bovine diseases, including bovine viral diarrhoea (BVD, a national eradication programme is in place), Johne's disease (JD, under voluntary control) and infectious bovine rhinotracheitis (IBR, where eradication is currently being considered).

Application of Whole Genome Sequencing to BVD virus in Ireland, to understand transmission and to investigate outbreaks

Guelbenzu, M. et al.

Animal Health Ireland

Genetic characterization and phylogenetic analysis of virus isolates provide a unique opportunity to trace routes of infection. Such methods have been used to investigate the molecular epidemiological characteristics of BVDV in several countries including Italy South Korea, Canada and Switzerland. This project aims to determine the predominant BVD viral types and subtypes circulating in Ireland and relate this to current diagnostics and vaccines. This will be addressed by collating the BVD 5'UTR sequence data available to date and linking movement/location data with the sequences, producing phylogenetic trees and exploring the population dynamics within the 5'UTR sequences. In addition, the application of whole genome sequencing to investigate transmissions pathways to help resolve the relationship between outbreaks and routes of spread of virus will be explored both for BVD and BoHV-1.

Early warning models for detecting re-emergence of BVD

McAloon, C.G. et al.

UCD School of Veterinary Medicine

The mandatory phase of the Irish BVD eradication programme, coordinated by Animal Health Ireland (AHI), was launched in 2013. Since then, the prevalence of BVD at herd- and individual-level has fallen dramatically. Consequently, and in line with recent regulatory changes in the EU, the BVD programme aims to move towards official recognition of freedom. Currently, the national BVD programme is entering the final stages towards eradication. The movement from endemicity to eradication and freedom of disease, is associated with a shift in the immune status of the national herd both at population and individual level. In addition, freedom under the Animal Health Law requires a vaccination ban. Increasing proportions of immunologically naive animals and herds create opportunity for the rapid transmission of infection should the disease be (re)introduced into the population or herd. For any re-emerging disease, early detection is an important 'pre-requisite' for intervention strategies aimed at mitigating the animal health, welfare and economic costs of disease (re)emergence. Disease surveillance strategies have different strengths and weaknesses, and a combination of surveillance strategies is important to achieve a balance between costs, ease of implementation and efficacy. Whilst there is significant expertise nationally on the development of targeted surveillance strategies, there is significant, as yet underutilised potential to harness the existing large databases on animal registration, health and production. In some cases, early manifestations of infection may yield non-specific animal and herd level impacts that may be difficult to detect with conventional surveillance methods. However, it is possible that these early signals could be detected in near to real-time analysis of aberrations in routinely collected data. Accordingly, a comprehensive strategy is required, and is currently being developed by AHI, for the ongoing surveillance of the re-emergence of the infection within Irish cattle herds. However, individual surveillance strategies have corresponding strengths and weaknesses associated with cost, ease of implementation and sample bias. Recent work has demonstrated that for surveillance of both endemic and exotic diseases, subject experts recommend a combination of both passive and active surveillance methods. There is an important opportunity for the real time (or close to real time) analysis of routinely collected data to augment surveillance efforts for the detection of BVD re-emergence. Since syndromic surveillance systems are non-specific in nature, the system could be useful for the detection of other emerging or exotic diseases, or as an early warning welfare alarm, for example when linked to mortality. This project will address this challenge by developing a Syndromic Surveillance system as a complimentary strategy augmenting existing and proposed surveillance approaches for the detection of the re-emergence of BVD.

Johne’s disease

The effect of risk-based trading and within-herd measures on *Mycobacterium avium* subspecies *paratuberculosis* spread within and between Irish dairy herds

Biemans, F.[1, 2], Arnoux, S.[2], More, S.J.[1, 3], Tratalos, J.A.[1], Gavey, L.[4], Ezanno, P.[2]

[1] UCD CVERA, [2] INRAE, Oniris, BIOEPAR, Nantes, France, [3] UCD School of Veterinary Medicine, [4] Animal Health Ireland

***Preventive Veterinary Medicine* 209, 105779 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105779

Johne’s disease (bovine paratuberculosis) is an endemic disease caused by *Mycobacterium avium* subspecies *paratuberculosis (Map). Map* is transmitted between herds primarily through movement of infected but undetected animals. Within infected herds, possible control strategies include improving herd hygiene by reducing calf exposure to faeces from cows, reducing stress in cows resulting in a longer latently infected period where shedding is minimal, or culling highly test-positive cows soon after detection. Risk-based trading can be a strategy to reduce the risk that *Map* spreads between herds. Our objective was to assess whether within-herd measures combined with risk-based trading could effectively control *Map* spread within and between dairy cattle herds in Ireland. We used a stochastic individual-based and between-herd mechanistic epidemiological model to simulate *Map* transmission. Movement and herd demographic data were available from 1st January 2009–31st December 2018. In total, 13,353 herds, with 4,494,768 dairy female animals, and 72,991 bulls were included in our dataset. The movement dataset consisted of 2,304,149 animal movements. For each herd, a weekly indicator was calculated that reflected the probability that the herd was free from infection. The indicator value increased when a herd tested negative, decreased when animals were introduced into a herd, and became 0 when a herd tested positive. Based on this indicator value, four Johne’s assurance statuses were distinguished: A) ≥ 0.7 – 1.0, B) ≥ 0.3 – < 0.7, C) > 0.0 – < 0.3, and D) 0.0. A is the highest and D the lowest Johne’s assurance status. With risk-based trading some of the observed movements between herds were redirected based on Johne’s assurance status with the aim of reducing the risk that a non-infected herd acquired an infected animal. Risk-based trading effectively reduced the increase in herd prevalence over a 10-year-period in Ireland: from 50% without risk-based trading to 42% with risk-based trading in the metapopulation only, and 26% when external purchases were risk-based as well. However, for risk-based trading to be effective, a high percentage of dairy herds had to participate. The most important within-herd measures were improved herd hygiene and early culling of highly infectious cows. These measures reduced both herd and within-herd prevalence compared to the reference scenario. Combining risk-based trading with within-herd measures reduced within-herd prevalence even more effectively.

Modelling transmission of *Mycobacterium avium* subspecies *paratuberculosis* between Irish dairy cattle herds

Biemans, F.[1, 2], Tratalos, J.[1], Arnoux, S.[2], Ramsbottom, G.[3], More, S.J.[1, 4], Ezanno, P.[2]

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***Veterinary Research* 53, 45 (2022)**

https://doi.org/10.1186/s13567-022-01066-5

Bovine paratuberculosis is an endemic disease caused by *Mycobacterium avium* subspecies *paratuberculosis (Map)*. *Map* is mainly transmitted between herds through movement of infected but undetected animals. Our objective was to investigate the effect of observed herd characteristics on *Map* spread on a national scale in Ireland. Herd characteristics included herd size, number of breeding bulls introduced, number of animals purchased and sold, and number of herds the focal herd purchases from and sells to. We used these characteristics to classify herds in accordance with their probability of becoming infected and of spreading infection to other herds. A stochastic individual-based model was used to represent herd demography and *Map* infection dynamics of each dairy cattle herd in Ireland. Data on herd size and composition, as well as birth, death, and culling events were used to characterize herd demography. Herds were connected with each other through observed animal trade movements. Data consisted of 13 353 herds, with 4 494 768 dairy female animals, and 72 991 breeding bulls. We showed that the probability of an infected animal being introduced into the herd increases both with an increasing number of animals that enter a herd via trade and number of herds from which animals are sourced. Herds that both buy and sell a lot of animals pose the highest infection risk to other herds and could therefore play an important role in *Map* spread between herds.

