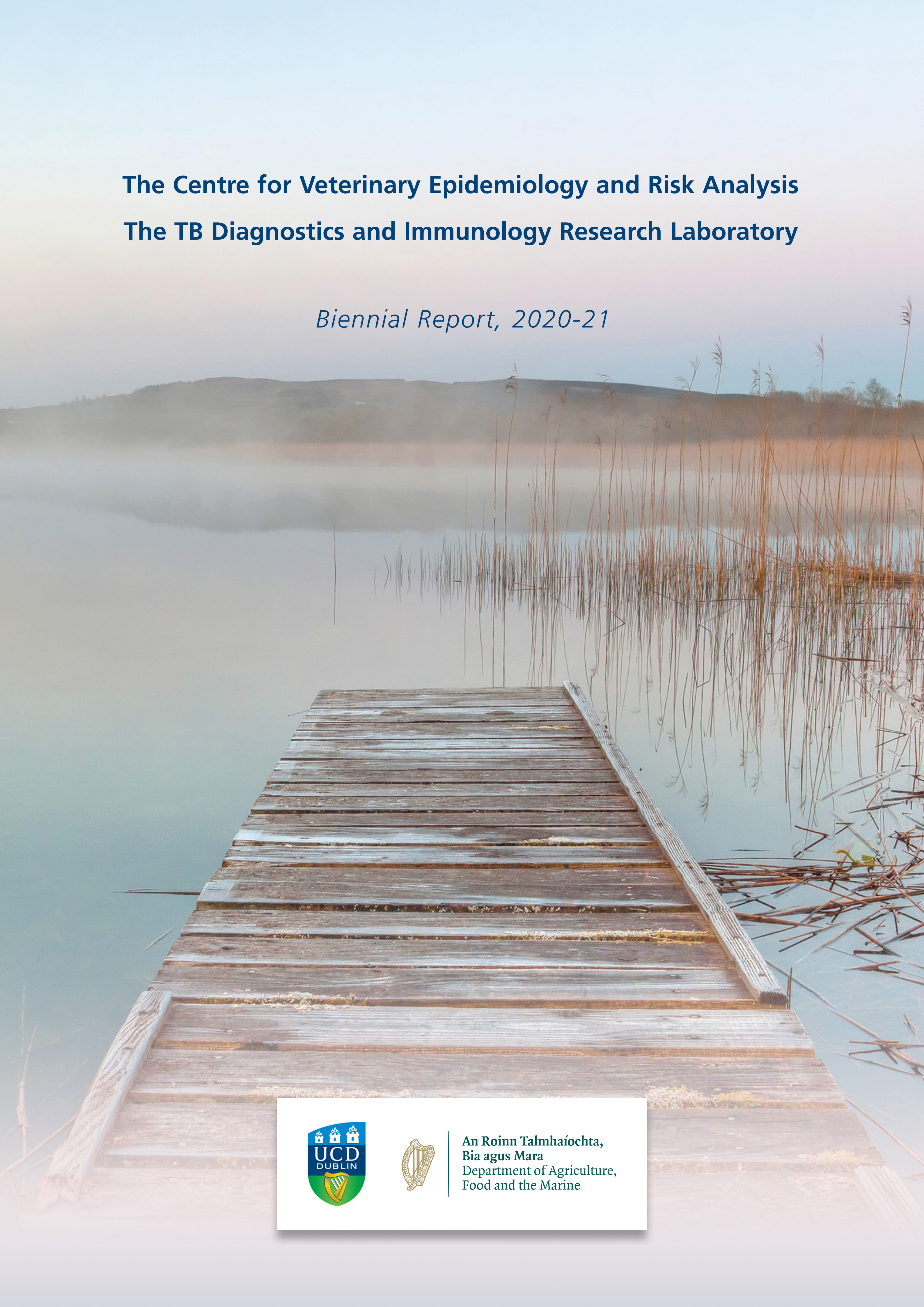

The Centre for Veterinary Epidemiology and Risk Analysis
The TB Diagnostics and Immunology Research Laboratory

Biennial Report, 2020-21

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, 2020-21

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

H.K. Tin (illustrations)

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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 (pre- and post-graduation). 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 2020 and 2021.

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Acknowledgements

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- UCD Animal Genomics Laboratory
- UCD Centre for Food Safety
- UCD Conway Institute of Biomolecular and Biomedical Research
- UCD School of Biosystems and Food Engineering
- UCD School of Mathematics and Statistics
- UCD School of Public Health, Physiotherapy and Sports Science

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- University of Copenhagen, Denmark
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- University of Zurich, Zurich, Switzerland
- 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 Kevin Kenny, Naomi Fogarty and colleagues at the mycobacteriology laboratory (DAFM Veterinary Laboratory Service, Backweston, Celbridge, Co. Kildare, Ireland). Also to the staff at Longtown farm for managing the BROC facility. Sandrine Lesellier (ANSES, France) is thanked for contributing technical expertise for the research programme.

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- June Fanning (DAFM) (from March 2021)
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- Laura Boyle (Teagasc)
- Jonas Brock (Helmholtz Centre for Environmental Research GmbH – UFZ, Germany & Animal Health Ireland)
- John Griffin (Private consultant)
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- Annika van Roon (Utrecht University, Netherlands)
- Tadaishi Yatabe (University of California, Davis, CA, USA)

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- Mart de Jong (Wageningen University, The Netherlands)
- Blain Murphy & Claire McKernan (Queen's University Belfast, Northern Ireland)

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
- Leigh Corner
- Naomi Fogarty
- Kevin Kenny (DAFM)
- Tara Fitzsimons
- Kevina McGill
- Anthony Duignan (DAFM)

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 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 strategic review, 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 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 UCD 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 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. The laboratory was responsible for providing scientific direction to the Co. Kilkenny vaccine field trial. 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, which includes those projects where relevant peer-reviewed papers, or equivalent, have been published in 2020/21, or

- Current, which includes the balance of active projects covering the spectrum from an advanced research concept through to final write-up or manuscript in press.

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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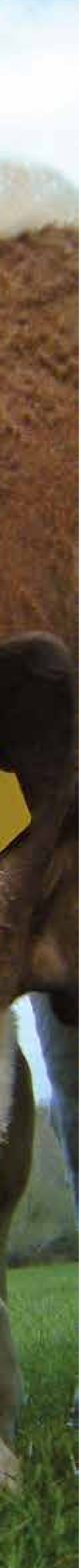

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Bovine tuberculosis

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, the Cork Blood Testing Laboratory (BTL) provides full IFN-γ testing in infected herds from the southern regions of the country. 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. The UCD laboratory has also provided assistance to Farmslabs (Co. Roscommon) in setting up the IFN-γ assay in their laboratory. Farmlabs will provide full IFN-γ testing starting in January 2022. In the period 2020-2021, approx. 91,000 blood samples were submitted to the UCD laboratory for IFN-γ testing. Apart from a few weeks between late March and mid-April 2020, the UCD laboratory maintained a full diagnostic service during lockdown restrictions imposed because of the covid-19 pandemic.

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).
- SICTT reactor animals where the IFN-γ test is used to confirm the exposure status of SICTT positive animals.

The laboratory continues to conduct research with a view to improving the performance of the assay under Irish conditions. A number of key studies have been completed and published in the past two years.

The development of a molecularly defined tuberculin skin test to detect Mycobacterium bovis *infected cattle*

In collaboration with APHA – Weybridge we tested a molecularly defined tuberculin (MDT) by skin testing and IFN-γ testing of DAFM Longtown farm reactors. Test and slaughter strategies are conventionally based on active surveillance through the application of tuberculin Purified Protein Derivate (PPD)-based skin testing, with IFN-γ tests often applied as ancillary tests to maximise the detection of infected cattle. The PPDs exhibit multiple limitations: they are crude extracts from mycobacterial cultures with largely unknown active components; their production depends on culture of mycobacteria requiring expensive BL3 production facilities; and their potency depends on the technically demanding guinea pig assay. APHA have a developed a molecularly defined tuberculin (MDT) by adding further antigens to the prototype reagent composed of ESAT-6, CFP-10 and Rv3615c (DIVA skin test, DST). The antigens were formulated together with the three DST antigens into the MDT to test cattle experimentally and naturally infected with *M. bovis*, uninfected cattle and MAP vaccinated calves. The study demonstrated significant increases in MDT-induced skin responses compared to DST in infected animals, whilst maintaining high specificity in unvaccinated or MAP vaccinated calves. Further, MDT could also be applied in *in vitro* blood-based interferon-gamma release assays. Thus, MDT promises to be a robust diagnostic skin and blood test reagent overcoming some of the limitations of PPDs and warrants full validation.

Additional IFN-γ laboratory research

The laboratory continues to carry 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 ready to be tested and evaluated in high-risk herds. The laboratory, along with CVERA and DAFM, is 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. 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.

RNA-Seq transcriptome analysis of peripheral blood from cattle infected with *Mycobacterium bovis* across an experimental time course

McLoughlin, K.E.[1], Correia, C.N.[1], Browne, J.A.[1], Magee, D.A.[1], Nalpas, N.C.[1], Rue-Albrecht, K.[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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[3] UCD School of Veterinary Medicine, [4] UCD Conway Institute of Biomolecular and Biomedical Research

Frontiers in Veterinary Science 8, 662002 (2021)

Bovine tuberculosis, caused by infection with members of the *Mycobacterium tuberculosis* complex, particularly *Mycobacterium bovis*, is a major endemic disease affecting cattle populations worldwide, despite the implementation of stringent surveillance and control programs in many countries. The development of high-throughput functional genomics technologies, including RNA sequencing, has enabled detailed analysis of the host transcriptome to *M. bovis* infection, particularly at the macrophage and peripheral blood level. In the present study, we have analysed the transcriptome of bovine whole peripheral blood samples collected at −1 week pre-infection and +1, +2, +6, +10, and +12 weeks post-infection time points. Differentially expressed genes were catalogued and evaluated at each post-infection time point relative to the −1 week pre-infection time point and used for the identification of putative candidate host transcriptional biomarkers for *M. bovis* infection. Differentially expressed gene sets were also used for examination of cellular pathways associated with the host response to *M. bovis* infection, construction of de novo gene interaction networks enriched for host differentially expressed genes, and time-series analyses to identify functionally important groups of genes displaying similar patterns of expression across the infection time course. A notable outcome of these analyses was identification of a 19-gene transcriptional biosignature of infection consisting of genes increased in expression across the time course from +1 week to +12 weeks post-infection.

A molecularly defined skin test reagent for the diagnosis of bovine tuberculosis compatible with vaccination against Johne's Disease

Middleton, S.[1], Steinbach, S.[1], Coad, M.[1], McGill, K.[2], Brady, C.[3], Duignan, A.[3], Wiseman, J.[2, 3], Gormley, E.[2], Jones, G.J.[1], Vordermeier, H.M.[1]

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Scientific Reports 11, 2929 (2021)

Tuberculin Purified Protein Derivatives (PPDs) exhibit multiple limitations: they are crude extracts from mycobacterial cultures with largely unknown active components; their production depends on culture of mycobacteria requiring expensive BCL3 production facilities; and their potency depends on the technically demanding guinea pig assay. To overcome these limitations, we developed a molecularly defined tuberculin (MDT) by adding further antigens to our prototype reagent composed of ESAT-6, CFP-10 and Rv3615c (DIVA skin test, DST). In vitro screening using PBMC from infected and uninfected cattle shortlisted four antigens from a literature-based list of 18 to formulate the MDT. These four antigens plus the previously identified Rv3020c protein, produced as recombinant proteins or overlapping synthetic peptides, were formulated together with the three DST antigens into the MDT to test cattle experimentally and naturally infected with *M. bovis*, uninfected cattle and MAP vaccinated calves. We demonstrated significant increases in MDT-induced skin responses compared to DST in infected animals, whilst maintaining high specificity in unvaccinated or MAP vaccinated calves. Further, MDT can also be applied in in vitro blood-based interferon-gamma release assays. Thus, MDT promises to be a robust diagnostic skin and blood test reagent overcoming some of the limitations of PPDs and warrants full validation.

Post-mortem surveillance of bovine tuberculosis in Ireland: herd-level variation in the probability of herds disclosed with lesions at routine slaughter to have skin test reactors at follow-up test

Byrne, A.W.[1], Barrett, D.[1], Breslin, P.[2], Madden, J.M.[3], O'Keeffe, J.[2], Ryan, E.[2]

[1] DAFM One Health Scientific Support Unit, [2] DAFM, [3] UCD CVERA

Veterinary Research Communications 44, 131-136 (2020)

Post-mortem surveillance in Ireland discloses skin-test negative cattle with presumptive evidence of infection of *Mycobacterium bovis* (lesions at routine slaughter (LRS)), the causative agent of bovine tuberculosis (bTB). Laboratory confirmation of lesions has impacts on trade restrictions for herds, therefore if laboratory capacity was diminished, how herds are treated would require an informed risk policy. Here we report the proportion of herds with subsequent evidence of within-herd transmission, based on skin-test results. We assess how herd-size, herd-type, and bTB-history affect the probability of additional reactors at follow-up test using univariable and multivariable random-effects models. The study represents a rapid response to developing an evidential base for policy demands during an extraordinary event, the COVID-19 epidemic in Ireland. A dataset from 2005 to 2019 of breakdowns were collated. Overall, 20,116 breakdowns were initiated by LRS cases. During the index tests of these breakdowns, 3931 revealed ≥1 skin-test reactor animals (19.54%; ≥1 standard reactors: 3827; 19.02%). Increasing herd-size was associated with reactor disclosure on follow-up. For small herds (<33 animals), 11.74% of follow-up tests disclosed ≥1 reactor; 24.63% of follow-up tests from very large herds (>137) disclosed ≥1 reactors. Beef (13.87%) and "other" (13%) herd production types had lower proportion of index tests with reactors in comparison with dairy (28.27%) or suckler (20.48%) herds. Historic

breakdown size during the previous 3-years was associated reactor disclosure risk on follow-up. Our results are useful for rapid tailored policy development aimed at identifying higher risk herds.

Reprinted by permission from Springer Nature: Springer Nature B.V. Veterinary Research Communications, *Post-mortem surveillance of bovine tuberculosis in Ireland: herd-level variation in the probability of herds disclosed with lesions at routine slaughter to have skin test reactors at follow-up test, Byrne et al © 2020.*

Re-evaluating the performance of the interferon gamma test on *Mycobacterium bovis* infected herds

Madden, J.M. et al.
UCD CVERA

The interferon gamma (IFN-γ) diagnostic test has become a critical tool for Ireland's bovine tuberculosis (bTB) eradication programme. It is used in conjunction with the single intradermal comparative tuberculin test (SICTT) to detect additional animals infected with *Mycobacterium bovis* that would have been missed and considered negative, if the SICTT alone had been utilized. However, as neither approach is deemed fully efficient, care must be taken when interpreting results and IFN-γ positive / SICTT negative animals have been detected with no visible lesions at slaughter suggesting that these animals may not actually be infected i.e., test false positive. Therefore, it is important to continually monitor the performance of this diagnostic test to unsure we are maximizing its potential. Thus, the aim of this study will be to re-evaluate the cut-off values currently being used and to develop a risk prediction tool to aid the decision-making process.

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

McGrath, G. et al.
UCD CVERA

This project aims to test the commonly believed idea that some areas in Ireland are prone to having positive SICCT tests caused by non-tuberculous mycobacteria. If these areas are detectable, herds occurring within them could be flagged which will assist with interpretation of herds with persistent single reactor tests and ultimately provide evidence to shape TB eradication policy both nationally and internationally.

bTB control

Spatio-temporal models of bovine tuberculosis in the Irish cattle population, 2012-2019

Madden, J.M.[1], McGrath, G.[1], Sweeney, J.[2], Murray, G.[3], Tratalos, J.A.[1], More, S.J.[1]

[1] UCD CVERA, [2] UL Department of Mathematics and Statistics, [3] DAFM

Spatial and Spatio-temporal Epidemiology 39, 100441 (2021)

Bovine tuberculosis (bTB) is an important zoonotic disease which has serious and sometimes fatal effects on both human and non-human animals. In many countries it is endemic in the cattle population and has a considerable economic impact through losses in productivity and impacts on trade. The incidence rate in Ireland varies by herd and location and it is hoped that statistical disease-mapping models accounting for both spatio-temporal correlation and covariates might contribute towards explaining this variation. Ireland was divided into equally sized hexagons for computational efficiency (n = 997). Different spatio-temporal random-effects models (e.g., negative binomial Besag-York-Mollié) were explored, using comprehensive data from the national bTB eradication programme to examine the association between covariates and the number of bTB cattle. Leveraging a Bayesian framework, model parameter estimates were obtained using the integrated nested Laplace approximation (INLA) approach. Exceedance probabilities were calculated to identify spatial clusters of cases. Models accounting for spatial correlation significantly improved model fit in comparison to non-spatial versions where independence between regions was assumed. In our final model at hexagon level, the number of cattle (IR = 1.142, CrI: 1.108 – 1.177 per 1000), the capture of badgers (IR = 5.951, CrI: 4.482 – 7.912), percentage of forest cover (IR = 1.031, CrI: 1.020 – 1.042) and number of farm fragments (IR = 1.012, CrI: 1.009 – 1.015 per 10 fragments) were all associated with an increased incidence of bTB. Habitat suitability for badgers, percentage of dairy herds and the number of cattle movements into the herd were not. As an epidemiological tool and to suggest future work, an interactive online dashboard was developed to monitor disease progression and disseminate results to the general public. Accounting for spatial correlation is an important consideration in disease mapping applications and is often ignored in statistical models examining bTB risk factors. Over time, the same regions in Ireland generally show highest incidences of bTB and allocation of more resources to these areas may be needed to combat the disease. This study highlights national bTB incidence rates. Shifting from national level analysis to smaller geographical regions may help identify localised high-risk areas.

Bovine tuberculosis *(Mycobacterium bovis)* outbreak duration in cattle herds in Ireland: a retrospective observational study

Byrne, A.W.[1], Barrett, D.[1], Breslin, P.[2], Madden, J.M.[3], O'Keeffe, J.[2], Ryan, E.[2]

[1] DAFM One Health Scientific Support Unit, [2] DAFM, [3] UCD CVERA

Pathogens 9, 815 (2020)

Bovine tuberculosis (bTB) outbreaks, caused by *Mycobacterium bovis* infection, are a costly animal health challenge. Understanding factors associated with the duration of outbreaks, known as breakdowns, could lead to better disease management policy development. We undertook a retrospective observational study (2012–2018) and employed Finite Mixture Models (FMM) to model the outcome parameter, and to investigate how factors were associated with duration for differing subpopulations identified. In addition to traditional risk factors (e.g., herd size, bTB history), we also explored farm geographic area, parcels/farm fragmentation, metrics of intensity via nitrogen loading, and whether herds were designated controlled beef finishing units (CBFU) as potential risk factors for increased duration. The final model fitted log-normal distributions, with two latent classes (k) which partitioned the population into a subpopulation around the central tendency of the distribution, and a second around the tails of the distribution. The latter subpopulation included longer breakdowns of policy interest. Increasing duration was positively associated with recent (<3 years) TB history and the number of reactors disclosed, (log) herd size, beef herd-type relative to other herd types, number of land parcels, area, being designated a CBFU ("feedlot") and having high annual inward cattle movements within the "tails" subpopulation. Breakdown length was negatively associated with the year of commencement of breakdown (i.e., a decreasing trend) and non-significantly with the organic nitrogen produced on the farm (N kg/hectare), a measure of stocking density. The latter finding may be due to confounding effects with herd size and area. Most variables contributed only moderately to explaining variation in breakdown duration, that is, they had moderate size effects on duration. Herd-size and CBFU had greater effect sizes on the outcome. The findings contribute to evidence-based policy formation in Ireland.

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

Byrne, A.W.[1], Barrett, D.[1], Breslin, P.[2], Madden, J.M.[3], O'Keeffe, J.[2], Ryan, E.[2]

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Microorganisms 9, 1004 (2021)

Bovine tuberculosis (bTB) remains a significant endemic pathogen of cattle herds, despite multi-decadal control programmes being in place in several countries. Understanding the risks of future bTB breakdown (BD) and the associated characteristics of herds and index breakdowns could help inform risk categorisation. Such risk categories could then contribute to tailored management and policies. Here, we estimated the future risk of herd BD for the cohort of herds that were derestricted during 2013 in Ireland using multivariable logit regression models, with a dominance analysis approach. One third of herds that were derestricted in 2013 experienced a breakdown during the follow-up five year period (1469/4459; 33%). BD length was a significant predictor of future risk, primarily driven by long BDs > 230 days relative to short BDs < 130 days (OR 95%CI: 1.157–1.851), as was having had a previous BD (OR 95%CI: 1.012–1.366). Herd-size was the dominant predictor of future risk (accounted for 46% of predicted variance), suggesting significant increase in risk of future breakdown with increasing (log) herd-size (OR 95%CI: 1.378–1.609). There was significant spatial variation in future risk across counties, and it was the second most dominant predictor of future risk (25% of predicted variance). The size of index breakdowns was not a strong predictor of future risk over a 5-year period. These findings can inform a risk-based policy development.

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], Ryan, E.[2], Byrne, A.W.[4], Barrett, D.[4]

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Preventive Veterinary Medicine 198, 105542 (2022)

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.

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Estimating the hidden burden of bovine tuberculosis in Ireland

Casey, M. et al.

UCD CVERA

This project will combine a within-herd model of bovine tuberculosis (bTB) transmission with a model of the Irish diagnostic and control regime in cattle. Specifically, we will adapt and develop the methodology of Conlan et al. (2012) in the paper “Estimating the hidden burden of bovine tuberculosis in Great Britain” - PLoS *Computational Biology* 8, e1002730. We aim to infer key transmission and diagnostic parameters and predict missed cattle infections. We will use the validated model to explore the potential impact of different diagnostic regimes and cattle controls on missed infections and the resolution of breakdowns. In this background section, we present (1) the science supporting our proposal, (2) policy implications and (3) a summary of the proposed project. Currently, we are conducting preliminary work for this project including organising the dataset, defining the study populating, generating a model of the Irish bTB diagnostic testing and control process and initial summary statistics. We hope to progress towards replicating and developing the model of Conlan et al. (2012) later in 2022.

Diagnosis and risk of bovine tuberculosis in young cattle stock

Byrne, A.W. et al.
DAFM One Health Scientific Support Unit

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, remains a high priority pathogen of concern worldwide. Despite long-term intensive programs of eradication in several countries, the pathogen has persisted. The role of youngstock in the epidemiology of bTB has not been a central focus of recent research. Therefore, here the aim is to collate and summarise what is known about the diagnosis of bTB, in youngstock (for the purposes of this review youngstock being up to 1 year of age, with particular interest in animals up to 4 months or 120 days old) and the subsequent risk associated with this cohort in relation to disease control programs. A narrative review will be developed based on primary literature and in reference to closely related review of bTB diagnostics and risk factors. In a separate part of the overall project, an exportation of young calves that test positive will be undertaken.

Whole Genome Sequencing (WGS) analysis of *M. bovis* in a bTB cluster in Co. Monaghan

Farrell, D. et al.
UCD School of Veterinary Medicine

This study will utilise Whole Genome Sequencing (WGS) to identify whether badgers and cattle present in Monaghan share common strains of *Mycobacterium bovis*. Strains sequenced will be added to a national database. Techniques will be designed which will enable WGS methodologies to be utilise as a tool in epidemiological investigations.

A spatial epidemiological analysis of Bovine TB in cattle herds in The Burren, County Clare

Tratalos, J.A. et al.
UCD CVERA

The incidence of bovine tuberculosis (bTB) in cattle herds in the Burren (County Clare) is higher than the national average, and this has been the case at least since 2005. This analysis will form part of a larger stakeholder engagement with herd owners in the Burren to identify the causes of this phenomenon, which will include the use of a herd owner questionnaire led by colleagues in DAFM. The CVERA component of this project will examine the relationship between bTB incidence in Burren herds and data available in national scale datasets.

Bayesian modelling of bTB transmission factors in Irish cattle herds

Hurley, A. et al.
University of Limerick

This project (as part of a PhD) will involve the construction of a detailed simulation model to examine the impact of individual disease prevention measures on the spread of bovine tuberculosis (bTB) in Ireland. The factors explored will include the impact of improved testing performance and harnessing information from multiple sources to predict disease outbreaks as a follow on to More et al (2019), *"Can bovine TB be eradicated from the Republic of Ireland? Could this be achieved by 2030"*. The aim of the project is to both guide and allow for concrete policy changes, as well as provide further validation for existing policy decisions through the development of spatio-temporal statistical models.

Animal level analysis – age-dependent patterns of bTB in cattle

Madden, J.M. et al.
UCD CVERA

Most infectious diseases are age-dependent (e.g., in people, the young are at more risk of severe disease from whooping cough while the elderly are at increased risk of mortality from influenza like illnesses). However, for bTB in Ireland, age-dependent risks have not yet been quantified. This project is focused 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, determine if this association varies by breed and herd type.

Irish cattle movements

Spatial and network characteristics of Irish cattle movements

Tratalos, J.A.[1], Madden, J.M.[1], McGrath, G.[1], Graham, D.A.[2], Collins, Á.B.[1, 3], More, S.J.[1]

[1] UCD CVERA, [2] Animal Health Ireland, [3] DAFM

Preventive Veterinary Medicine 183, 105095 (2020)

Our aim was to examine, for the first time, the spatial and network characteristics of cattle movements between herds in the Republic of Ireland (ROI), to inform policy and research of relevance to the surveillance and management of disease in Irish cattle. We analysed movements in 2016 as discrete herd to herd pairings (degree), herd to herd pairings by date of move (contacts) and herd to herd pairings by date and individual animal (transfers), and looked at each of these as movements out of a herd (out degree, out contacts, out transfers) and into a herd (in degree, in contacts, in transfers). We found that the frequency distributions, by herd, of these six move types were all heavily right skewed but in the case of the 'out' data types more closely followed a log-normal than the scale free distribution often reported for livestock movement data. For each distinct herd to herd contact in a given direction, over 90 % occurred only once, whereas the maximum number of occurrences was 62. Herd-level Spearman rank correlations between inward moves (represented as in degree, in contacts, in transfers) and outward moves (out degree, out contacts, out transfers) were weak or even negative whereas correlations between different measures of outward moves or inward moves (e.g. out degree vs. out contacts, in transfers vs. in degree) were stronger. Correlations between these variables and the network measure betweenness varied between r = 0.513 and r = 0.587. Some herds took part in a relatively large number of movements whilst also retaining their cattle for long periods (> 100 days) between moves. In and out degree, contacts and transfers were mapped across Ireland on a 5 km grid, and additionally normalized per 1000 animals and per herd. We found considerable variation in the number of movements by county. Approximately half of transfers were conducted within a single county, but the number and distance of between county movements varied considerably by county of origin and county of destination, with the proportion of moves completed within a single county correlated with its size. Herds exchanging cattle via a market were generally further apart than when moves were made directly herd to herd. For contacts, the distances moved away from the herd were on average greater for origin herds in the west of ROI whereas distances moved to a herd were generally greater for destination herds in the centre-east and the north-west.

A systematic framework of modelling epidemics on temporal networks

Humphries, R.[1], Mulchrone, K.[1], Tratalos, J.[2], More, S.J.[2], Hövel, P.[1]

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Applied Network Science 6, 23 (2021)

We present a modelling framework for the spreading of epidemics on temporal networks from which both the individual-based and pair-based models can be recovered. The proposed temporal pair-based model that is systematically derived from this framework offers an improvement over existing pair-based models by moving away from edge-centric descriptions while keeping the description concise and relatively simple. For the contagion process, we consider the susceptible–infected–recovered (SIR) model, which is realized on a network with time-varying edges. We show that the shift in perspective from individual-based to pair-based quantities enables exact modelling of Markovian epidemic processes on temporal tree networks. On arbitrary networks, the proposed pair-based model provides a substantial

increase in accuracy at a low computational and conceptual cost compared to the individual-based model. From the pair-based model, we analytically find the condition necessary for an epidemic to occur, otherwise known as the epidemic threshold. Due to the fact that the SIR model has only one stable fixed point, which is the global non-infected state, we identify an epidemic by looking at the initial stability of the model.

An analysis of the role of cattle movements in TB transmission

Tratalos, J.A. et al.
UCD CVERA

This project will examine the relationship between network derived cattle movement metrics and bovine tuberculosis (bTB), building on work conducted in the UK. Likelihood of experiencing a breakdown during 2018 – 2019 will be examined using the following inputs: bTB status, 2013-2017, of herds in the ingoing contact chains (ICCs) of cattle movements into the herd, 2015-2017; the betweenness centrality measure of the herd, in degree, total number of movements into the herd, prior TB history of the herd; TB incidence in neighbouring herds; herd type, herd size, altitude, rainfall, county, and modelled probability of a badger social group on the farm. Residuals from the models will be mapped in order to assess their performance across Ireland and to flag potential problem areas where bTB prevalence is unusually high, suggesting that some factors not accounted for in the model may operate locally, such as farm management practices or the presence of alternative (non-badger) wildlife hosts such as deer.

A systematic framework of modelling epidemics on temporal networks - A network model of bovine TB

Humphries, R. et al.
University College Cork

Further to the work conducted by Humphries et al (2021), the authors will proceed to use the modelling framework to examine the relationship between cattle movements and bTB spread in Irish herds and consider the implications of the findings for a trading system guided by bTB risk among trading herds.

Badger ecology

Emergence counts of badgers *(Meles meles)* in lowland Co. Wicklow

Sleeman, D.P.[1], Collins, D.M.[2], O'Keeffe, J.J.[2, 3], Mackey, M.[1]

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Irish Naturalists' Journal 37, 150-154 (2021)

Emergence counts of badgers were conducted by trained volunteers. Such counts or 'badger watching' are a relatively easy, non-invasive method of estimating numbers in a specific area, without some of the disadvantages, such as animal welfare and trap shyness, associated with other methods, such as restraint or cage capturing and mark- re-capture. The results are variable, numbers of badgers per sett differed per night, and no badgers were seen at three setts. The variation is discussed with reference to monitoring badgers.