An observational study of ear-tagged calf mortality (1 to 100 days) on Irish dairy farms and associations between biosecurity practices and calf mortality on farms participating in a Johne's disease control program

McAloon, C.G.[1], Tratalos, J.A.[2], O'Grady, L.[1, 3], Green, M.J.[3], Gavey, L.[4], Graham, D.[4], More, S.J.[1, 2], McGrath, G.[2], Mee, J.F.[5]

[1] UCD School of Veterinary Medicine, [2] UCD CVERA, [3] School of Veterinary Science and Medicine, University of Nottingham, Leicestershire, United Kingdom, [4] Animal Health Ireland, [5] Teagasc

***Journal of Dairy Science* 106, 4966-4977 (2023)**

https://doi.org/10.3168/jds.2022-22519

Postnatal mortality among replacement stock has a detrimental effect on the social, economic, and environmental sustainability of dairy production. Calf mortality rates vary between countries and show differences in temporal trends; most, however, are characterized by high levels of between-farm variability. Explaining this variation can be difficult because herd-level information on management practices relevant to calf health is often not available. The Irish Johne's Control Programme (IJCP) contains a substantial on-farm monitoring program called the Veterinary Risk Assessment and Management Plan (VRAMP). Although this risk assessment is largely focused on factors relevant to the transmission of paratuberculosis, many of its principles are good practice biocontainment policies that are also advocated for the protection of calf health. The objectives of this study were (1) to quantify mortality in ear-tagged Irish dairy calves between 2016 and 2020 using both survival and risk approaches, (2) to determine risk factors for 100-d cumulative mortality hazard in ear-tagged Irish dairy calves between 2016 and 2020, (3) to determine whether 100-d cumulative mortality hazard was higher in ear-tagged calves within herds registered in the IJCP versus those that were not registered in the IJCP and whether there were differences between these cohorts over time, and (4) within IJCP herds, to determine whether VRAMP score or changes in VRAMP score were associated with 100-d cumulative mortality hazard. Excluding perinatal mortality, the overall 100-d cumulative mortality hazard was 4.1%. Calf mortality was consistently underestimated using risk approaches that did not account for calf censoring. Cox proportional hazards models showed that cumulative mortality hazard was greater in male calves; particularly, calves born to Jersey breed dams and those with a beef breed sire. Mortality hazard increased with increasing herd size, was highest in calves born in herds that contract-reared heifers, and lowest in those born in mixed dairy-beef enterprises. Mortality hazard decreased over time with the mortality hazard in 2020 being 0.83 times that of 2016. Mortality hazard was higher in IJCP-registered herds than nonregistered herds (hazard ratio 1.06, 95% CI 1.01–1.12), likely reflecting differences in herds that enrolled in the national program. However, we detected a significant interaction between IJCP status (enrolled vs. not enrolled) and year (hazard ratio 0.96, 95% CI 0.92–1.00), indicating that the decrease in mortality hazard between 2016 and 2020 was greater in IJCP herds versus non-IJCP herds. Finally, increasing VRAMP scores (indicating higher risk for paratuberculosis transmission) were positively associated with increased calf mortality hazard. Postnatal calf mortality rates in Irish dairy herds declined between 2016 and 2020. Our study suggests that implementation of recommended biocontainment practices to control paratuberculosis in IJCP herds was associated with a reduction in calf mortality hazard.

Mycoplasma bovis infection

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

McAloon, C.I.[1], McAloon, C.G.[1], Tratalos, J.[2], O'Grady, L.[1], McGrath, G.[2], Guelbenzu, M.[3], Graham, D.A.[3], O'Keeffe, K.[4], Barrett, D.J.[5], More, S.J.[1, 2]

[1] UCD School of Veterinary Medicine, [2] UCD CVERA, [3] Animal Health Ireland, [4] DAFM Blood Testing Laboratory, [5] DAFM National Disease Control Centre

Journal of Dairy Science **6, 5410-5419 (2022)**

https://doi.org/10.3168/jds.2021-21334

Mycoplasma bovis is a serious disease of cattle worldwide; mastitis, pneumonia, and arthritis are particularly important clinical presentations in dairy herds. *Mycoplasma bovis* was first identified in Ireland in 1994, and the reporting of *Mycoplasma*-associated disease has substantially increased over the last 5 years. Despite the presumed endemic nature of *M. bovis* in Ireland, there is a paucity of data on the prevalence of infection, and the effect of this disease on the dairy industry. The aim of this observational study was to estimate apparent herd prevalence for *M. bovis* in Irish dairy herds using routinely collected bulk milk surveillance samples and to assess risk factors for herd seropositivity. In autumn 2018, 1,500 herds out of the 16,858 herds that submitted bulk tank milk (BTM) samples to the Department of Agriculture testing laboratory for routine surveillance were randomly selected for further testing. A final data set of 1,313 sampled herds with a BTM ELISA result were used for the analysis. Testing was conducted using an indirect ELISA kit (ID Screen *Mycoplasma bovis*). Herd-level risk factors were used as explanatory variables to determine potential risk factors associated with positive herd status (reflecting past or current exposure to *M. bovis*). A total of 588 of the 1,313 BTM samples were positive to *M. bovis*, providing an apparent herd prevalence of 0.45 (95% CI: 0.42, 0.47) in Irish dairy herds in autumn 2018. Multivariable analysis was conducted using logistic regression. The final model identified herd size, the number of neighboring farms, in-degree and county as statistically significant risk factors for herd BTM seropositivity to *M. bovis*. The results suggest a high apparent herd prevalence of seropositivity to *M. bovis*, and evidence that *M. bovis* infection is now endemic in the Irish dairy sector. In addition, risk factors identified are closely aligned to what we would expect of an infectious disease. Awareness raising and education about this important disease is warranted given the widespread nature of exposure and likely infection in Irish herds. Further work on the validation of diagnostic tests for herd-level diagnosis should be undertaken as a matter of priority.

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

McAloon, C.I. et al.

UCD School of Veterinary Medicine

There are important knowledge gaps about *Mycoplasma bovis* infection, which is endemic in cattle in Ireland. This study seeks an understanding of herd prevalence and risk factors associated with positive herd status, an estimation of the characteristics of several tests for herd-level diagnosis of infection, an understanding of the strain types of *M. bovis* present in Ireland and Scotland, and quantification of the impact of *M. bovis* infection at herd-level.

Infectious bovine diseases in general

Output-based assessment of confidence of freedom from infection

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

Madouasse, A.[1], Mercat, M.[1], van Roon, A.[2], Graham, D.[3], Guelbenzu, M.[3], Santman Berends, I.[2, 4], van Schaik, G.[2, 4], Nielen, M.[2], Frössling, J.[5, 6], Ågren, E.[5, 6], Humphry, R.[7], Eze, J.[7], Gunn, G.[7], Henry, M.K.[7], Gethmann, J.[8], More, S.J.[9, 10], Toft, N.[11], Fourichon, C.[1]

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***Peer Community Journal* 2, e4 (2022)**

https://doi.org/10.24072/pcjournal.80

The collective control programmes (CPs) that exist for many infectious diseases of farm animals rely on the application of diagnostic testing at regular time intervals for the identification of infected animals or herds. The diversity of these CPs complicates the trade of animals between regions or countries because the definition of freedom from infection differs from one CP to another. 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, using either Stan or JAGS. 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. When risk factors are available, prior distributions need to be provided for the coefficients of the logistic regression, replacing the prior for the probability of becoming positive. From these prior distributions and from the longitudinal data, the model returns posterior probability distributions for being status positive for all herds on the current month. Data from the previous months are used for parameter estimation. 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.