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Two-tier badgers' *(Meles meles)* territories in lowland Wicklow, Ireland

Sleeman, D.P.[1], Mackey, M.[1], O'Keeffe, J.J.[2, 3], Collins, D.M.[3]

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Irish Naturalists' Journal (in press) (2022)

Nine badger territories were estimated using bait-marking in Wicklow in 2009. The territories varied in size between 8.6 and 85.4 hectares (ha) and presented in a variety of shapes. Cubs were only detected in the bigger territories, suggesting a two-tier badger social system between those that breed and those that do not. It is proposed that non-breeding, small unstable setts be called peripheral setts. Bait-marking followed by counts can provide useful information on badgers.

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The challenge of estimating wildlife populations at scale: the case of the European badger *(Meles meles)* in Ireland

Byrne, A.W.[1], Parnell, A.[2], O'Keeffe, J.[3], Madden, J.M.[4]

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European Journal of Wildlife Research 67, 85 (2021)

Estimating population size in space and time is essential for applied ecology and wildlife management purposes; however, making accurate and precise estimates at large scales is highly challenging. An example is the European badger *(Meles meles)*, a widespread and abundant mammal in Ireland. Due to their role in the epidemiology of bovine tuberculosis, the species has been culled in agriculturally dominant landscapes with the intention of reducing spillback infection to local cattle populations. Despite several studies using different approaches having estimated badger populations at different time points and scales, there remains considerable uncertainty regarding the current population and its future trajectory. To explore this uncertainty, we use published data and expert opinion to estimate a snapshot of probable badger population size using a Monte Carlo approach, incorporating variation in three key components: social group numbers, group size, and culling efficacy. Using this approach, we estimate what the badger population in Ireland would be with/without culling, assuming a steady-state population at carrying capacity, and discuss the limitations of our current understanding. The mean estimate for the badger population size was 63,188 (5–95th percentile, 48,037–79,315). Population estimates were sensitive to the assumption of mean group size across landscape type. Assuming a cessation of culling (in favour of vaccination, for example) in agricultural areas, the mean estimated population size was 92,096 (5–95th percentile, 67,188–118,881). Despite significant research being conducted on badgers, estimates on population size at a national level in Ireland are only approximate, which is reflected in the large uncertainty in the estimates from this study and inconsistencies between recording of data parameters in previous studies. Focusing on carefully estimating group size, factors impacting its variation, in addition to understanding the dynamics of repopulation post-culling, could be a fruitful component to concentrate on to improve the precision of future estimates.

The epidemiology of Mycobacterium bovis *in badgers*

Mycobacterium bovis genomics reveals transmission of infection between cattle and deer in Ireland

Crispell, J.[1, 2], Cassidy, S.[1], Kenny, K.[3], McGrath, G.[4], Warde, S.[3], Cameron, H.[3], Rossi, G.[5, 6], MacWhite, T.[7], White, P.C.L.[8], Lycett, S.[6], Kao, R.R.[5, 6], Moriarty, J.[3], Gordon, S.V.[1,9]

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Microbial Genomics 6, 8 (2020)

Control of bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, in the Republic of Ireland costs €84 million each year. Badgers are recognized as being a wildlife source for *M. bovis* infection of cattle. Deer are thought to act as spillover hosts for infection; however, population density is recognized as an important driver in shifting their epidemiological role, and deer populations across the country have been increasing in density and range. County Wicklow represents one specific area in the Republic of Ireland with a high density of deer that has had consistently high bTB prevalence for over a decade, despite control operations in both cattle and badgers. Our research used whole-genome sequencing of *M. bovis* sourced from infected cattle, deer and badgers in County Wicklow to evaluate whether the epidemiological role of deer could have shifted from spillover host to source. Our analyses reveal that cattle and deer share highly similar *M. bovis* strains, suggesting that transmission between these species is occurring in the area. In addition, the high level of diversity observed in the sampled deer population suggests deer may be acting as a source of infection for local cattle populations. These findings have important implications for the control and ultimate eradication of bTB in Ireland.

Evaluation of the Dual Path Platform (DPP) VetTB assay for the detection of *Mycobacterium bovis* infection in badgers

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Preventive Veterinary Medicine 180, 105005 (2020)

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, represents a major animal health issue. In the United Kingdom and the Republic of Ireland, European badgers *(Meles meles)* have been shown to act as a reservoir of *M. bovis* infection, hindering the eradication of bTB in livestock. The availability of suitable diagnostic assays, particularly those that may be applied in a “trap-side” setting, would facilitate the implementation of a wider range of disease control strategies. Here we evaluate the Dual Path Platform (DPP) VetTB assay, a lateral-flow type test for detecting antibodies to *M. bovis* antigens (MPB83 and ESAT-6/CFP-10). Both serum and whole blood were evaluated as diagnostic samples. Additionally, two methods were evaluated for interpretation of test results (qualitative interpretation by eye and quantitative measurement using an optical reader). The antibody response to MPB83 detected by the DPP VetTB assay increased significantly following experimental *M. bovis* infection of badgers, whilst the response to ESAT-6/CFP-10 showed no significant change. In sera from TB-free captive and naturally *M. bovis* infected wild badgers the MPB83 response exhibited a sensitivity of 55 % by eye and quantitative reader (95 % CI: 40–71 and 38–71, respectively), with slightly lower specificity when read by eye (93 % compared to 98 %; 95 % CI: 85–100 and 90–100, respectively). In whole blood, the DPP VetTB assay MPB83 response exhibited a sensitivity of 65 % (95 % CI: 50–80) when interpreted by eye and 53 % (95 % CI: 36–69) using quantitative values, whilst the specificity was 94 % and 98 % respectively (95 % CI: 88–100 and 90–100). Comparison with contemporaneous diagnostic test results from putatively naturally infected and TB-free badgers demonstrated varying levels of agreement. Using sera from naturally *M. bovis* infected and TB-free badgers, with post mortem confirmation of disease status, the DPP VetTB assay exhibited a sensitivity of 60 % (95 % CI: 41–77) when interpreted using quantitative values (specificity 95 %; 95 % CI: 76–100), and 67 % (95 % CI: 50–84) when read by eye (specificity 95 %; 95 % CI: 86–100). Further work is required to robustly characterize the DPP VetTB assay’s performance in a wider selection of samples, and in the practical and epidemiological contexts in which it may be applied.

BCG vaccination in badgers

The badger vaccine development programme

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

The role of badgers in the transmission of tuberculosis to cattle herds has created much interest in Ireland, the UK and elsewhere in Europe where the problems of tuberculosis and how to deal with them are often quite controversial. Our internationally advocated strategy has been to develop a vaccine for badger populations against tuberculosis in the expectation that it will protect badgers and reduce infection transmission rates to cattle. The team at UCD has published much work on development of the BCG vaccine for use in badgers most of which was carried out in an experimental setting.

In this study, we have published the first detailed pathological report of the impact of oral BCG vaccination on progression of infection / disease in free-living badgers during the largest wildlife BCG vaccine study ever conducted worldwide (covering approx. 755 km^2). We analysed detailed pathological, histological and bacteriological data from the full cohort of badgers removed at the end of the trial to determine if vaccination a) protected badgers from infection and b) reduced the likelihood of infected badgers developing severe disease. In addition, by including non-treated badgers in the study group we were able to look for evidence of any indirect effect of vaccination that might impact on the prevalence of infection in the population. The results provided strong evidence of the BCG vaccine effectiveness in badgers as measured by a reduction in susceptibility to infection and an indirect protective effect conferred on the non-vaccinated proportion of the population. The results suggest that BCG vaccination of badgers could be a highly effective means of reducing the incidence of tuberculosis in badger populations.

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 managed by Ann Barber (Wageningen University & UCD CVERA) by assisting to process field blood samples for antibody testing and conducting ancillary lateral flow testing to monitor test performance in the field.

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

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.[1], Murphy, D.[1, 2], Corner, L.[1]

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Transboundary and Emerging Diseases (in press) (2022)

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.

Is moving from targeted culling to BCG-vaccination of badgers *(Meles meles)* associated with an unacceptable increased incidence of cattle herd tuberculosis in the Republic of Ireland? A practical non-inferiority wildlife intervention study in the Republic of Ireland (2011-2017)

Martin, S.W.[1], O'Keeffe, J.[2], Byrne, A.W.[2, 3, 4], Rosen, L.E.[5], White, P.W.[2, 6], McGrath, G.[6]

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Preventive Veterinary Medicine 179, 105004 (2020)

Bovine tuberculosis (BTB) remains as a costly disease of cattle-herds in the Republic of Ireland (ROI). This persistence is partially attributable to the presence of *M. bovis* infection in a wildlife reservoir, the European badger *(Meles meles)*. Thus, both area-wide and limited-area targeted-badger-culling have been part of the ROI-BTB control/eradication program to help reduce the future incidence of a cattle-herd BTB breakdown (i.e., a "new herd-level occurrence of BTB"). However, neither badger-culling practice can be sustained as a major component in the ongoing BTB eradication program in the ROI. Vaccination of badgers with Bacille Calmette-Guérin (BCG) has been proposed as an alternative to badger culling. Thus, in 2011, a five-year non-inferiority study was implemented in seven counties in the ROI. This study was designed to compare and contrast the cattle-herd-BTB-incidence in areas where intramuscular badger vaccination would be implemented versus the cattle-herd-BTB-incidence in the remaining area of the same county where targeted-badger-culling was maintained as the standard treatment response to probable badger-sourced BTB breakdowns. Our outcome of interest was a new cattle-herd-BTB-episode (breakdown) with a total of >2 standard skin-test (SICTT) reactors detected during the episode. Treatments (badger vaccination or targeted badger culling) were cluster allocated based on where the majority of the herd owner's land was located. To assess the impact of the two treatments, we compared the incidence-risk, of our defined outcome, for cattle herds in the area under vaccination to the outcome incidence-risk for cattle herds in the remainder of the same county after 4 and 5 years of having implemented badger vaccination. A random-effects logit model with adjustment for clustering by treatment, and statistical control of herd-type, herd-size and five-year prior-BTB-episode history was used for our analyses. Although not included in the logistic model, a relative badger density metric based on the annual number of badgers captured-per-sett-night of capturing effort was developed for each treatment area; this metric indicated that relative badger density was approximately 40 % higher in vaccination areas than in the targeted badger-culling areas during our study. Overall, our study results indicated that vaccination was not inferior to targeted badger-culling in four counties and badger vaccination was deemed to produce ambivalent results in one (County Cork North) of the seven study sites in the ROI. A post-study investigation, in County Galway, where vaccination was deemed inferior to target culling, revealed that widespread purchases of cattle from a nearby cattle mart, by herd owners in the vaccination-area, was associated with the increased herd and vaccination-area risk of BTB. No single "biasing hypothesis" was evident for the apparent vaccine inferiority in the second study site (County Monaghan) where vaccination was deemed inferior to targeted culling; hence no further investigations were conducted.

Infection control strategies in a multi-host system

Quantification of multi-host transmission based on endemic prevalence: *Mycobacterium bovis* in badgers and cattle as an example

Aznar, I.[1, 2, 3], de Jong, M.C.M. et al.[1]

[1] Wageningen University, Wageningen, The Netherlands, [2] DAFM & [3] UCD CVERA

In Ireland, in spite of a comprehensive control/eradication programme for *Mycobacterium bovis*, tuberculosis in cattle (bTB) has remained endemic in cattle at a low prevalence for the last 20 years. Badgers *(Meles meles)* are considered to be the main wildlife reservoir for *M. bovis* infection in Ireland and Great Britain. To select strategies that allow eradication of the infection in cattle, knowledge of the quantitative role of each of these two host species in the transmission of *M. bovis* is essential. Here, we derive algorithms that show how the Next Generation Matrix (NGM) and the reproduction ratio *(RR)* for the cattle-badger system can be calculated from prevalence data and the number of cattle herds and badgers, collected at the endemic steady state. By exploring the system at the endemic equilibrium, we can set bounds for the possible transmission scenarios between cattle and badgers in Ireland. By constructing these boundaries, we can examine the scenarios where BCG vaccination of badgers in addition to current controls could successfully achieve eradication of *M. bovis* infection in the system.

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)

Barber, A. et al.

Wageningen University, Wageningen, The Netherlands & UCD CVERA

Badger vaccination is progressively replacing culling as part of the national strategy in controlling the spread of bTB. An understanding of the local dynamics is key to ensure the success of the vaccination programme. A test, vaccinate and removed or release field trial is ongoing to quantify local transmission and evaluate the effects of local factors on badger vaccination. The results of this trial will help to inform national policy in relation to the vaccination programme.

Modelling local bTB transmission in a two-host disease dynamic system

Chang, Y. et al.

Wageningen University, Wageningen, The Netherlands

With the ongoing badger vaccination, it is important to have an early identification where badger vaccination might be insufficient to eradicate TB in this cattle-badger system. An understanding of the local dynamics is important for predicting high-risk areas. Although *Mycobacterium bovis* is known to be persistent in the environment, the importance of the environment in the transmission has not been considered in many models. Therefore, we will build an environmental transmission model to understand the local transmission with consideration of badger, cattle and environment. The estimated parameters will be used to generate an R map that can predict high-risk areas and highlight where extra interventions might be needed.

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 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 and farm fragmentation

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

Brock, J. et al.

Helmholtz Centre for Environmental Research GmbH-UFZ, Dept Ecological Modelling, PG Ecological Epidemiology, Leipzig, Germany, Animal Health Ireland & UCD CVERA

A new approach to herd classification was recently described, capturing the different herd types within the Irish cattle industry. This approach utilised machine learning and knowledge-based interpretation. In the current study, this classification system was applied to Irish herds during 2015-19, with the aim to provide an overview of the Irish cattle population, exploring changes in herd types over this period, and describing movements between herd types and to slaughter.

Spatial structure of farms in Ireland (fragmentation)

McGrath, G. et al.

UCD CVERA

The project will provide an in-depth analysis and description of the extent of farm fragmentation in Ireland, including information regarding the number of neighbours and the length of shared boundary with neighbours. Methodologies will be explored to mitigate against operational difficulties DAFM experience due to fragmentation. The metadata will be made available as an online resource accompanying a scientific publication, providing a reference point for future epidemiological studies and important metrics for disease modelling for use nationally and internationally.