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

Mercat, M.[1], van Roon, A.M.[2], Santman-Berends, I.[2, 3], van Schaik, G.[2, 3], Nielen, M.[2], Graham, D.[4], More, S.J.[5, 6], Guelbenzu-Gonzalo, M.[4], Fourichon, C.[1], Madouasse, A.[1]

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***Preventive Veterinary Medicine* 200, 105582 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105582

Control programmes against non-regulated infectious diseases of farm animals are widely implemented. Different control programmes have different definitions of “freedom from infection” which can lead to difficulties when trading animals between countries. When a disease is still present, in order to identify herds that are safe to trade with, estimating herd-level probabilities of being infected when classified “free from infection” using field data is of major interest. 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. Two different indexes were used to categorize herds from the probability of being infected into a herd predicted status. 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. Model convergence did not occur for 39 % of the scenarios, mainly in association with low herd test sensitivity. 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 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.

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Output-based assessment of herd-level freedom from infection in endemic situations: Application of a Bayesian Hidden Markov model

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Preventive Veterinary Medicine **204, 105662 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105662

Countries have implemented control programmes (CPs) for cattle diseases such as bovine viral diarrhoea virus (BVDV) that are tailored to each country-specific situation. Practical methods are needed to assess the output of these CPs in terms of the confidence of freedom from infection that is achieved. As part of the STOC free project, a Bayesian Hidden Markov model was developed, called STOC free model, to estimate the probability of infection at herd-level. In the current study, the STOC free model was applied to BVDV field data in four study regions, from CPs based on ear notch samples. The aim of this study was to estimate the probability of herd-level freedom from BVDV in regions that are not (yet) free. We additionally evaluated the sensitivity of the parameter estimates and predicted probabilities of freedom to the prior distributions for the different model parameters. First, default priors were used in the model to enable comparison of model outputs between study regions. Thereafter, country-specific priors based on expert opinion or historical data were used in the model, to study the influence of the priors on the results and to obtain country-specific estimates. The STOC free model calculates a posterior value for the model parameters (e.g. herd-level test sensitivity and specificity, probability of introduction of infection) and a predicted probability of infection. The probability of freedom from infection was computed as one minus the probability of infection. For dairy herds that were considered free from infection within their own CP, the predicted probabilities of freedom were very high for all study regions ranging from 0.98 to 1.00, regardless of the use of default or country-specific priors. The priors did have more influence on two of the model parameters, herd-level sensitivity and the probability of remaining infected, due to the low prevalence and incidence of BVDV in the study regions. The advantage of STOC free model compared to scenario tree modelling, the reference method, is that actual data from the CP can be used and estimates are easily updated when new data becomes available.

A framework for assessing the confidence in freedom from infection in animal disease control programmes

van Schaik, G.[1, 2], Madouasse, A.[3], van Roon, A.M.[1], More, S.J.[4, 5], Graham, D.A.[6], Frössling, J.[7], Gethmann, J.[8], Fourichon, C.[3], Mercat, M.[3], Ågren, E.[6], Sauter-Louis, C.[8], Gunn, G.[9], Eze, J.[9], Humphry, R.[9], Henry, M.[9], Guelbenzu, M.[6], Nielen, M.[1], Santman-Berends, I.M.G.A.[1, 2]

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https://doi.org/10.20506/rst.42.3364

***OIE Scientific and Technical Review* 42, 210-217 (2023)**

In the Surveillance Tool for Outcome-based Comparison of FREEdom from infection (STOC free) project (**https://www.stocfree.eu**), a data collection tool was constructed to facilitate standardised collection of input data, and a model was developed to allow a standardised and harmonised comparison of the outputs of different control programmes (CPs) for cattle diseases. The STOC free model can be used to evaluate the probability of freedom from infection for herds in CPs and to determine whether these CPs comply with the European Union's pre-defined output-based standards. Bovine viral diarrhoea virus (BVDV) was chosen as the case disease for this project because of the diversity in CPs in the six participating countries. Detailed BVDV CP and risk factor information was collected using the data collection tool. For inclusion of the data in the STOC free model, key aspects and default values were quantified. A Bayesian hidden Markov model was deemed appropriate, and a model was developed for BVDV CPs. The model was tested and validated using real BVDV CP data from partner countries, and corresponding computer code was made publicly available. The STOC free model focuses on herd-level data, although that animal-level data can be included after aggregation to herd level. The STOC free model is applicable to diseases that are endemic, given that it needs the presence of some infection to estimate parameters and enable convergence. In countries where infection-free status has been achieved, a scenario tree model could be a better suited tool. Further work is recommended to generalise the STOC free model to other diseases.

Syndromic surveillance

Development of a syndromic surveillance system for Irish dairy cattle using milk recording data

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***Preventive Veterinary Medicine* 204, 105667 (2022)**

https://doi.org/10.1016/j.prevetmed.2022.105667

In the last decade and a half, emerging vector-borne diseases have become a substantial threat to cattle across Europe. To mitigate the impact of the emergence of new diseases, outbreaks must be detected early. However, the clinical signs associated with many diseases may be nonspecific. Furthermore, there is often a delay in the development of new diagnostic tests for novel pathogens which limits the ability to detect emerging disease in the initial stages. Syndromic Surveillance has been proposed as an additional surveillance method that could augment traditional methods by detecting aberrations in non-specific disease indicators. The aim of this study was to develop a syndromic surveillance system for Irish dairy herds based on routinely collected milk recording and meteorological data. We sought to determine whether the system would have detected the 2012 Schmallenberg virus (SBV) incursion into Ireland earlier than conventional surveillance methods. Using 7,743,138 milk recordings from 730,724 cows in 7,037 herds between 2007 and 2012, linear mixed-effects models were developed to predict milk yield and alarms generated with temporally clustered deviations from predicted values. Additionally, hotspot spatial analyses were conducted at corresponding time points. Using a range of thresholds, our model generated alarms throughout September 2012, between 4 and 6 weeks prior to the first laboratory confirmation of SBV in Ireland. This system for monitoring milk yield represents both a potentially useful tool for early detection of disease, and a valuable foundation for developing similar tools using other metrics.

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Other animal health and welfare issues

Milk quality and intramammary antimicrobial stewardship

Antimicrobial usage

Prescribing and sales of intramammary antimicrobials in Ireland in 2019 and 2020: the role of milk purchasers

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Irish Veterinary Journal **75, 20 (2022)**

https://doi.org/10.1186/s13620-022-00227-4

In Ireland between 2008 and 2022, intramammary antimicrobial (AM) products could be prescribed by a veterinary practitioner under what was known as Schedule 8 (or remote) prescribing. Under this prescribing route, an annual herd visit was not required when criteria were met as outlined in Animal Remedies Regulation 2007 to 2017 (statutory instruments No. 786/2007 and 558/2017). Under this prescribing route, the responsibilities of the milk purchaser, the farmer and the veterinary practitioner were each outlined, and a written mastitis control programme (MCP) was required. Milk purchasers implemented MCPs on participating farms (so-called MCP herds) with support from veterinary practitioner(s) who undertook Schedule 8 prescribing of intramammary AM tubes. This study seeks a clearer understanding of the role of milk purchasers in the prescribing and sale of intramammary AM products in Ireland during 2019 and 2020, whilst this Regulation was in force. Specifically, the study sought insights into the role of milk purchasers in the prescribing and sale of intramammary AM products in the Irish dairy industry during 2019 and 2020, using anonymised and highly aggregated milk purchaser data. The study also provided insights into milk quality among supplying herds during this period. For this study, we had access to anonymised, highly aggregated data from all milk purchasers that operated a MCP on at least some of their supplying herds during 2019 or 2020. Data collection was undertaken by the Department of Agriculture, Food and Marine. Data analysis was primarily descriptive. Data were available on 11 milk purchasers (64.7% of all) and 13,251 supplying herds. Of these, 52% were MCP herds. The quality of milk from supplying herds varied significantly by month, year and milk purchaser. During 2019 and 2020, there was a single Schedule 8 prescriber (a private veterinary practitioner prescribing intramammary AMs as part of a MCP), on average, for 549.3 herds. The sale of intramammary AM products through milk purchasers represented 15.2% and 26.9% of national sales in in-lactation and dry cow tubes, respectively. There was an overall 2% increase in sales through milk purchasers between 2019 and 2020. Few European Medicines Agency (EMA) category B *('Restrict')* intramammary AM products were sold by milk purchasers. For both in-lactation and dry cow tubes, there was a statistically significant association between EMA classification and route of sale (through milk purchasers or otherwise). The study findings provide important insights into mastitis control and intramammary AM stewardship in the Irish dairy industry. Significant differences between milk purchasers were observed in the quality of milk, as measured through somatic cell count (SCC) values, from supplying herds. This warrants further research. In the context of intramammary AM prescribing, veterinary oversight under the Animal Remedies Regulation 2007 to 2017 was very limited during 2019 and 2020. There were also significant associations between EMA classification and route of sale during 2019 and 2020, reinforcing the need for Irish veterinary practitioners to move away from EMA category B intramammary AMs. Higher quality data are needed to address important industry questions. Specifically it is recommended that national bulk tank SCC data are made available for public good research. Past experiences with Schedule 8 prescribing (no longer permitted from 28 January 2022) may influence current efforts towards improved intramammary AM stewardship.

Intramammary antimicrobial sales in Ireland: a descriptive 2020 update

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***Irish Veterinary Journal* 75, 5 (2022)**

https://doi.org/10.1186/s13620-022-00213-w

Intramammary (IM) antimicrobial sales data are currently the only feasible means to gain broad insights into on-farm usage of antimicrobials (AMs) relevant to mastitis control within the Irish dairy industry. The aim of this study was to update earlier work describing sales data of intramammary antimicrobial usage in the Irish dairy industry in 2020. Previously reported data from 2013 to 2019 is included for reference and 2020 sales data is reported using similar methodology to previously published work in this area. Data on IM AMs sold in Ireland during 2013-2020 were obtained from two sources, believed to represent 99% of all sales of IM AMs in Ireland, and analyses were undertaken to evaluate patterns in IM AM sales. We report an increase in overall sales of both lactating cow (LC) and dry cow (DC) IM AMs. We observed a large increase in the use of DC IM AMs, from 0.95 to 1.13 defined course dose (DCDvet) per cow per year in 2019 and 2020 respectively, as well as evidence of ongoing usage of highest priority critically important AMs, as defined by the World Health Organization. There was also a slight increase in LC use of IM AMs, from 0.43 to 0.44 defined course dose (DCDvet) per cow per year. We believe that our results provide an accurate reflection of IM sales in Ireland in 2020. In common with any study of this type, caution is needed when interpreting national IM AM sales data, noting the potential discrepancies between AM sales and on-farm usage. Nonetheless, the sales pattern described here, most importantly the increased use of DC products and ongoing and increasing use of HP CIA products in both DC and LC therapy raise significant concerns for the Irish dairy industry. This study provides an evidence base to inform current policy discussions, particularly in the context of the new Veterinary Medicines Regulation (Regulation (EU) 2019/6), which comes into force on 28 January 2022.

Antimicrobial stewardship

The new Veterinary Medicines Regulation: rising to the challenge

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***Irish Veterinary Journal* 75, 2 (2022)**

https://doi.org/10.1186/s13620-022-00209-6

This article 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. In the Irish dairy industry, as elsewhere, successful implementation of the Regulation will require a high level of mastitis control across all herds, and measures to support high standards in antibiotic stewardship. National actions will be critical, to support optimal mastitis control throughout the national herd. 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. Further, prescribing choices will need 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. A herd health approach will be critical, within a Client-Patient-Practice Relationship as outlined by the Veterinary Council of Ireland. On those farms with sub-optimal mastitis control, mastitis issues 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.

Mastitis control and intramammary antimicrobial stewardship in Ireland: challenges and opportunities

More, S.J.[1, 2], McAloon, C.[2], Silva Boloña, P.[3], O'Grady, L.[2, 4], O'Sullivan, F.[5], McGrath, M.[6], Buckley, W.[7], Downing, K.[8], Kelly, P.[9], Ryan, E.G.[2], McCoy, F.[6]

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***Frontiers in Veterinary Science* 9, 748353 (2022)**

https://doi.org/10.3389/fvets.2022.748353

The Veterinary Medicines Regulation (EU 2019/6) came into force in all EU member states on 28 January 2022. This regulation places particular emphasis on prudent and responsible antimicrobial use in food animal production. Key changes include restrictions on the prophylactic use of antimicrobials in animals, and the possibility to reserve certain antimicrobials for humans only. The Regulation presents challenges to the Irish dairy industry, particularly with respect to current approaches to dry cow therapy. In response, the CellCheck technical working group (TWG, a technical group working in support of CellCheck, the national mastitis control programme) have developed pragmatic national and farm-level recommendations in support of improved mastitis control and intramammary antimicrobial stewardship in the Irish dairy industry. This paper outlines these recommendations, and provides an overview of the evidence considered to inform the TWG during its work (including the Regulation, policy perspectives, international best-practice, international scientific reviews and specific Irish challenges). In many key areas of concern, the TWG recognises the challenges in seeking to shape recommendations in the absence of robust and practical scientific evidence. For this reason, some of the recommended actions are pragmatic in nature, informed by national and international experiences. Periodic programme review will be needed, informed by ongoing monitoring of key performance indicators, to identify those actions that are most effective in an Irish context.

The opinions of farm animal veterinarians in Ireland on antimicrobial use and their role in antimicrobial stewardship

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***Irish Veterinary Journal* 76, 28 (2023)**

https://doi.org/10.1186/s13620-023-00253-w

Antibiotic use and resistance in animal production are a concern to public health, and there is an urgent need to reduce antibiotic use in farm animals. To prevent blame shifting, professionals from human medicine, animal medicine and environmental backgrounds must collaborate to tackle this issue. Veterinarians are typically responsible for overseeing and prescribing antibiotic use in animals. There are currently no available studies on the opinions of Irish farm animal veterinarians on antibiotic use, reduction opportunities and their relationships with farmers. A digital survey was developed and sent out to Irish farm animal veterinarians. This paper presents the results of a cross-sectional study of Irish farm animal veterinarians' attitudes towards antimicrobial stewardship, their prescribing behaviours, antibiotic reduction opportunities and their attitudes for the future of antibiotic use. The veterinarian-farmer relationship is examined and potential interventions to reduce antibiotic use on farms are identified. In total, 114 complete questionnaires were received, representing approximately 11 per cent of all farm animal veterinarians in Ireland. Respondents were aware of the problem of antibiotic resistance and recognise their role in the fight against it. They realise what actions they must take to reduce antibiotic use and identify barriers that prevent their farmer clients from implementing their advice. Many of them say that they can reduce antibiotic use on farms in the future, but some remain doubtful. There was no statistical difference between veterinarians that had less experience working than those that had more experience in their attitudes towards future reduction in antibiotic use. Most of the respondents seek to use antibiotics as judiciously as they can. The majority agree that antibiotic overuse is the main contributor to antibiotic resistance. Possible solutions to reduce antibiotic use include the development of antibiotic treatment guidelines, assigning one unique practice to each farm and compulsory CPD (Continuous Professional Development) courses.