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

Collins, Á.B.[1, 2], Floyd, S.[3], Gordon, S.V.[4], More, S.J.[1]

[1] UCD CVERA, [2] DAFM, [3] London School of Hygiene & Tropical Medicine, London, United Kingdom, [4] UCD School of Veterinary Medicine

Tuberculosis (in press) (2022)

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

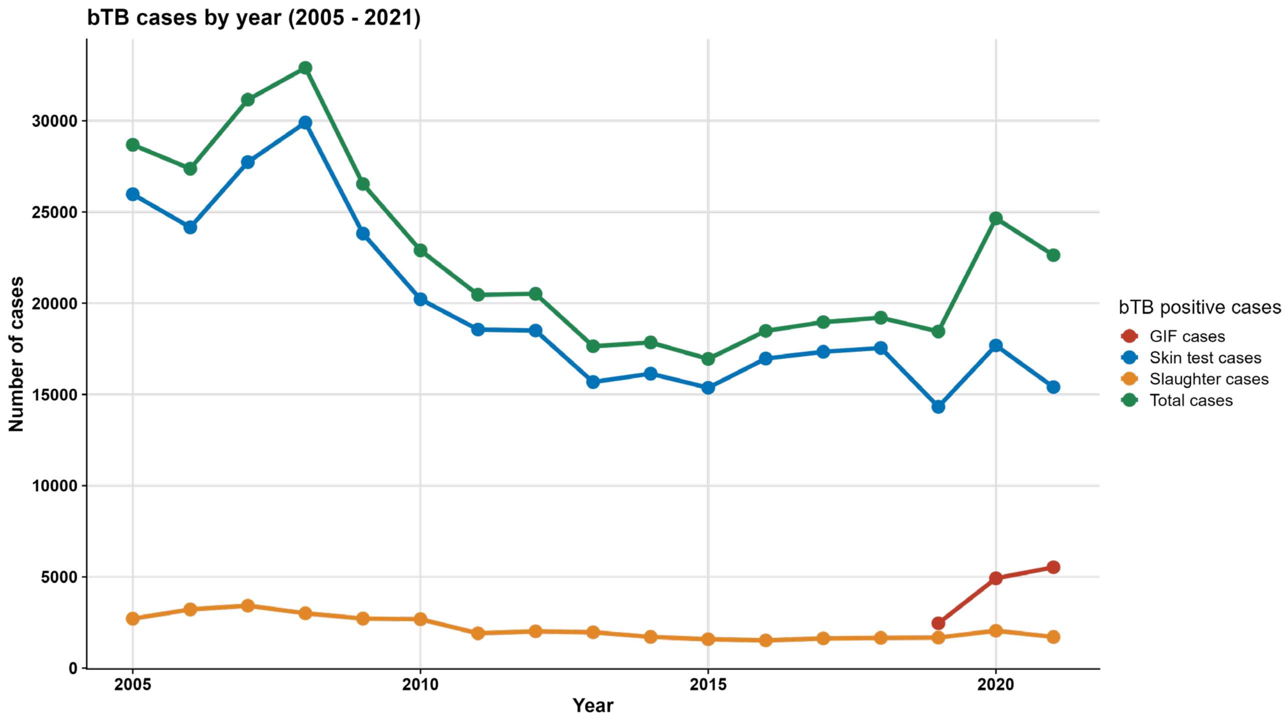
Collins, Á. et al.
DAFM & UCD CVERA

The aim of this study was to determine parameter estimates to support the future risk assessment of *Mycobacterium bovis* in raw milk cheese. In this study, the hazard was identified as viable *M. bovis* organisms in raw milk cheese, parameter estimation for exposure assessment was undertaken using systematic literature reviews and meta-analyses, and EU and Irish legislation were consulted for hazard characterisation. Estimates could be derived for many parameters, but not all. 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.

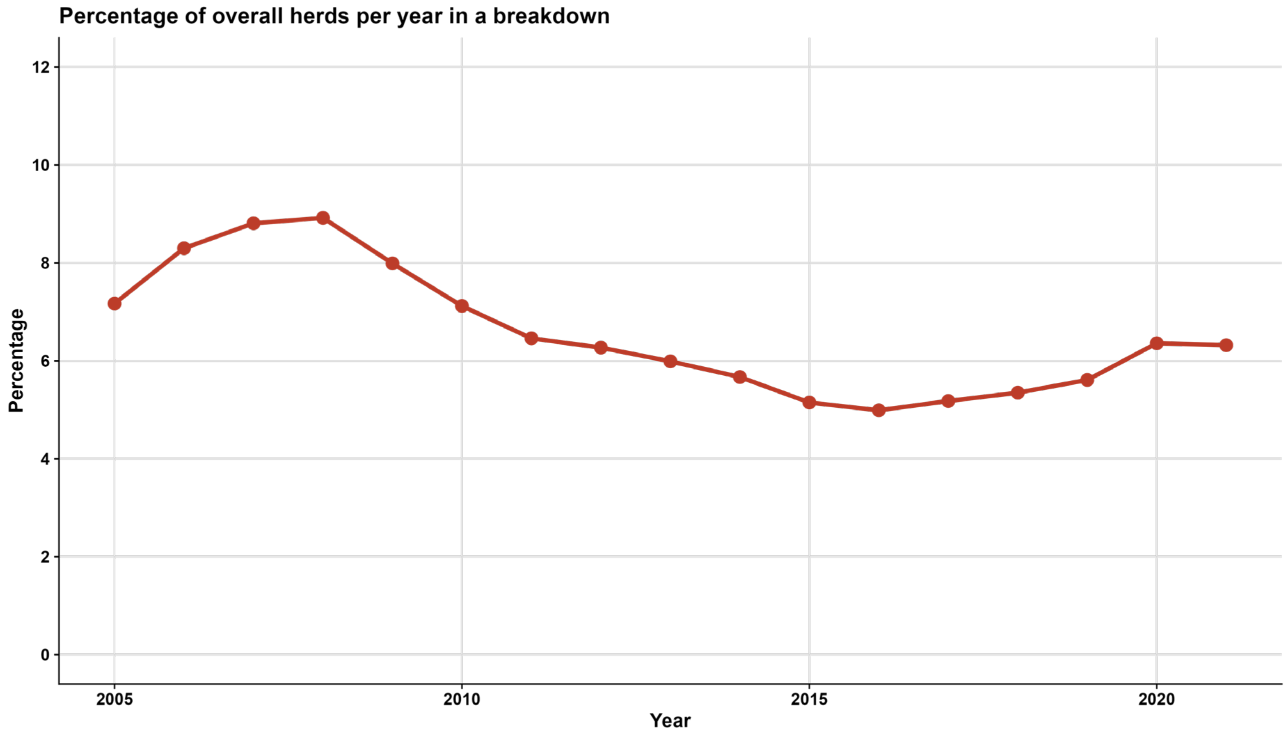
A microbial risk analysis of the public health risk posed by *Mycobacterium bovis* from the consumption of cheese produced from raw milk originating in infected bovine herds

McGee, C. et al.
DAFM

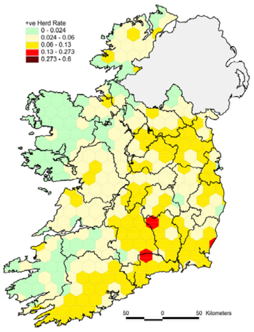
In many countries, including Ireland, human cases of zoonotic tuberculosis caused by *Mycobacterium bovis* are rare, due to pasteurisation of milk and national programmes to control *M. bovis* infection in cattle. Nonetheless, specialty cheeses, which are often produced using raw milk, present a challenge to risk managers. A key concern is the potential risk of zoonotic tuberculosis from consuming dairy products produced using raw milk originating from herds infected with *M. bovis*. The aim of this study is to develop a risk assessment tool to quantify this risk in support of policy decision-making. Complementary projects have been undertaken to determine the parameter estimates that will be needed for this work.



Plot developed from various AHCS data sources supplied to CVERA.
Total cases = GIF + skin + 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).
GIF cases prior to May 2019 were interpreted as skin cases.



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.



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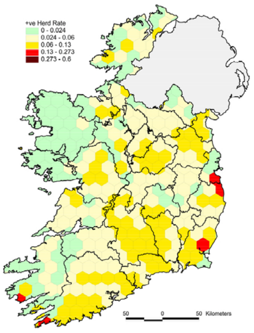

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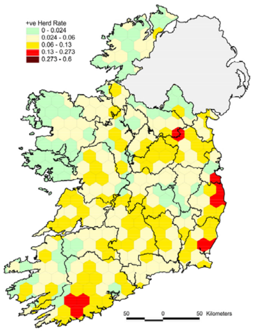

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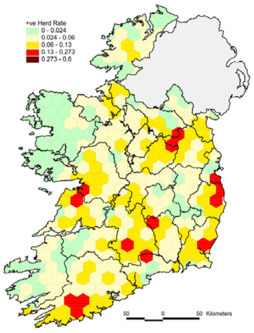

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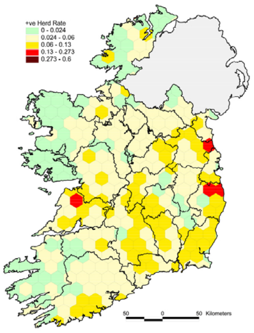

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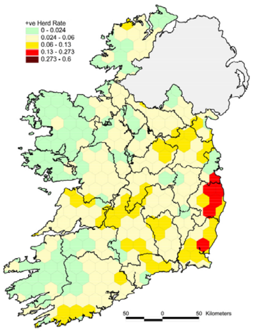

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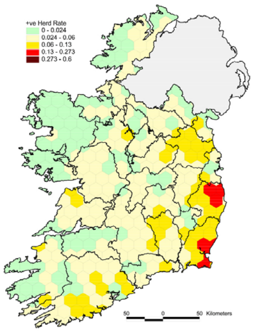

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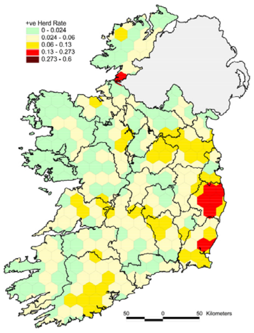

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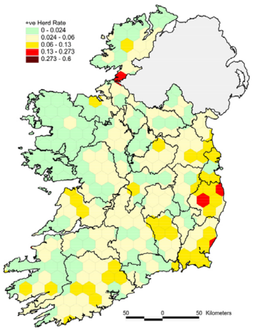

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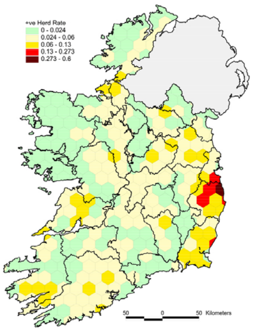

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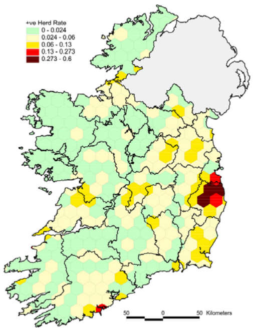

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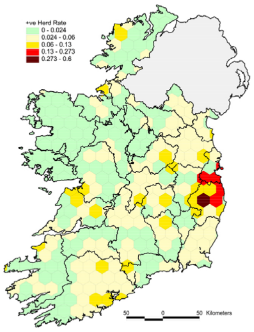

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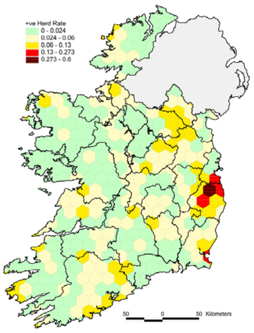

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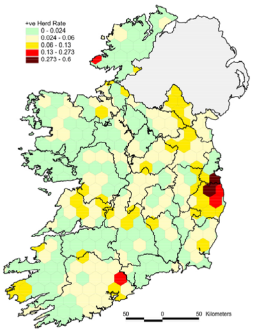
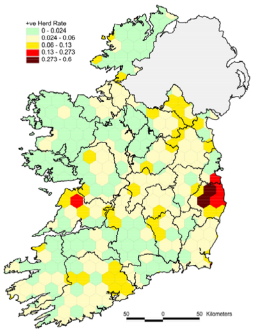
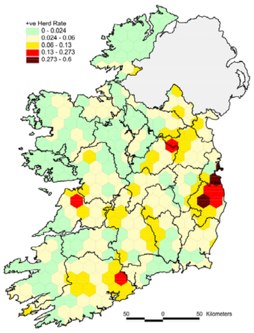


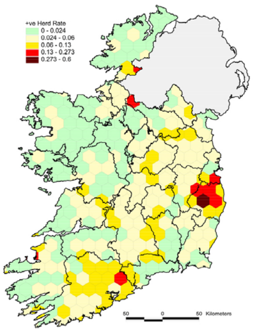
2018



2019



2020

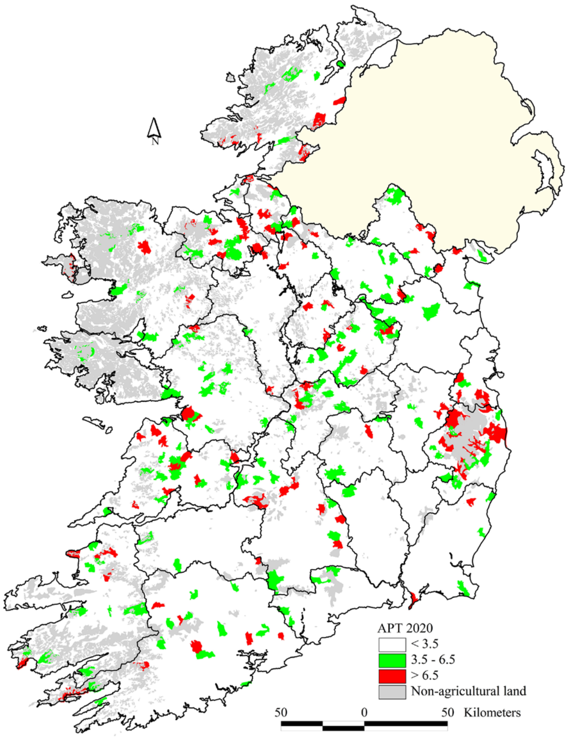


2021

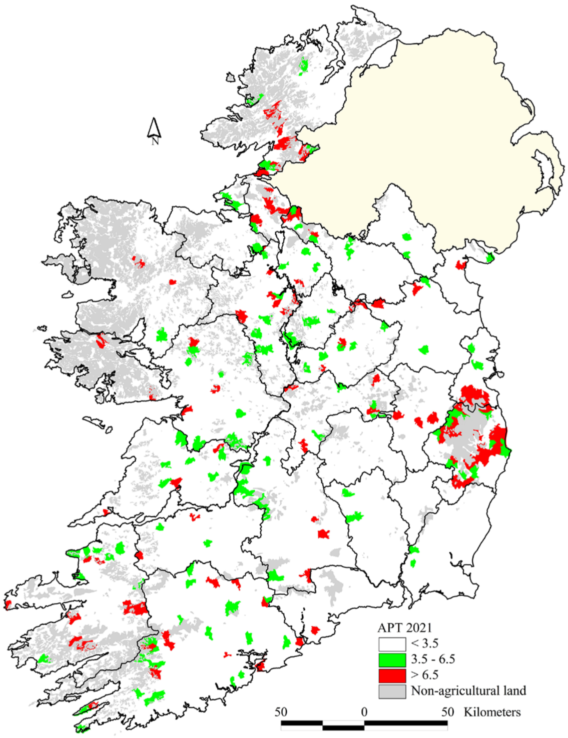
+ve Herd Rate
🟩 0 - 0.024
▨ 0.024 - 0.06
🟨 0.06 - 0.13
🟥 0.13 - 0.273
■ 0.273 - 0.6

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)

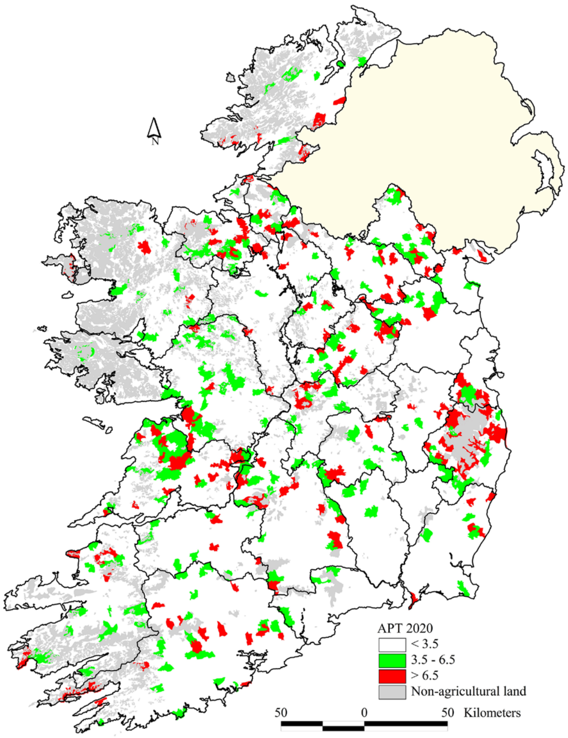


The total number of standard reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2020

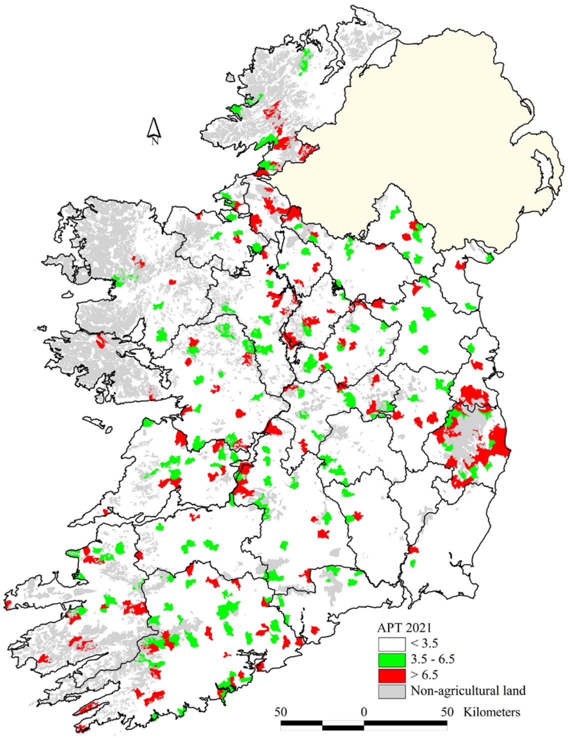


The total number of standard reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2021

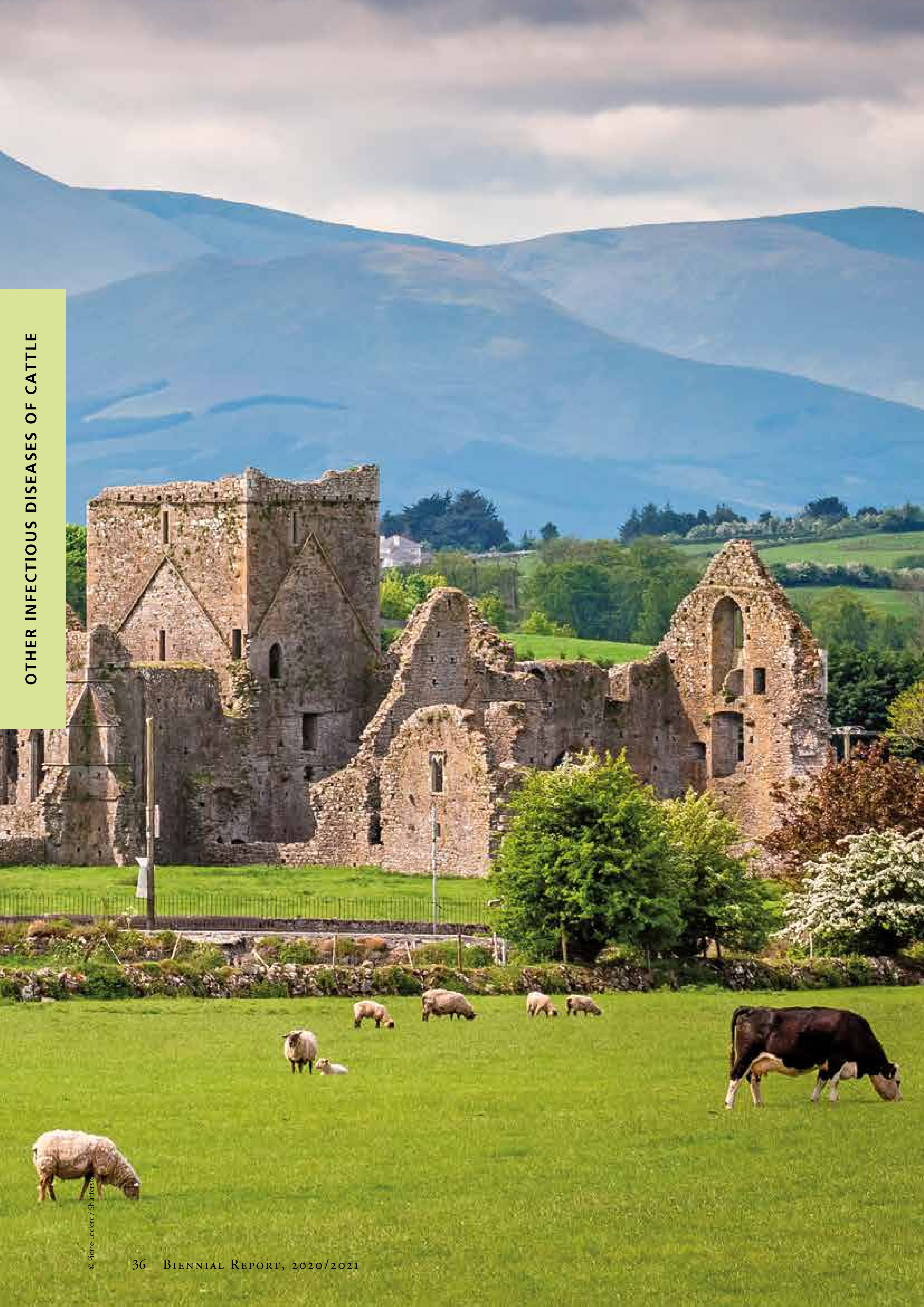
APT per DED (total reactors)



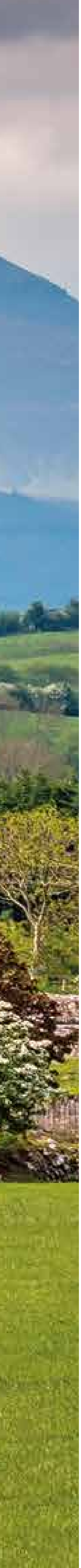
The total number of reactors divided by the total number of Single Intradermal Comparative Tuberculin Tests "skin tests" (x 1,000) per District Electoral Division for 2020



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 2021



© Pierre Leclerc / Shutterst



© Hannah More 2014

Other infectious diseases of cattle

Infectious bovine diseases in general

Bovine viral diarrhoea (BVD)

The Irish programme to eradicate bovine viral diarrhoea virus – organization, challenges and progress

Graham, D.[1], More, S.J.[2], O'Sullivan, P.[3], Lane, E.[4], Barrett, D.[4], Lozano, J.-M.[5], Thulke, H.-H.[6], Verner, S.[7], Guelbenzu, M.[1]

[1] Animal Health Ireland, [2] UCD CVERA, [3] Irish Cattle Breeding Federation, [4] DAFM, [5] DAFM Central Veterinary Research Laboratory, [6] Helmholtz Centre for Environmental Research GmbH - UFZ, Leipzig, Germany, [7] Animal Health and Welfare NI, Dungannon, Northern Ireland

Frontiers in Veterinary Science 8, 674557 (2021)

A mandatory national Irish bovine viral diarrhoea (BVD) eradication programme, coordinated by Animal Health Ireland, commenced in 2013. Key decisions and programme review are undertaken by a cross-industry Implementation Group (BVDIG) supported by a Technical Working Group. Ear notch tissue is collected from all new-born calves using modified official identity tags, supplemented by additional blood sampling, including for confirmatory testing of calves with initial positive results and testing of their dams. Testing is delivered by private laboratories in conjunction with the National Reference Laboratory, with all results reported to a central database. This database manages key elements of the programme, issuing results to herdowners by short message service messaging supplemented by letters; assigning and exchanging animal-level statuses with government databases of the Department of Agriculture, Food and the Marine to enable legislated restrictions on animal movements; assigning negative herd status based on test results; generating regular reports for programme management and evaluation and providing herd-specific dashboards for a range of users. Legislation supporting the programme has been in place throughout but has not thus far mandated the slaughter of persistently infected (PI) calves. A key challenge in the early years, highlighted by modeling, was the retention of PI animals by some herd owners. This has largely been resolved by measures including graduated financial supports to encourage their early removal, herd-level movement restrictions, ongoing programme communications and the input of private veterinary practitioners (PVPs). A framework for funded investigations by PVPs in positive herds was developed to identify plausible sources of infection, to resolve the status of all animals in the herd and to agree up to three measures to prevent re-introduction of the virus. The prevalence of PI calves in 2013 was 0.66%, within 11.3% of herds, reducing in each subsequent year, to 0.03 and 0.55%, respectively, at the end of 2020. Recent regulatory changes within the European Union for the first time make provision for official approval of national eradication programmes, or recognition of BVD freedom, and planning is underway to seek approval and, in due course, recognition of freedom within this framework by 2023.

Herd-level factors associated with detection of calves persistently infected with bovine viral diarrhoea virus (BVDV) in Irish cattle herds with negative herd status (NHS) during 2017

Barrett, D.[1], Clegg. T.[2], McGrath, G.[2], Guelbenzu, M.[3], O'Sullivan, P.[4], More, S.J.[2], Graham, D.A.[3]

[1] DAFM, [2] UCD CVERA, [3] Animal Health Ireland, [4] Irish Cattle Breeding Federation

Preventive Veterinary Medicine 179, 104990 (2020)

A compulsory national BVD eradication programme commenced in Ireland in 2013. Since then considerable progress has been made, with the animal-level prevalence of calves born persistently infected (PI) falling from 0.67 % in 2013 to 0.06 % in 2018. The herd-level prevalence fell from 11.3 % in 2013 to 1.1 % in 2018. In the Irish programme, herds in which all animals have a known negative status and which have not contained any PI animals for 12 months or more are assigned a negative herd status (NHS). While considerable progress towards eradication has been made, PI calves have been identified in a small proportion of herds that had previously been assigned NHS. Given this context, a case-control study was conducted to investigate potential risk factors associated with loss of NHS in 2017. 546 herds which had NHS on 1 January 2017 and lost that status during 2017 (case herds) were matched with 2191 herds (control herds) that retained their NHS status throughout 2017. Previous history of BVD infection, herd size, herd expansion, the purchase of cattle including potential Trojan cattle and the density of BVD infection within 10 km of the herd emerged as significant factors in a multivariable logistic regression model. This work adds to the evidence base in support of the BVD eradication programme, particularly establishing why BVD re-emerged in herds which had been free of BVD for at least the previous 12 months prior to the identification of a BVD positive calf. This information will be especially important in the context of identifying herds which may be more likely to contain BVD positive animals once the programme moves to herd-based serology status for trading purposes in the post-eradication phase.

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. et al.
UCD CVERA

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. This study will involve a case-control study comprised of bovine herds that had calves born and tested negative for BVD virus (BVDV) every year from 2013 to 2019. We defined cases as herds which had one or more test positive calves for the first time in 2019. Controls 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, will be investigated. Network analysis approaches will be 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, will be used to explore these risk factors. This study will suggest elements at farm which may help prevent the introduction of BVDV to low-risk herds. At policy level, other considerations will be highlighted which may help target surveillance measures towards the end of the eradication programme.

Post-eradication options for BVD surveillance

Graham, D. et al.
Animal Health Ireland

Bovine viral diarrhoea virus (BVD) is the cause of an important viral disease of cattle that is estimated to cost Irish farmers around €102 million each year. A mandatory national Irish bovine viral diarrhoea (BVD) eradication programme, coordinated by Animal Health Ireland, commenced in 2013. Since the programme was introduced, animal-level BVD incidence has decreased from 0.77% among calves born in 2013 to 0.03% in 2021. As the programme moves toward achieving the goal of eradication, and the requirement for compulsory tissue tag testing of all calves born, there is a need to develop alternative surveillance strategies. This study is exploring the potential of a variety of potential strategies, either alone or in combination, and considering factors such as time to detection and cost to inform decisions on future surveillance.

Infectious Bovine Rhinotracheitis (IBR)

Epidemiology of age-dependent prevalence of Bovine Herpes Virus Type 1 (BoHV-1) in dairy herds with and without vaccination

Brock, J.[1, 2], Lange, M.[1], Guelbenzu-Gonzalo, M.[2], Meunier, N.[2], Vaz, A.M.[3], Tratalos, J.A.[4], Dittrich, P.[5], Gunn, M.[2], More, S.J.[4], Graham, D.[2], Thulke, H.-H.[1]

[1] Helmholtz Centre for Environmental Research GmbH-UFZ, Dept Ecological Modelling, PG Ecological Epidemiology, Leipzig, Germany, [2] Animal Health Ireland, [3] Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal, [4] UCD CVERA, [5] Department of Mathematics and Computer Sciences, Friedrich Schiller University, Jena, Germany

Veterinary Research 51, 124 (2020)

Many studies report age as a risk factor for BoHV-1 infection or seropositivity. However, it is unclear whether this pattern reflects true epidemiological causation or is a consequence of study design and other issues. Here, we seek to understand the age-related dynamics of BoHV-1 seroprevalence in seasonal calving Irish dairy herds and provide decision support for the design and implementation of effective BoHV-1 testing strategies. We analysed seroprevalence data from dairy herds taken during two Irish seroprevalence surveys conducted between 2010 and 2017. Age-dependent seroprevalence profiles were constructed for herds that were seropositive and unvaccinated. Some of these profiles revealed a sudden increase in seroprevalence between adjacent age-cohorts, from absent or low to close to 100% of seropositive animals. By coupling the outcome of our data analysis with simulation output of an individual-based model at the herd scale, we have shown that these sudden increases are related to extensive virus circulation within a herd for a limited time, which may then subsequently remain latent over the following years. BoHV-1 outbreaks in dairy cattle herds affect animals independent of age and lead to almost 100% seroconversion in all age groups, or at least in all animals within a single epidemiological unit. In the absence of circulating infection, there is a year-on-year increase in the age-cohort at which seroprevalence changes from low to high. The findings of this study inform recommendations regarding testing regimes in the context of contingency planning or an eradication programme in seasonal calving dairy herds.