Mastitis control

Insights into Irish mastitis control: describing somatic cell count patterns using anonymised data

Madden, J. et al.
UCD CVERA

Mastitis is a common production disease in dairy farming which can cause compromised animal welfare as well as high economic losses. Somatic cell counts (SCC), due to inflammation of the udder, are an important indicator of udder health and milk quality and are used to define chronic mastitis (SCC elevated for at least 3–4 weeks). Mastitis control also significantly impacts antimicrobial stewardship in the dairy industry. Relevant to this, the new Veterinary Medicines Regulation (EU 2019/6) places particular emphasis on responsible antimicrobial use, particularly in the context of antimicrobial therapy at drying off. This study will describe and quantify SCC patterns across the national dairy cow population, providing insights into herd-level milk quality changes and knowledge gaps. It will be conducted using anonymised herd-level milk quality data and associated demographic variables.

Dog welfare

Understanding the dog population of the Republic of Ireland: insight from existing data sources?

More, S.J.[1, 2], Collins, D.M.[1], Meunier, N.V.[3], Messam, L.L.McV.[2], Doyle, R.[4], Maguire, A.[4], Murray, S.[4], Reilly, P.[4], Lawler, C.[4]

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***Irish Veterinary Journal* 75, 16 (2022)**

https://doi.org/10.1186/s13620-022-00223-8

Reliable information about national pet dog populations is an important contributor to informed decision-making, both by governments and national dog welfare organisations. In some countries, there is an improved understanding of aspects of the national pet dog population, but as yet limited published information is available in Ireland. The current study reviews the utility of existing data to inform our understanding of recent changes to the pet dog population in Ireland, including both biological and organisational processes. Based on national data on dog licencing and microchipping registration, pet dog numbers have remained relatively stable in recent years (i.e. prior to the COVID-19 pandemic). Since 2015, there has been a substantial decrease in the number of dogs managed through dog control centres. Although the completeness of the data are likely variable, there appears to be substantial, and increasing, number of dogs moving from Ireland to other countries, including UK, Sweden, Italy, Germany and Singapore. We also note an increase (albeit much smaller) in the number of dogs being moved into Ireland. This study highlights the challenges faced when using existing national data to gain insights into the dog population of Ireland. The linking of existing national databases (individual dog identification, dog licencing, dog control statistics) has the potential to improve both the representativeness and accuracy of information about the Irish pet dog population. In the next phases of our work, we will focus on the work of dog welfare organisations, given both the increased role played by these organisations and the substantial public funding that has been committed in this sector.

A qualitative exploration of challenges and opportunities for dog welfare in Ireland post COVID-19, as perceived by dog welfare organisations

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***Animals* 12, 3289 (2022)**

https://doi.org/10.3390/ani12233289

This novel qualitative study identifies challenges and opportunities to improve dog welfare in Ireland, as perceived by dog welfare organisations (DWOs), a previously underutilised stakeholder. This study sought the views of this predominantly voluntary sector of the next steps for policy and action in dog welfare, in light of the effects of the "puppy pandemic", increased costs and COVID-19 restrictions. An integrated online focus group and interview design involving DWOs was analysed using inductive thematic analysis. Thematic analysis identified 2 key themes: (1) Key challenges and solutions in general dog welfare and (2) Challenges and opportunities in the welfare organisation sector. DWOs perceived poor public awareness of appropriate dog-husbandry, inadequate legislation enforcement, negative impact of puppy farms, and increased financial and volunteer burden. DWOs helped construct a best practice rehoming pathway, identified how overall standards could be improved and recommendations to enhance dog welfare. The DWOs perceived an increased numbers of households acquiring dogs, difficulties in rehoming, and financial challenges as threatening their viability as organisations and Irish dog welfare. Greater enforcement of legislation, greater communication between organisations and the government, and more media awareness were seen as helpful by the DWOs to improve dog welfare standards and their organisations.

A mixed-method survey to understand the role of dog welfare organisations in Ireland, including reported challenges and potential solutions

McKernan, C.[1], Lawler, C.[2], Murphy, B.[1], Collins, D.M.[3], More, S.J.[3, 4], Murray, S.[2], Reilly, P.[2], Doyle, R.[2], Meunier, N.V.[5], Maguire, A.[2], Messam, L.L.McV.[4]

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***Irish Veterinary Journal* 76, 27 (2023)**

https://doi.org/10.1186/s13620-023-00249-6

This novel study forms part of a larger research programme seeking an improved understanding of aspects of the owned dog population in Ireland. Dog welfare organisations (DWOs) in Ireland are recognised as an instrumental pillar of the animal welfare sector with some receiving substantial public funding. We conducted a survey of DWOs in Ireland ($n=39$) to gain a better understanding of their role and function, including their policies and procedures and the rehoming of dogs to other regions. In addition, we wanted to get a better understanding of the challenges experienced by DWOs in fulfilling their role and their perspectives on potential solutions to these challenges. The survey questions consisted of closed and open-ended items. Closed items were analysed quantitively; open-ended items were analysed thematically. Most DWOs (> 80%) had written protocols for important welfare actions including rehoming procedures, assessment of owner suitability and euthanasia. DWOs sent dogs to Northern Ireland (13%), Great Britain (38.5%) and to other countries outside the United Kingdom (36%, including Germany, Sweden, Italy, the Netherlands and Czechia). Reported challenges included a general lack of funding, limited public awareness of the importance of dog welfare and insufficient capacity to handle dog numbers. To address these challenges, the DWOs highlighted the potential contribution of subsidised programmes and access to resources to educate potential owners. In a further qualitative evaluation to capture perceptions of appropriate solutions by DWOs, several themes emerged, relating to legislation, education, an overwhelmed workforce, and funding. This study provides important insights into the roles and functions of DWOs and challenges they experience in Ireland. It is hoped that the findings from this research will inform future research investigating potential solutions to these challenges as well as the development of policy in Ireland.

Further animal health and welfare research

Honey bee colony health

High accuracy monitoring of honey bee colony development by image analysis

Capela, N.[1], Dupont, Y.L.[2], Rortais, A.[3], Sarmento, A.[1], Papanikolaou, A.[3], Topping, C.J.[2], Arnold, G.[4], Pinto, M.A.[5], Rodrigues, P.J.[6], More, S.J.[7, 8], Tosi, S.[9], Alves, T.S.[6], Sousa, J.P.[1]

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***Journal of Apicultural Research* 62, 741-750 (2023)**

https://doi.org/10.1080/00218839.2022.2098899

Honey bees are key insect pollinators, providing important economic and ecological value for human beings and ecosystems. This has triggered the development of several monitoring methods for assessing the temporal development of colony size, food storage, brood and pathogens. Nonetheless, most of these methods are based on visual assessments that are observer-dependent and prone to bias. Furthermore, the impact on colony development (invasiveness), as well as accuracy, were rarely considered when implementing new methods. In this study, we present and test a novel accurate and observer-independent method for honey bee colony assessment, capable of being fully standardized. Honey bee colony size is quantified by assessing the weight of adult bees, while brood and provision are assessed by taking photos and conducting image analysis of the combs with the image analysis software Deepbee®. The invasiveness and accuracy of the method were investigated using field data from two experimental apiaries in Portugal, comparing results from test and control colonies. At the end of each field experiment, most of the tested colonies had the same colony size, brood levels and honey production as the control colonies. Nonetheless, continuous weight data indicated some disturbance in tested colonies in the first year of monitoring. The overall accuracy of the image analysis software was improved by training, indicating that it is possible to adapt the software to local conditions. We conclude that the use of this fully quantitative method offers a more accurate alternative to classic visual colony assessments, with negligible impact on colony development.