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

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

[1] Helmholtz Centre for Environmental Research GmbH - UFZ, Dept Ecological Modelling, PG Ecological Epidemiology, Leipzig, Germany, [2] Animal Health Ireland, [3] UCD CVERA

Preventive Veterinary Medicine 192, 105375 (2021)

We present a new modelling framework to address the evaluation of national control/surveillance programs planned in line with the European Animal Health Law (AHL) for livestock diseases. Our modelling framework is applied to the cattle sector in Ireland where there is need for policy support to design an optimal programme to achieve bovine herpesvirus type 1 (BoHV-1) free status under the AHL. In this contribution, we show how our framework establishes a regional model that is able to mechanistically reproduce the demography, management practices and transport patterns of an entire cattle population without being dependent on continuous livestock registry data. An innovative feature of our model is the inclusion of herd typing, thereby extending these beyond the categories of dairy, beef and mixed herds that are frequently considered in other regional modelling studies. This detailed representation of herd type-specific management facilitates comparative assessment of BoHV-1 eradication strategies targeting different production types with individual strategy protocols. Finally, we apply our model to support current discussions regarding the structure and implementation of a potential national BoHV-1 eradication programme in Ireland.

Johne's disease

Johne's disease in Irish dairy herds: considerations for an effective national control programme

Jordan, A.G.[1], Citer, L.R.[2], McAloon, C.G.[3], Graham, D.A.[2], Sergeant, E.S.G.[1], More, S.J.[4]

[1] Ausvet Pty Ltd, Canberra, Australia, [2] Animal Health Ireland, [3] UCD School of Veterinary Medicine, [4] UCD CVERA

Irish Veterinary Journal 73, 18 (2020)

The Irish dairy industry has established a reputation for the production of safe and healthy dairy products and is seeking to further expand its export market for high value dairy products. To support its reputation, stakeholders aim to control Johne's disease. To assist decision-makers determine the most appropriate design for an Irish programme, a narrative review of the scientific literature on the epidemiology of Johne's disease, and selected control programmes throughout the world was undertaken. Two modelling studies specifically commissioned by Animal Health Ireland to assess testing methods used to demonstrate confidence of freedom in herds and to evaluate a range of possible surveillance strategies provided additional information. The majority of control programmes tend to be voluntary, because of the unique epidemiology of Johne's disease and limited support for traditional regulatory approaches. While acknowledging that test performance and sub-clinical sero-negative shedders contributes to the spread of infection, a range of socio-political issues also exist that influence programme activities. The paper provides a rationale for the inclusion of a Veterinary Risk Assessment and Management Plan (VRAMP), including voluntary whole herd testing to identify infected herds and to support assurance-based trading through repeated rounds of negative testing, national surveillance for herd-level case-detection, and improved understanding of biosecurity management practices. Identification and promotion of drivers for industry and producer engagement in Ireland is likely to guide the future evolution of the Irish Johne's Control Programme (IJCP) and further enhance its success. The provision of training, education and extension activities may encourage farmers to adopt relevant farm management practices and help them recognize that they are ultimately responsible for their herd's health and biosecurity.

The Irish Johne's control programme

Gavey, L.[1], Citer, L.[1], More, S.J.[2], Graham, D.[1]

[1] Animal Health Ireland, [2] UCD CVERA

Frontiers in Veterinary Science 8, 703843 (2021)

The Irish Johne's Control Programme (IJCP) provides a long-term approach to the voluntary control of Johne's disease (JD) in Ireland, strongly supported by Irish cattle industry leadership. It leverages the establishment of Animal Health Ireland for control of animal diseases not regulated by the European Union. The IJCP has four objectives: facilitate protection against spread of JD to uninfected farms; reduce the level of infection when present; assure markets of JD control in Ireland; and improve calf health and farm biosecurity. Key IJCP elements are an annual veterinary risk assessment and management plan (VRAMP), annual whole herd test (WHT) by ELISA on blood or milk samples with ancillary faecal PCR testing of ELISA reactors, and Targeted Advisory Service on Animal Health (TASAH) investigations of infected herds. There are pathways for assurance of herds with continuing negative tests and for management of test-positive herds. Herdowners are responsible for on-farm activities, and specifically-trained (approved) veterinary practitioners have a pivotal role as technical advisors and service providers. The programme is supported by training of veterinarians, performance of testing in designated laboratories, documentation of policies and procedures, innovative data management for herd and test activities and for programme administration, training, and broad communication and awareness activities. Tools and systems are refined to address emerging issues and enhance the value of the programme. An Implementation Group comprising industry, government and technical leaders sets strategic direction and policy, advised by a Technical Working Group. Shared funding responsibilities are agreed by key stakeholders until 2022 to support herds in the programme to complete requirements. Herd registrations have increased steadily to exceed 1,800. National bulk tank milk surveillance is also being deployed to identify and recruit test-positive herds with the expectation that they have a relatively high proportion of seropositive animals. The programme will continue to innovate and improve to meet farmer and industry needs.

Individual and herd-level milk ELISA test status for Johne's disease in Ireland after correcting for non-disease-associated variables

McAloon, C.G.[1], O'Grady, L.[1], Botaro, B.[2], More, S.J.[3], Doherty, M.[1], Whyte, P.[1], Nielsen, S.S.[4], Citer, L.[5], Kenny, K.[6], Graham, D.[5], Green, M.[7]

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Journal of Dairy Science 103, 9345-9354 (2020)

Antibody-detecting tests for *Mycobacterium avium* ssp. *paratuberculosis (MAP)* have low sensitivity and imperfect specificity for detection of infection. Sensitivity increases as the disease progresses. Aside from infection status and stage of disease, several factors affect test performance. These factors have not yet been studied in dairy cows producing lower volumes of milk with higher solids concentration, such as those managed in low-input, pasture-based production systems. Furthermore, the effect of correcting for these associations on individual and herd test status is also unknown. The first objective of this study was to examine the relationship between *MAP* antibody response in milk and milk yield, somatic cell count (SCC), fat and protein contents, and stage of lactation in dairy cows enrolled in the national Johne's Disease Control Programme (JDCP) in Ireland. The second objective was to examine the effect of correcting the antibody

response for these associations on the test status of individual cows and herds, given that individual tests are often used to define a herd's status. Data were extracted for herds in the JDCP from January 2014 to December 2015 inclusive, consisting of 42,657 milk recordings from 18,569 cows across 187 dairy herds. Two linear regression models were constructed to investigate the association between log-transformed *MAP* sample-to-positive ratio and milk recording data and in primi- and multiparous cows. Days in milk was modeled as a B-spline in each model, and cow and herd were included as random effects. Across both models, natural log-transformed *MAP* antibody response was negatively associated with milk yield, positively associated with protein and fat production, and had a curvilinear association with log-transformed SCC. The association between *MAP* antibody response and days in milk varied over the course of the lactation. However, when combined, these variables explained only 5.1% of the variation in the antibody response of the population. After correcting for these associations, 93 multiparous cows and 20 primiparous cows changed category (negative, suspect, or positive). When considered at the herd-test level, out of a total of 531 herd tests, 1 herd changed from negative to positive, and 5 herds changed from positive to negative. This study provides useful information to aid in the interpretation of antibody results for herds testing animals for the presence of *MAP* infection. At an overall population level, correction of the serological response for non-disease-associated factors has the potential to change the status of only a small number of cows. At the herd level, the proportion of herds changing status was minimal. However, depending on the implications of a herd-level serological diagnosis, consideration should be given to correcting for these non-disease-associated variables within the context of national JD control programs.

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Modelling transmission and control of *Mycobacterium avium* subspecies *paratuberculosis* within Irish dairy herds with compact spring calving

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Preventive Veterinary Medicine 186, 105228 (2021)

Paratuberculosis is a chronic bacterial infection of the intestine in cattle caused by *Mycobacterium avium* subspecies *paratuberculosis (Map).* To better understand *Map* transmission in Irish dairy herds, we adapted the French stochastic individual-based epidemiological simulation model to account for seasonal herd demographics. We investigated the probability of *Map* persistence over time, the within-herd prevalence over time, and the relative importance of transmission pathways, and assessed the relative effectiveness of test-and-cull control strategies. We investigated the impact on model outputs of calf separation from cows (calves grazed on pasture adjacent to cows vs. were completely separated from cows) and test-and-cull. Test-and-cull scenarios consisted of highly test-positive cows culled within 13 or 4 weeks after detection, and calf born to highly test-positive cows kept vs removed. We simulated a typical Irish dairy herd with on average 82 lactating cows, 112 animals in total. Each scenario was iterated 1000 times to adjust variation caused by stochasticity. *Map* was introduced in the fully naive herd through the purchase of a moderately infectious primiparous cow. Infection was considered to persist when at least one infected animal remained in the herd or when *Map* was present in the environment. The probability of *Map* persistence 15 years after introduction ranged between 32.2–42.7% when calves and cows had contact on pasture, and between 18.9–29.4% when calves and cows were separated on pasture. The most effective control strategy was to cull highly test-positive cows within four weeks of detection (absolute 10% lower persistence compared to scenarios without control). Removing the offspring of highly test-positive dams did not affect either *Map* persistence or within-herd prevalence of *Map.* Mean prevalence 15 years after *Map* introduction was highest (63.5%) when calves and cows had contact on pasture. Mean prevalence was 15% lower (absolute decrease) when cows were culled within 13 weeks of a high test-positive result, and 28% lower when culled within 4 weeks. Around calving, the infection rate was high, with calves being infected *in utero* or via the general indoor environment (most important transmission routes). For the remainder of the year, the incidence rate was relatively low with most calves being infected on pasture when in contact with cows. Testing and culling was an effective control strategy when it was used prior to the calving period to minimize the number of highly infectious cows present when calves were born.

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

Biemans, F. et al.
INRAE, Oniris, BIOEPAR, Nantes, France & UCD CVERA

Mycobacterium avium subspecies *paratuberculosis (Map)* is mainly transmitted between herds through movement of infected but undetected animals. Our objective was to investigate the effect of herd characteristics on *Map* spread and persistence on a national scale in Ireland. This was done using a stochastic, individual-based model to represent herd demography and *Map* infection dynamics of each dairy cattle herd in Ireland. 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.

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

Biemans, F. et al.
INRAE, Oniris, BIOEPAR, Nantes, France & UCD CVERA

Mycobacterium avium subspecies *paratuberculosis (Map)* is mainly transmitted between herds through movement of infected but undetected animals. Our objective is to investigate the effect of risk-based trading on *Map* transmission. Herds are assigned a classification (score/indicator) for the probability that a herd is free of infection. Based on this classification, movements between herds are redirected with the aim to reduce the risk that carriers enter a herd (bio-exclusion). Furthermore, risk-based trading is combined with other control measures like improved herd hygiene and early culling of detected highly infectious animals.

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. et al.
UCD School of Veterinary Medicine

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

Latent class analysis of bulk tank milk PCR and two ELISA tests for herd level diagnosis of *Mycoplasma bovis*

McAloon, C.I. et al.
UCD School of Veterinary Medicine

The objective of this study is to estimate the sensitivity and specificity of the two ELISA tests using a non-gold standard Bayesian latent class analysis, using a 3-test, 2-population approach assuming conditional dependence between the two ELISAs, for determination of herd *Mycoplasma bovis* infection status using bulk milk samples randomly selected for national surveillance.

Profile the strain types of *Mycoplasma bovis* and associated antimicrobial resistance profile associated with *Mycoplasma bovis* associated bovine respiratory disease in Ireland and Scotland

McAloon, C.I. et al.
UCD School of Veterinary Medicine

The objectives of this study are two-fold. Firstly, the study aims to profile the strain types of *Mycoplasma bovis* present in clinical cases of *Mycoplasma*-associated bovine respiratory disease in cattle in Ireland and Scotland. Secondly, the study will characterise the genotypic antimicrobial resistance profiles in *M. bovis* isolates from bovine clinical BRD cases in Ireland and Scotland.

Schmallenberg virus infection

Schmallenberg virus in Poland endemic or re-emerging? A six-year serosurvey

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Transboundary and Emerging Diseases 68, 2188-2198 (2021)

A novel arbovirus, called Schmallenberg virus (SBV), emerged in Europe in 2011 infecting domestic as well as wild ruminants. The virus was first detected in Poland during the 2012 vector season. In order to study the SBV post-epidemic period in Poland, over twenty-one thousand domestic ruminants (cattle, sheep, goats) were tested for SBV infection between 2013 and 2018. Samples were collected as part of the national Bluetongue virus (BTV) surveillance programme. Thirteen per cent of all samples were collected from animals between 6 months and one year of age. Overall, 37.5% of ruminants tested seropositive. The seroprevalence fluctuated yearly and was highest in 2014 and 2017; however, seroconversion was detected in younger animals throughout the study indicating continuous virus circulation during the 6-year study period. A significantly higher proportion of seropositive animals were detected among cattle and older animals. Uneven distribution of seropositive animals between provinces was identified and may be a result of different housing and breeding practices and/or meteorological conditions influencing local and regional vector abundances, rather than farm stocking densities. A small number of animals were identified as being exposed to both SBV and BTV; this is likely due to the fact that the same Culicoides species transmit these two viruses thus increasing the risk of co-exposure. Considering these results, in addition to virological and entomological studies carried out in Poland previously, it can be concluded that SBV is endemic in Poland with cyclical waves of virus circulation happening every 3–4 years.

Infectious bovine diseases in general

Output-based assessment of confidence of freedom from infection

A description and qualitative comparison of the elements of heterogeneous bovine viral diarrhea control programs that influence confidence of freedom

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For endemic infections in cattle that are not regulated at the European Union level, such as bovine viral diarrhea virus (BVDV), European Member States have implemented control or eradication programs (CEP) tailored to their specific situations. Different methods are used to assign infection-free status in CEP; therefore, the confidence of freedom associated with the "free" status generated by different CEP are difficult to compare, creating problems for the safe trade of cattle between territories. Safe trade would be facilitated with an output-based framework that enables a transparent and standardized comparison of confidence of freedom for CEP across herds, regions, or countries. The current paper represents the first step toward development of such a framework by seeking to describe and qualitatively compare elements of CEP that contribute to confidence of freedom. For this work, BVDV was used as a case study. We qualitatively compared heterogeneous BVDV CEP in 6 European countries: Germany, France, Ireland, the Netherlands, Sweden, and Scotland. Information about BVDV CEP that were in place in 2017 and factors influencing the risk of introduction and transmission of BVDV (the context) were collected using an existing tool, with modifications to collect information about aspects of control and context. For the 6 participating countries, we ranked all individual elements of the CEP and their contexts that could influence the probability that cattle from a herd categorized as BVDV-free are truly free from infection. Many differences in the context and design of BVDV CEP were found. As examples, CEP were either mandatory or voluntary, resulting in variation in risks from neighboring herds, and risk factors such as cattle density and the number of imported cattle varied greatly between territories. Differences were also found in both testing protocols and definitions of freedom from disease. The observed heterogeneity in both the context and CEP design will create difficulties when comparing different CEP in terms of confidence of freedom from infection. These results highlight the need for a standardized practical methodology to objectively and quantitatively determine confidence of freedom resulting from different CEP around the world.

Quantification of risk factors for bovine viral diarrhea virus in cattle herds: A systematic search and meta-analysis of observational studies

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Journal of Dairy Science 103, 9446-9463 (2020)

Bovine viral diarrhea virus (BVDV) is endemic in many parts of the world, and multiple countries have implemented surveillance activities for disease control or eradication. In such control programs, the disease-free status can be compromised by factors that pose risks for introduction or persistence of the virus. The aim of the present study was to gain a comprehensive overview of possible risk factors for BVDV infection in cattle herds in Europe and to assess their importance. Papers that considered risk factors for BVDV infection in cattle were identified through a systematic search. Further selection of papers eligible for quantitative analysis was performed using a predefined checklist, including (1) appropriate region (i.e., studies performed in Europe), (2) representativeness of the study population, (3) quality of statistical analysis, and (4) availability of sufficient quantitative data. In total, 18 observational studies were selected. Data were analyzed by a random-effects meta-analysis to obtain pooled estimates of the odds of BVDV infection. Meta-analyses were performed on 6 risk factors: herd type, herd size, participation in shows or markets, introduction of cattle, grazing, and contact with other cattle herds on pasture. Significant higher odds were found for dairy herds (odds ratio, OR = 1.63, 95% confidence interval, CI: 1.06–2.50) compared with beef herds, for larger herds (OR = 1.04 for every 10 extra animals in the herd, 95% CI: 1.02–1.06), for herds that participate in shows or markets (OR = 1.45, 95% CI: 1.10–1.91), for herds that introduced cattle into the herd (OR = 1.41, 95% CI: 1.18–1.69), and for herds that share pasture or have direct contact with cattle of other herds at pasture (OR = 1.32, 95% CI: 1.07–1.63). These pooled values must be interpreted with care, as there was a high level of heterogeneity between studies. However, they do give an indication of the importance of the most frequently studied risk factors and can therefore assist in the development, evaluation, and optimization of BVDV control programs.

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

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Frontiers in Veterinary Science 8, 656336 (2021)

Various European Member States have implemented control or eradication programmes for endemic infectious diseases in cattle. The design of these programmes varies between countries and therefore comparison of the outputs of different control programmes is complex. Although output-based methods to estimate the confidence of freedom resulting from these programmes are under development, as yet there is no practical modeling framework applicable to a variety of infectious diseases. Therefore, a data collection tool was developed to evaluate data availability and quality and to collect actual input data required for such a modeling framework. The aim of the current paper is to present the key learnings from the process of the development of this data collection tool. The data collection tool was developed by experts from two international projects: STOC free (Surveillance Tool for Outcome-based Comparison of FREEdom from infection, **www.stocfree.eu**) and SOUND control (Standardizing OUtput-based surveillance to control Non-regulated Diseases of cattle in the EU, **www.sound-control.eu**). Initially a data collection tool was developed for assessment of freedom of bovine viral diarrhea virus in six Western European countries. This tool was then further generalized to enable inclusion of data for other cattle diseases i.e., infectious bovine rhinotracheitis and Johne's disease. Subsequently, the tool was pilot-tested by a Western and Eastern European country, discussed with animal health experts from 32 different European countries and further developed for use throughout Europe. The developed online data collection tool includes a wide range of variables that could reasonably influence confidence of freedom, including those relating to cattle demographics, risk factors for introduction and characteristics of disease control programmes. Our results highlight the fact that data requirements for different cattle diseases can be generalized and easily included in a data collection tool. However, there are large differences in data availability and comparability across European countries, presenting challenges to the development of a standardized data collection tool and modeling framework. These key learnings are important for development of any generic data collection tool for animal disease control purposes. Further, the results can facilitate development of output-based modeling frameworks that aim to calculate confidence of freedom from disease.

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

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Countries have implemented control programmes (CPs) for cattle diseases such as bovine viral diarrhea virus (BVDV) that are tailored to each country specific situation. 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 to estimate the probability of infection on herd level was developed. In the current study, this model was applied to BVDV field data from CPs based on ear notch samples in four countries. The aim of this study was to test the performance of the STOC free model and to estimate the probability of herd level freedom from BVDV.

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

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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

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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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Animal health surveillance

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 testing of routinely collected bulk tank milk can contribute to surveillance of the national dairy herd for a range of animal health issues. Testing of bulk tank milk is currently being undertaken twice-yearly for bovine viral diarrhoea (BVD), infectious bovine rhinotracheitis (IBR) and Johne's disease (JD). This project is being undertaken to analyse and interpret these test results, to inform national control and eradication programmes.

Irish dairy farmers' engagement with animal health surveillance services: Factors influencing sample submission

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A high-quality animal health surveillance service is required to inform policy and decision-making in food-animal disease control, to substantiate claims regarding national animal health status and for the early detection of exotic or emerging diseases. In Ireland, the Department of Agriculture, Food and the Marine provides partially subsidized testing of farm animal samples and postmortem examinations to the Irish agriculture sector (farmers) at 6 regional veterinary laboratories (RVL) throughout the country. Diagnoses and data from these submissions are recorded and reported monthly and annually to enable animal health monitoring and disease surveillance. In a passive surveillance model, both the veterinary practitioner and the farmer play a vital role in sample submission by determining which cases are sent to the laboratory for postmortem or diagnostic testing. This paper identified factors influencing Irish dairy farmers' decisions to submit carcasses to RVL. Behavioral determinants of the submission of samples where veterinary professionals are concerned has been studied previously; however, limited work has studied determinants among farmers. This study conducted qualitative analyses of decisions of Irish dairy farmers relevant to diagnostic sample submission to an RVL and to examine the herd-level characteristics of farmers that submitted cases to an RVL. The biographical narrative interpretive method was used to interview 5 case-study farmers who were classified nonsubmitters, medium, or high submitters to the postmortem service based on the proportion of on-farm mortalities submitted to the laboratory service in 2016. The data obtained from these interviews were supplemented and triangulated through dairy farmer focus groups. The data were thematically analyzed and described qualitatively. In addition, quantitative analysis was undertaken. Data for herds within the catchment area of a central RVL were extracted, and a multivariable logistic regression model was constructed to examine the relationship between herds from which carcasses were submitted to the laboratory and those from which none were submitted. Results from the analysis show that the farmer's veterinary practitioner was the primary influence on submission of carcasses to the laboratory. Similarly, the type of incident, logistical issues with transporting carcasses to the laboratory, influence of peers, presence of alternative private laboratories, and a fear of government involvement were key factors emerging from the case-study interview and focus group data. Herd size was identified in both the qualitative and quantitative analysis as a factor determining submission. In the logistic regression model, herd size and increased levels of expansion were positively correlated with the odds of submission, whereas distance from the laboratory was negatively associated with odds of submission. These results identify the main factors influencing the use of diagnostic services for surveillance of animal health, signaling how services may be made more attractive by policy makers to a potentially wider cohort of users.

General modelling considerations

Combining expert knowledge and machine-learning to classify herd types in livestock systems

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Scientific Reports 11, 2989 (2021)

A detailed understanding of herd types is needed for animal disease control and surveillance activities, to inform epidemiological study design and interpretation, and to guide effective policy decision-making. In this paper, we present a new approach to classify herd types in livestock systems by combining expert knowledge and a machine-learning algorithm called self-organising-maps (SOMs). This approach is applied to the cattle sector in Ireland, where a detailed understanding of herd types can assist with on-going discussions on control and surveillance for endemic cattle diseases. To our knowledge, this is the first time that the SOM algorithm has been used to differentiate livestock systems. In compliance with European Union (EU) requirements, relevant data in the Irish livestock register includes the birth, movements and disposal of each individual bovine, and also the sex and breed of each bovine and its dam. In total, 17 herd types were identified in Ireland using 9 variables. We provide a data-driven classification tree using decisions derived from the Irish livestock registration data. Because of the visual capabilities of the SOM algorithm, the interpretation of results is relatively straightforward and we believe our approach, with adaptation, can be used to classify herd type in any other livestock system.

Reviewing age-structured epidemiological models of cattle diseases tailored to support management decisions: guidance for the future

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Preventive Veterinary Medicine 174, 104814 (2020)

Mechanistic simulation models are being increasingly used as tools to assist with animal health decision-making in the cattle sector. We reviewed scientific literature for studies reporting age-structured cattle management models in application to infectious diseases. Our emphasis was on papers dedicated to support decision making in the field. In this systematic review we considered 1290 manuscripts and identified 76 eligible studies. These are based on 52 individual models from 10 countries addressing 9 different pathogens. We provide an overview of these models and present in detail their theoretical foundations, design paradigms and incorporated processes. We propose a structure of the characteristics of cattle disease models using three main features: [1] biological processes, [2] farming-related processes and [3] pathogen-related processes. It would be of benefit if future cattle disease models were to follow this structure to facilitate science communication and to allow increased model transparency.

Biosecurity and infectious disease control

SWAB - Surveillance Welfare and Biosecurity of farmed animals in Ireland

McAloon, C. et al.

UCD School of Veterinary Medicine

This project aims to develop a syndromic surveillance tool that will enable more rapid detection of emerging disease outbreaks in cattle herds. This can theoretically allow for the earlier treatment and prevention of outbreaks before they become severe. This would have economic benefits for farmers and the country as a whole. In addition, this study will contribute to the investigation of the impact of biosecurity methods in the SWAB project task 8 and the development of a biosecurity scoring for Irish cattle herds. Promoting good biosecurity is a key goal highlighted in DAFM strategic objectives and is of fundamental importance to maintaining high standards of animal health for Irish cattle.

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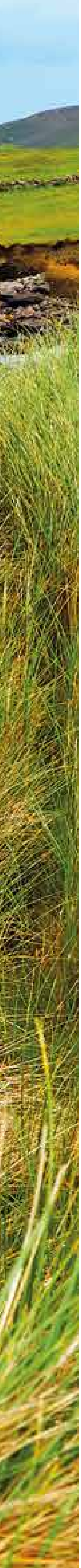

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Other animal health and welfare issues

Milk quality and intramammary antimicrobial stewardship

Antimicrobial usage

Short Communication: Trends in estimated intramammary antimicrobial usage in the Irish dairy industry from 2003 to 2019

McAloon, C.I.[1], McCoy, F.[2], More, S.J.[3]

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JDS Communications 2, 271-276 (2021)

The objective of this study is to update earlier work on intramammary (IM) antimicrobial (AM) usage in Ireland. There is a need to measure AM usage in food-producing animals given increasing societal concerns about AM resistance as well as recent regulatory changes that dictate changes in how AM are used in food-producing animals and how AM sales and usage are recorded. National sales data were collected and used in this analysis. Sales of the number of IM AM tubes and amount of active ingredient sold were analyzed each year by product type [in-lactation (LC) therapy and dry cow (DC) therapy] and classification system (World Health Organization and more recent European Medicine Agency). Descriptive trends in estimated IM AM use are presented, including defined course dose (DCDvet; a technical unit for on-farm usage). There has been a decrease in estimated on-farm usage of IM AM during lactation, from 0.48 DCDvet/cow per year in 2015 to 0.43 DCDvet/cow per year in 2019. Almost all LC therapies sold include critically important AM (CIA), with 98% of the total DCDvet administered for LC therapy in 2019 containing at least 1 CIA. There has been a slow increase in tubes containing at least 1 highest priority CIA in LC therapies, from 0.01 DCDvet/cow per year in 2003, accounting for 2% of the total DCDvet administered for LC therapy, to 0.03 DCDvet/cow per year in 2019, accounting for 7% of the total DCDvet administered for LC use. The estimated usage of IM AM DC therapy has decreased from 1.09 DCDvet/cow per year in 2015 to 0.95 DCDvet/cow per year in 2019. In the last 5 yr, more than 40% of the total DC DCDvet administered contained at least 1 CIA, and there has been an increase in recent years in the percentage of the total DC DCDvet administered that contains at least 1 highest priority CIA, driven mainly by use of fourth-generation cephalosporin. This work provides further insights into IM AM usage in Ireland and highlights some important areas for attention, including availability of farm-level usage data, prescribing practices, and usage of important AM.

Current antimicrobial use in farm animals in the Republic of Ireland

Martin, H.[1], Manzanilla, E.G.[1, 2], More, S.J.[3], O'Neill, L.[1, 2], Bradford, L.[1], McAloon, C.I.[1], Collins, Á.B.[3, 4], McAloon, C.G.[1]

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Irish Veterinary Journal 73, 11 (2020)

Antimicrobial resistance has been recognised as one of the most difficult challenges facing human and animal health in recent decades. The surveillance of antimicrobial use in animal health plays a major role in dealing with the growing issue of resistance. This paper reviews current data available on antimicrobial use in farmed animals in the Republic of Ireland, including each of the major livestock production sectors; pigs, poultry, dairy, beef and sheep. A systematic literature search was conducted to identify relevant published literature, and ongoing research was identified through the network of authors and searches of each of the research databases of the main agriculture funding bodies in Ireland. The varying quantities and quality of data available across each livestock sector underlines the need for harmonisation of data collection methods. This review highlights the progress that has been made regarding data collection in the intensive production sectors such as pigs and poultry, however, it is clear there are significant knowledge gaps in less intensive industries such as dairy, beef and sheep. To comply with European regulations an antimicrobial data collection system is due to be developed for all food-producing animals in the future, however in the short-term surveillance studies have allowed us to build a picture of current use within the Republic of Ireland. Further studies will allow us to fill current knowledge gaps and build a more comprehensive overview of antimicrobial use in farm animals in Ireland.

Intramammary antimicrobial sales in Ireland: a 2020 update

McAloon, C.I. et al.
UCD School of Veterinary Medicine

Intramammary (IM) antimicrobial sales data are currently the only feasible means to gain broad insights into on-farm AM usage relevant to mastitis control within the Irish dairy industry. Published information is available for the period 2003-19, with key themes including near-universal blanket dry cow therapy across the national herd until very recently, a progressive fall in in-lactation therapy since 2013, and ongoing concerns about both the use and trend in use of highest priority critically important antimicrobials (HP CIA) in intramammary products, both with in-lactation and dry-cow therapies. This paper updates this earlier work, describing trends in intramammary AM usage in Ireland during 2020.

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

More, S.J. et al.
UCD CVERA

Milk purchasers (cooperatives etc) have played an important role in the prescribing and sales of intramammary antimicrobial (AM) products in Ireland. Their role in the prescribing of intramammary AM products was outlined under SI No. 558/2017 (previously SI No. 786/2007). They have an ongoing role in the sale of intramammary AM products, which can be dispensed in Ireland by licensed agricultural merchants. The aim of this study was to provide insights into the role of Irish milk purchasers in the prescribing and sale of intramammary AM products during 2019 and 2020. With the introduction of SI No. 36/2022, some aspects of this study will relate to past, rather than current, practices.