Bovine abortion

Bovine foetal death in Ireland: gaps in our knowledge of pathogens that are difficult to diagnose

Hayes, C. et al.

DAFM Regional Veterinary Laboratory Service

Bovine foetal death encompasses the death of a foetus at any stage between 42 days of gestation and the calving event. However, any foetal death results in an impactful reduction in calves produced per cow. Additional possible sequelae include reduced milk production (Keshavarzi et al., 2020), impaired reproductive performance (Mahnani et al., 2018) and the associated economic consequences (Cantón et al., 2022). Further, there is an internationally recognised problem of low rates of diagnosis in cases of bovine foetal death. The overall objective of this project is to improve these diagnostic rates. The first part of the project aims to determine the prevalence of the infectious abortifacients *Coxiella burnetii*, *Mycoplasma bovis* and *Chlamydia abortus* in bovine foetuses submitted to the Irish Regional Veterinary Laboratories service during the winter-spring season 2020-2021. Further work will attempt to determine the potential role of *C. burnetii* in these foetal deaths using histopathology of the membranes. PCR testing for *M. bovis* and *C. abortus* in these foetal membranes is ongoing. The second part of the project looks at the diagnosis of *Neospora caninum* in bovine foetuses and aborted cows. The animal-level true prevalence of *N. caninum* in bovine foetuses will be estimated using three diagnostic techniques: PCR, foetal blood/ thoracic fluid antibody ELISA and histopathology. The median number of days from foetal expulsion to the day the cow achieves non-seropositivity to *Neospora caninum* will be estimated in cows that abort a foetus PCR-positive for *N. caninum*. Bovine abortion is an under-researched area, in spite of its major implications for farm productivity, animal health, and in the case of zoonotic agents, even human health. This study aims to fill knowledge gaps in the literature.

Culicoides dispersion modelling

Culicoides dispersion model

McGrath, G. et al.

UCD CVERA

Met Éireann and CVERA have created an operational model for forecasting potential incursion of windborne *Culicoides* spp. (midges) to Ireland. There is strong evidence that the introduction of Schmallenberg virus into Ireland in the summer of 2012 was due to the arrival of infected midges carried on the wind from southwest England. By forecasting midge dispersion, we can assess the risk of future potential incursion events which can then assist in active surveillance, particularly for Bluetongue virus, which is active on mainland Europe but has yet to reach Ireland. The model is built on the HYSPLIT atmospheric dispersion model driven by the European Centre for Medium-Range Weather Forecasts (ECMWF). The model is run daily with the 3-day forecast results distributed to a list of relevant associates. The model has been enhanced to improve emission estimates and to simplify the output. The next steps will be to further enhance the model to include biological parameters and to add rainfall, thereby making prediction estimates more realistic. The forecasts from the model inform DAFM risk assessments, early warning surveillance and risk mitigation actions to prevent or reduce the impact of a potential incursion of Bluetongue virus into Ireland.

Highly Pathogenic Avian Influenza (HPAI)

Spatial and temporal monitoring and analysis of highly pathogenic avian influenza (HPAI) in Ireland

McGrath, G. et al.

UCD CVERA

Highly Pathogenic Avian Influenza (HPAI) is a virus that occurs mostly in birds. It is highly contagious among birds and generally has high mortality, especially in domestic poultry where contact rates are high. A HPAI epidemic would potentially have a substantial negative impact on the poultry industry in Ireland through the need for enhanced biosecurity and direct losses associated with outbreak control measures. CVERA provides mapping and administrative supports to the Department of Agriculture, Food and the Marine (DAFM) during HPAI outbreaks in commercial poultry units and assists with the public facing mapping of wild bird HPAI surveillance. An online interactive map viewer of the location of confirmed cases of avian influenza subtype H5N1 in captive and wild birds in Ireland is available at ***https://t.co/F9TwWTqVrG***

Nuclear contingency planning

Nuclear contingency planning

McGrath, G. et al.
UCD CVERA

CVERA, in conjunction with the Environmental Protection Agency (EPA), Met Éireann and the Department of Agriculture, Food and the Marine (DAFM), created a model for defining the extent and severity of contamination of Irish farm land, both during and after a nuclear accident scenario in the United Kingdom or continental Europe. An ongoing risk value will be assigned to all active herds/flocks which will be appraised by DAFM as part of their contingency management plan. Having an informed real-time risk value at a farm level would enable DAFM to offer relevant advice to the farming community. In the event of local to regionalised contamination, fodder could be moved from areas identified as negligible risk to higher risk areas for the period of highest risk. Knowing where high risk farms are would enable targeted testing of food products which would be essential as Ireland has limited testing capacity. Defining areas of negligible risk would allow for an uninterrupted supply of farming produce to the general public and for export. Having a system such as this in place would offer a degree of security in what would be a period of uncertainly in consumer confidence in agricultural produce.

An overview of research within the UCD School of Veterinary Medicine

Advancing national animal health and welfare policy

Graham, H.A.[1], Doherty, M.L.[1], More, S.J.[1, 2], Gordon, S.V.[1], Gormley, E.P.[1], Mooney, C.T.[1], Hanlon, A.J.[1], Mullan, S.M.[1], Leonard, F.C.[1], McAloon, C.G.[1]
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American Journal of Veterinary Research **83, ajvr.22.10.0179 (2022)**

https://doi.org/10.2460/ajvr.22.10.0179

The University College Dublin (UCD) School of Veterinary Medicine has a broad research agenda covering areas such as veterinary public health, epidemiology and national disease control, herd health management, drug delivery, pharmacology, parasitology, and One Health research. Staff work with national and international collaborators and, with the support of Zoetis, have a longstanding "UCD Squared" partnership with the University of California-Davis, which has established an ambitious program of research, drawing on expertise from a diverse community of veterinary and medical scientists and clinicians. The School works closely with national government , conducting research in support of national animal health and welfare policy. Key areas include bovine tuberculosis diagnostics and eradication; the assessment of alternative pig production system from the perspective of pigs, farmers and society; clinical academic training in human medicine, veterinary medicine, and dentistry; antimicrobial usage and resistance; and the eradication and control of other animal diseases. Further information on research in the UCD School of Veterinary Medicine is available here: www.ucd.ie/vetmed/research/.

This summary has been adapted from the original source.

Improving the safety of spinal fracture fixation in dogs

Mullins, R.A.[1], Graham, H.A.[1], Breathnach, R.M.[1], More, S.J.[2]

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***American Journal of Veterinary Research* 85, ajvr.23.10.0245 (2023)**

https://doi.org/10.2460/ajvr.23.10.0245

University College Dublin (UCD) undertakes a comprehensive program to support research at all levels, with a particular focus on building sustainable infrastructure for clinical research within the UCD Veterinary Hospital. In this article, Ronan Mullins (Head of Small Animal Surgery) offers an insight into research involving the freehand probing technique for stabilization of vertebral fractures in dogs and techniques aimed at improving the safety of spinal fracture fixation. If found to be reliable, the techniques could translate into decreased patient morbidity, reduced surgical interventions, decreased hospitalization, and reduced costs for clients.

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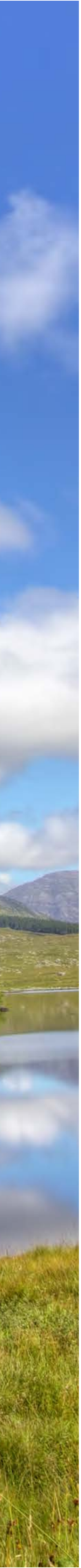

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Covid-19

COVID-19 epidemiological studies

Rapid antigen testing for SARS-CoV-2 infection in a university setting in Ireland: learning from a 6-week pilot study

Barry, G.[1], McCarney, C.[1], Farrelly, M.[1], Breathnach, R.[1], Mooney, C.[1], More, S.J.[1, 2]

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***Public Health in Practice* 3, 100255 (2022)**

https://doi.org/10.1016/j.puhip.2022.100255

With the ongoing circulation of SARS-CoV-2 in countries across the world it is essential to identify effective ways to reduce the risk of infection while allowing society to function as close to 'normal' as possible. Serial testing using rapid lateral flow antigen tests is a possible way to do this by screening populations in a targeted way, identifying infectious (both symptomatic and asymptomatic) people and removing them from circulation while infectious. To make rapid antigen testing effective, high levels of participation are important. This study was designed to evaluate the establishment of a testing programme in a university setting and assess some of the factors that impact participation in such a study among both staff and students. A trial period of SARS-CoV-2 rapid testing using the Abbott Panbio rapid antigen test was set up and staff and students based in the University College Dublin Veterinary Hospital were asked to take part voluntarily for 6 weeks. Following the trial period, we used a questionnaire to evaluate satisfaction and to understand some reasons behind participation or lack thereof. Overall, almost all respondents to the survey stated that they were happy with having a testing programme present in the workplace and it helped to reduce anxiety associated with COVID-19. Findings indicated that staff and students did not participate equally in the voluntary testing programme. The findings also highlighted that intrinsic motivations and extrinsic motivations for participation differ. For example, participation among staff was much higher than among students, motivational messaging focused on protecting others did not resonate with students as much as staff, convenience was a key factor driving participation in both cohorts and the pressure of being forced to miss class (if positive) close to exam time provided motivation to students to avoid testing. Introducing antigen testing into a workplace helped to reduce overall anxiety associated with the potential impact of COVID-19, but achieving good participation was challenging. Participation is key to a successful, campus wide antigen testing programme but reaching high levels of participation is not straightforward and cannot be taken for granted. Different motivations drive participation in different cohorts and different messaging/incentivisation is needed to encourage participation in those different cohorts. The findings reported here should inform any SARS-CoV-2 testing programme that will run in these types of settings in the future.

Assessing pandemic era stadium events and infections using mobile phone based population mobility data: An exploratory study from Ireland, 2021

Condron, A.J.[1], McGrath, G.[2], Madden, J.[2]

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***Statistical Journal of the IAOS* 38, 1143-1157 (2022)**

https://doi.org/10.3233/SJI-220045

Mass gathering events (MGEs) attracting local, national, or international crowds presented particular challenges in the context of the coronavirus disease 2019 (COVID-19) pandemic. Sporting, religious, music and other cultural events held during the early months of the pandemic, without social distancing or other safeguards, have been regarded as so-called 'super spreader' events. By the summer of 2020, MGEs were generally banned or subject to severe restrictions. Regular European sporting fixtures such as England's Football Association and Germany's Bundesliga matches began to return in the autumn with protective measures in place, such as matches initially held behind closed doors, and later with sub-capacity crowd limits and mandatory social distancing. With protective measures in place, and proof of COVID-19 vaccination or recovery required for entry, a series of six sporting MGEs, 'the All-Ireland Finals' were held in the Republic of Ireland's largest stadium, Croke Park in Dublin, during August-September 2021. This study draws on a high-resolution human population mobility dataset to quantify journeys to/from the stadium area on MGE days by destination. The anonymised, aggregated, data used is based on mobile phone usage, and consists of a series of fine-grained geographical origin-destination matrices presenting daily estimates of area to area journey numbers. With mobility from the stadium area serving as a proxy for MGE attendance, this study explores associations between MGE attendance numbers and local COVID-19 infections over subsequent five week periods. No evidence was found of association between attendance at any of the six 2021 All-Ireland MGEs and COVID-19 infections over subsequent five week periods. This finding contrasts with studies of comparable MGEs in 2020, such as English Association Football matches held during spring 2020, and German Bundesliga football matches held during autumn 2020. These differing outcomes may point to the effectiveness of transmission mitigation policies and behaviours.

Reprinted from the Statistical Journal of the IAOS *38, Condron, A.J., McGrath, G., Madden, J., Assessing pandemic era stadium events and infections using mobile phone based population mobility data: An exploratory study from Ireland, 2021, 1143-1157, © 2022, with permission from IOS Press. The publication is available at IOS Press through* ***https://doi.org/10.3233/SJI-220045***

Potential application of SARS-CoV-2 rapid antigen diagnostic tests for the detection of infectious individuals attending mass gatherings – a simulation study

McAloon, C.G.[1], Dahly, D.[2], Walsh, C.[3], Wall, P.[4], Smyth, B.[5], More, S.J.[1, 6], Teljeur, C.[7]

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***Frontiers in Epidemiology* 2, 862826 (2022)**

https://doi.org/10.3389/fepid.2022.862826

Rapid Antigen Diagnostic Tests (RADTs) for the detection of SARS-CoV-2 offer advantages in that they are cheaper and faster than currently used PCR tests but have reduced sensitivity and specificity. One potential application of RADTs is to facilitate gatherings of individuals, through testing of attendees at the point of, or immediately prior to entry at a venue. Understanding the baseline risk in the tested population is of particular importance when evaluating the utility of applying diagnostic tests for screening purposes. We used incidence data from January and from July-August 2021, periods of relatively high and low levels of infection, to estimate the prevalence of infectious individuals in the community at particular time points and simulated mass gatherings by sampling from a series of age cohorts. Nine different illustrative scenarios were simulated, small (n = 100), medium (n = 1,000) and large (n = 10,000) gatherings each with 3 possible age constructs: mostly younger, mostly older or a gathering with equal numbers from each age cohort. For each scenario, we estimated the prevalence of infectious attendees, then simulated the likely number of positive and negative test results, the proportion of cases detected and the corresponding positive and negative predictive values, and the cost per case identified. Our findings suggest that for each reported case on a given day, there are likely to be 13.8 additional infectious individuals also present in the community. Prevalence ranged from 0.26% for "mostly older" events in July-August, to 2.6% for "mostly younger" events in January. For small events (100 attendees) the expected number of infectious attendees ranged from <1 across all age constructs of attendees in July-August, to 2.6 for "mostly younger" events in January. For large events (10,000 attendees) the expected number of infectious attendees ranged from 27 (95% confidence intervals 12 to 45) for mostly older events in July-August, to 267 (95% confidence intervals 134 to 436) infectious attendees for mostly younger attendees in January. Given rapid changes in SARS-CoV-2 incidence over time, we developed an RShiny app to allow users to run updated simulations for specific events.

Risk factors for SARS-CoV-2 infection in Healthcare Workers following an identified nosocomial COVID-19 exposure during waves 1-3 of the pandemic in Ireland

McGrath, J.[1], McAloon, C.G.[2], More, S.J.[2, 3], Garrett, S.[1], Reidy, C.[1], Geary, U.[1], Noonan, N.[1], Bergin, C.[1]

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Epidemiology & Infection **150, e186 (2022)**

https://doi.org/10.1017/S0950268822001595

Healthcare workers (HCWs) have increased exposure and subsequent risk of infection with severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). This case-control study was conducted to investigate the contemporaneous risks associated with confirmed SARS-CoV-2 infection amongst HCWs following in-work exposure to a confirmed coronavirus disease-2019 (COVID-19) case. We assessed the influence of demographic (age, sex, nationality, high risk co-morbidities and vaccination status) and work-related factors (job role, exposure location, contact type, personal protective equipment (PPE) use) on infection risk following nosocomial SARS-CoV-2 exposure. All contact tracing records within the hospital site during waves 1–3 of the COVID-19 pandemic in Ireland were screened to identify exposure events, cases and controls. In total, 285 cases and 1526 controls were enrolled, as a result of 1811 in-work exposure events with 745 index cases. We demonstrate that male sex, Eastern European nationality, exposure location, PPE use and vaccination status all impact the likelihood of SARS-CoV-2 infection following nosocomial SARS-CoV-2 exposure. The findings draw attention to the need for continuing emphasis on PPE use and its persisting benefit in the era of COVID-19 vaccinations. We suggest that non-work-related factors may influence infection risk seen in certain ethnic groups and that infection risk in high-risk HCW roles (e.g. nursing) may be the result of repeated exposures rather than risks inherent to a single event.

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Scientific support

CVERA works to generate scientific information in support of national policy decision-making. This work is conducted in two ways, either as:

- defined *scientific projects* (as outlined in earlier sections of this Biennial Report [Bovine tuberculosis; Other infectious diseases of cattle; Other animal health and welfare issues]), or
- as more-general *scientific support*.

Each accounts for approximately 50% of available resources.

Our work draws on expertise within CVERA in epidemiology, statistics, geographic information systems, and database maintenance and interrogation.

CVERA provides scientific support to both *ad hoc* and ongoing activities, and to a range of national bodies including the Department of Agriculture, Food and the Marine (DAFM), University College Dublin (UCD), and Animal Health Ireland. During 2022/2023, CVERA continued to contribute to the national COVID-19 response, primarily in support of the Irish Epidemiological Modelling Advisory Group (IEMAG).

The following provide a broad, non-exhaustive overview of scientific support provided by CVERA during 2022 and 2023.

Epidemiological support

Simon J. More

European Food Safety Authority

- Chair of the Scientific Committee (SC)
- Chair of the EFSA Journal Editorial Advisory Board
- Chair of the MUST-B (multiple stressors on honey bee colony health) working group

Department of Agriculture, Food and the Marine

- Member, One Health Scientific Advisory Committee
- Member, TB Forum & TB Forum Scientific Working Group
- Member, One Health National Action Plan on the Antimicrobial Resistance (iNAP) Animal Health Implementation Committee
- Member, Animal Health Surveillance Steering Group
- Member, CVERA management board
- Epidemiological support on a broad range of animal health & welfare and One Health issues

Irish Epidemiological Modelling Advisory Group (IEMAG)

- IEMAG member

University College Dublin

- Associate Dean for Research, Innovation and Impact within the UCD School of Veterinary Medicine
    - Chair, Research, Innovation and Impact Committee, UCD School of Veterinary Medicine
    - Member, Research, Innovation and Impact Committee, UCD College of Health and Agricultural Sciences
    - Member, Research, Innovation and Impact Group, University College Dublin
    - Member, Senior Management Team, UCD School of Veterinary Medicine

- COVID-19
    - Member, UCD COVID-19 Medicine & Public Health Committee Subgroup
    - Chair, School COVID-19 Advisory Group

- Teaching
    - Undergraduate, including Agricultural Science (ANSC30130), Veterinary Medicine (VET30520, VET30550, VET30170, VET30280) and Medicine (MDSA10210)
    - Postgraduate, including Dairy Herd Health (VETS40180)

- Postgraduate supervision or support
    - You Chang (PhD Wageningen University) [bovine tuberculosis], Catherine McAloon (PhD) [*bovine mycoplasmosis*], Áine Collins (ECVPH) [epidemiology]

Animal Health Ireland (AHI)

- Chair of the Technical Work Group, member of the Implementation Group, Johne's disease
- Chair of the Technical Work Group, member of the Implementation Group, CellCheck programme
- Provision of scientific support to AHI on issues relating to the bovine viral diarrhoea (BVD), Johne's disease, CellCheck, and infectious bovine rhinotracheitis (IBR) programmes

General scientific community

- Scientific Advisory Board, *Preventive Veterinary Medicine*
- Deputy Editor, *Irish Veterinary Journal*
- Independent referee for a number of international peer reviewed journals
- Thesis examination (PhD), several universities
- Member, Scientific Committee, Seventh International Conference on *Mycobacterium bovis* (*M. bovis* 2022)

Statistical support

Jamie Madden

Department of Agriculture, Food and the Marine

- Statistical and geospatial support for a range of projects
- Continually processing and cleaning raw bTB testing data for research projects including development of a herd bTB breakdown file. These data are used:
  - for DAFM/CVERA projects
  - for DAFM/CVERA associate projects
  - by DAFM's One Health Unit
  - for annual bTB incidence maps
  - for bTB breakdown trends
  - to answer bTB related epidemiological questions
  - to assist with a variety of other bTB related projects

General research support

- Providing statistical, epidemiological, geospatial and statistical software support for a range of ongoing CVERA related projects and day to day issues
- Continually updating and development of various data dictionaries/manuals for various datasets for CVERA staff and CVERA associates

Other

- Independent referee for a number of international peer reviewed papers
- Member of the Irish Statistical Association

Geographic Information Systems (GIS) support

Guy McGrath & Daniel Collins

Department of Agriculture, Food and the Marine

- Wildlife Administration Unit
  DAFM's Wildlife Administration Unit (WAU) has had responsibility for the implementation of the Department's wildlife strategy for bovine tuberculosis since its foundation in 2002. The strategy is implemented under licence from, and in co-operation with, National Parks and Wildlife Service (NPWS). CVERA provides support to the WAU vaccination and control elements of the TB eradication programme. CVERA will continue to provide:
    - Daily approvals and monthly/yearly reports for vaccine tile turnover and control programme
    - Issue of permits for removals in vaccine areas
    - End of year progress maps for each District Veterinary Office (DVO)
    - TB quarterly maps
    - Resources for regional offices and problem areas
    - WAU annual calculations
    - Density metric data
    - Vaccine coverage metrics
    - Sett data and activity score work
    - Cattle access to setts report
    - County boundary report

- GIS support for a range of studies, including:
    - Foot & Mouth incursion preparedness work
    - Highly Pathogenic Avian Influenza mapping
    - Infectious Laryngotracheitis (ILT) virus map
    - Bluetongue incursion preparedness work

Animal Health Ireland

- GIS support for a range of studies, including:
    - Monthly BVD maps
    - All-island BVD maps
    - BVD clustering report

General research support

- GIS support for a range of studies, including:
    - Meteorological data stream and archive
    - Annual processing of Land Parcel Identification System data
    - GeoVet 2023
    - Seventh International Conference on *Mycobacterium bovis* (*M. bovis* 2022) - Scientific Committee and Organising Committee

Database and computer programming support

Jamie Tratalos

Department of Agriculture, Food and the Marine

- Annual Bluetongue freedom from infection analysis
- Provision of bovine movement datasets for use in a variety of projects

General research support

- Database support for a range of studies, including:
    - Development of Structured Query Language (SQL) data bases to ensure that CVERA is in compliance with EU and national Data Protection legislation and that data are readily available in standardised formats for analysis by CVERA staff

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Publications

During 2022 - 2023

Pear reviewed papers & book chapters

Barroso, P., Breslin, P., McGrath, G., Madden, J.M., Tratalos, J.A., More, S.J., Ryan, E., Byrne, A.W., Barrett, D., 2022. Is there an association between road building and bovine tuberculosis herd risk? A three time-points study in Ireland, 2011-2020. *Preventive Veterinary Medicine* 198, 105542. **https://doi.org/10.1016/j.prevetmed.2021.105542**

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ISBN: 978-1-910963-760

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