Antimicrobial stewardship

European perspectives on efforts to reduce antimicrobial usage in food animal production

More, S.J.[1]

[1] UCD CVERA

Irish Veterinary Journal 73, 2 (2020)

New regulations on veterinary medicines and medicated feed will substantially influence antimicrobial prescribing and usage throughout Europe into the future. These regulations have been informed by a very large body of work, including the substantial progress towards reduced antimicrobial usage in food animal production in a number of member states of the European Union (EU). This paper seeks to summarise European perspectives on efforts to reduce antimicrobial usage in food animal production. Work within the EU is informed by the global action plan of the World Health Organization, which includes a strategic objective to optimise the use of antimicrobial medicines in human and animal health. There is ongoing measurement of trends in antimicrobial usage and resistance throughout the EU, and detailed information on strategies to reduce the need to use antimicrobials in food animal production. Substantial scientific progress has been made on the measurement of antimicrobial usage, including at herd-level, and on the objective assessment of farm biosecurity. In a number of EU member states, monitoring systems for usage are well-established, allowing benchmarking for veterinarians and farms, and monitoring of national and industry-level trends. Several countries have introduced restrictions on antimicrobial prescribing and usage, including strategies to limit conflicts of interest around antimicrobial prescribing and usage. Further, a broad range of measures are being used across member states to reduce the need for antimicrobial usage in food animal production, focusing both at farm level and nationally. Veterinarians play a central role in the reduction of antimicrobial usage in farm animals. Ireland's National Action Plan on Antimicrobial Resistance 2017–20 (iNAP) provides an overview of Ireland's commitment to the development and implementation of a holistic, cross-sectoral 'One Health' approach to the problem of antimicrobial resistance. The new regulations offer an important springboard for further progress, in order to preserve the efficacy of existing antimicrobials, which are a critical international resource.

The new Veterinary Medicines Regulation: rising to the challenge

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Irish Veterinary Journal (in press) (2022)

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.

Intramammary antibiotic stewardship in the Irish dairy industry: challenges and opportunities

More, S.J. et al.
UCD CVERA

This paper outlines challenges to and opportunities for intramammary antibiotic stewardship in the Irish dairy industry, particularly in the context of the Veterinary Medicines Regulation, which is applicable across Member States from 28 January 2022. Key changes include a ban on the prophylactic use (and restriction on the metaphylactic use) of antibiotics in groups of animals, the possibility to reserve certain antibiotics for humans only, and the need for Member States to collect data on the sale and use of antimicrobials at prescriber and user level. This paper presents a proposal from the CellCheck technical working group (a group of experts providing technical information in support of CellCheck, the national mastitis control programme) to support intramammary antibiotic stewardship in Ireland, whilst also addressing mastitis and milk quality, and intramammary antibiotic usage.

Prioritising animal health and welfare

Stakeholder perceptions of non-regulatory bovine health issues in Ireland: past and future perspectives

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Irish Veterinary Journal 73, 25 (2020)

In recent years, there have been multiple (political, environmental, cultural) drivers of change in Irish agriculture, including the establishment of Animal Health Ireland (AHI) in 2009, to provide leadership of non-regulatory livestock health issues (diseases and conditions of livestock that are endemic in Ireland but which are not currently subject to international legislation). In this study, we describe the opinion of stakeholders (farmers, veterinary practitioners and agricultural industry professional service providers), elicited by means of a survey, on their perceptions of changes in selected non-regulatory bovine health issues over the last 10 years and priority issues relevant to non-regulatory bovine health to be tackled over the next 10 years. A total of 673 individuals participated in the online questionnaire. For the majority of the non-regulatory bovine health issues, most participants felt there had been improvements over the last 10 years. However, professional service providers were generally more conservative in their response to improvements on-farm compared to farmers. Several issues, particularly BVD and udder health/milk quality, were viewed more positively by all relevant respondents. There was reasonable agreement between responses from different respondent types and sectors regarding the top three priorities relevant to non-regulatory bovine animal health for the next 10 years in Ireland, which included antimicrobial resistance (highlighting measures to reduce both on-farm usage and resistance), anthelmintic resistance, greenhouse emissions and calf welfare. The results are encouraging, demonstrating a perception of improvement in a number of non-regulatory bovine health issues in Ireland over the last ten years. With respect to the next 10 years, stakeholders prioritised antimicrobial and anthelmintic resistance, greenhouse gas emissions and calf welfare, which aligns closely with broader societal concerns. This information is useful to AHI, particularly with respect to future priorities. However, these concerns are broad in scope and will require further considerations, including collaborations, between AHI and partnering organisations. Given that there were differences between farmers and professional service providers in responses, it is useful to consider how the aims and the benefits of future AHI programmes are framed and communicated to all stakeholders.

Development and application of a prioritisation tool for animal health surveillance activities in Ireland

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Frontiers in Veterinary Science 7, 596867 (2020)

Decisions around animal health management by stakeholders are often subject to resource limitation, therefore prioritization processes are required to evaluate whether effort is attributed appropriately. The objectives of this study were to develop and apply a surveillance prioritization process for animal health surveillance activities in Ireland. An exploratory sequential mixed research methods design was utilized. A prioritization tool was developed for surveillance activities and implemented over two phases. During the first phase, a survey was conducted which asked stakeholders to prioritize diseases/conditions by importance for Irish agriculture. In the second phase, experts identified the most important surveillance objectives, and allocated resources to the activities that they considered would best meet the surveillance objectives, for each disease/condition. This study developed a process and an accompanying user-friendly practical tool for animal disease surveillance prioritization which could be utilized by other competent authorities/governments. Antimicrobial resistance and bovine tuberculosis were ranked top of the endemic diseases/conditions in the Irish context, while African swine fever and foot and mouth disease were ranked top of the exotic diseases/conditions by the stakeholders. The study showed that for most of the diseases/conditions examined in the prioritization exercise, the respondents indicated a preference for a combination of active and passive surveillance activities. Future extensions of the tool could include prioritization on a per species basis.

Private animal health and welfare standards

An evaluation of four private animal health and welfare standards and associated quality assurance programmes for dairy cow production

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Food Policy 105, 102169 (2021)

Private standards in animal health and welfare (AHW) and associated quality assurance (QA) programmes are an important instrument for food policy with the potential to substantially improve AHW. However, there are concerns that they do not necessarily do so. In this study, we evaluated four private AHW standards and associated QA programmes for dairy cow production, from Denmark, Ireland, the Netherlands and the United Kingdom, using an existing (but adapted) conceptual framework. The framework considers criteria relating to programme goals including relevance to AHW, programme beneficiaries, effectiveness, efficiency and transparency. The current study focused on information that was publicly available online. We found limited objective information to support programme claims, although there were considerable differences between programmes. Across all programmes, problems were identified with respect to transparency, and attempts to scrutinise claims would not be a straightforward process for most consumers. Among the programmes, there were notable examples of best-practice in AHW, relating to science-based evidence, separation of risk assessment and risk management, animal-based measures, farm benchmarking, ongoing programme-level metrics and measurement, and ongoing programme review. There is a need for careful scrutiny of private standards and QA programmes, to provide consumers with assurance with respect to programme effectiveness and transparency. Further, it is important that programme efficiencies are maximised. There is a strong case for regulatory oversight of private standards in AHW and associated QA programmes. This could be within existing or defined policy instruments, both to facilitate the positive impact of these programmes and to build confidence among consumers of the validity of programme claims.

Dog welfare

Understanding the dog population in Ireland: insights from existing data sources

More, S.J. et al.
UCD CVERA

There is little information available in the peer-reviewed literature on the dog population in the Republic of Ireland. The current study was conducted using existing databases to gain a current understanding of biological and organisational factors affecting the dog population of Ireland and the movement of dogs into and from Ireland. Available data provide useful, but fragmented, insights, with the dog licensing and microchipping data being of greatest value with respect to trends over time. This study highlights the challenges faced when using existing national data to gain insights into the dog population of Ireland, noting that the assessed quality of existing databases is very variable, and often poor.

A quantitative study of dog welfare organisations in Ireland

McKernan, C. et al.
Queen's University Belfast, Belfast, Northern Ireland

A number of dog welfare charity organisations in Ireland are active recipients of public funding, by way of welfare grants from the national Department of Agriculture, Food and the Marine (DAFM). Many of these organisations also have alternative sources of funding, e.g. from charitable donations. In consideration of future policy planning and management of public expenditure, DAFM is seeking an improved understanding of the national dog population and the role of the animal welfare organisations in this area. The specific objective of this project is to gain an understanding of the roles and functions of dog welfare organisations in Ireland. The study will be conducted using a mixed modes approach to data collection, utilising phone interview and online questionnaire.

The current state of the Irish dog and dog welfare organisations. A qualitative investigation

Murphy, B. et al.
Queen's University Belfast, Belfast, Northern Ireland

As individual ownership of dogs has increased in Ireland, there has been greater involvement of various animal/dog welfare organisations. These organisations fulfill various duties in the system (welfare, importation/exportation, rehoming etc.), and receive varied funding from the Irish government (such as the Department of Agriculture, Food and the Marine, DAFM) and charitable funding. No previous research has explored the dog welfare landscape in an Irish context, using a mixed methods approach. This stakeholder-focused research project will seek to develop policy-based options and provide context on the Irish dog welfare sector. The project will be conducted using online focus groups and interviews.

Further animal health and welfare research

African swine fever in Romania

Risk factors for African swine fever incursion in Romanian domestic farms during 2019

Boklund, A.[1], Dhollander, S.[2], Chesnhoiu Vasile, T.[3], Abrahantes, J.C.[2], Bøtner, A.[4, 5], Gogin, A.[6], Gonzalez Villeta, L.C.[2], Gortázar, C.[7], More, S.J.[8], Papanikolaou, A.[2], Roberts, H.[9], Stegeman, A.[10], Ståhl, K.[11], Thulke, H.H.[12], Viltrop, A.[13], Van der Stede, Y.[2], Mortensen, S.[14]

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Scientific Reports 10, 10215 (2020)

African swine fever (ASF) entered Georgia in 2007 and the EU in 2014. In the EU, the virus primarily spread in wild boar *(Sus scrofa)* in the period from 2014–2018. However, from the summer 2018, numerous domestic pig farms in Romania were affected by ASF. In contrast to the existing knowledge on ASF transmission routes, the understanding of risk factors and the importance of different transmission routes is still limited. In the period from May to September 2019, 655 Romanian pig farms were included in a matched case-control study investigating possible risk factors for ASF incursion in commercial and backyard pig farms. The results showed that close proximity to outbreaks in domestic farms was a risk factor in commercial as well as backyard farms. Furthermore, in backyard farms, herd size, wild boar abundance around the farm, number of domestic outbreaks within 2 km around farms, short distance to wild boar cases and visits of professionals working on farms were statistically significant risk factors. Additionally, growing crops around the farm, which could potentially attract wild boar, and feeding forage from ASF affected areas to the pigs were risk factors for ASF incursion in backyard farms.

Biosecurity in the Irish farmed Atlantic salmon industry

Data-driven network modelling as a framework to evaluate the transmission of piscine myocarditis virus (PMCV) in the Irish farmed Atlantic salmon population and the impact of different mitigation measures

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Frontiers in Veterinary Science 7, 385 (2020)

Cardiomyopathy syndrome (CMS) is a severe cardiac disease of Atlantic salmon caused by the piscine myocarditis virus (PMCV), which was first reported in Ireland in 2012. In this paper, we describe the use of data-driven network modeling as a framework to evaluate the transmission of PMCV in the Irish farmed Atlantic salmon population and the impact of different mitigation measures. Input data included live fish movement data from 2009 to 2017, population dynamics events and the spatial location of the farms. With these inputs, we fitted a network-based stochastic infection spread model. After assumed initial introduction of the agent in 2009, our results indicate that it took 5 years to reach a between-farm prevalence of 100% in late 2014, with older fish being most affected. Local spread accounted for only a small proportion of new infections, being more important for sustained infection in a given area. Spread via movement of subclinically infected fish was most important for explaining the observed countrywide spread of the agent. Of the targeted intervention strategies evaluated, the most effective were those that target those fish farms in Ireland that can be considered the most connected, based on the number of farm-to-farm linkages in a specific time period through outward fish movements. The application of these interventions in a proactive way (before the first reported outbreak of the disease in 2012), assuming an active testing of fish consignments to and from the top 8 ranked farms in terms of outward fish movement, would have yielded the most protection for the Irish salmon farming industry. Using this approach, the between-farm PMCV prevalence never exceeded 20% throughout the simulation time (as opposed to the simulated 100% when no interventions are applied). We argue that the Irish salmon farming industry would benefit from this approach in the future, as it would help in early detection and prevention of the spread of viral agents currently exotic to the country.

Bovine abortion

Bovine abortion: risk factors, pathogens and diagnostics

Hayes, C. et al.

DAFM

Cattle abortions represent significant economic and welfare impacts to the Irish farming industry. In spite of this, there are important knowledge gaps relating to the prevalence of and risk factors for infectious causes of abortion. Further, diagnostic limitations, for example declining antibody levels against *Neospora caninum* tachyzoites in the weeks and months after abortion, may present obstacles to detection of this pathogen in cattle herds. However, there have been few large scale studies to investigate and address these issues. Utilising (1) post-mortem and pathogen detection data from foetuses submitted to the Irish Veterinary Laboratories Service, (2) detailed individual and herd level data from the dams of the submitted foetuses and (3) field epidemiological data and serological samples subsequent to known N. caninum abortions, the aim of this PhD project is to improve our understanding of bovine abortion, the pathogens that cause it and the diagnostic techniques used to detect them.

Campylobacter *infection in chickens*

The relationship between *Campylobacter* prevalence and biosecurity on Irish broiler farms

Gomes, C. et al.

Animal Health Ireland

Campylobacter is a naturally occurring bacterium found in the intestinal tract of wild and domesticated birds and mammals. It is the most common cause of bacterial gastroenteritis in Ireland and Europe. In 2020, 66.3% of the carcases sampled through official monitoring in Ireland were positive for *Campylobacter*, with 10.7% exceeding the limit of 1,000 CFU/g. This study will link biosecurity data with *Campylobacter* results at farm level and the outcomes of this project are expected to describe the prevalence of *Campylobacter* in Irish poultry flocks and to identify herd-level risk factors associated with *Campylobacter* prevalence. These will be used by the broiler industry and government to progress the journey into the reduction of prevalence in Irish flocks.

Culicoides dispersion modelling

Culicoides dispersion model

McGrath, G. et al.

UCD School of Veterinary Medicine

This study will build on the existing Culicoides Dispersion Model which is run daily by Met Éireann. Additional parameters will be added to the model to better reflect potential dispersion events. The forecasts from the model inform DAFM of periods of potential high risk for culicoides incursion. This early warning system can assist with targeted surveillance and prompt risk mitigation actions to prevent or reduce the impact of a potential incursion of bluetongue virus into Ireland.

Foot and mouth disease modelling

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

Casey, M. et al.

UCD CVERA, DAFM National Disease Control Centre (NDCC) in collaboration with the European Commission

CVERA worked with the National Disease Control Centre (NDCC) of the Department of Agriculture, Food and the Marine (DAFM) and with the European Commission for the Control of Foot and Mouth Disease (EuFMD) to parameterise the EuFMDiS model for Ireland. This model can be used to evaluate various control options to eradicate the foot-and-mouth disease (FMD). It can also evaluate available resource and vaccine supply issues. CVERA collated cattle, pig, sheep and goat population, movement and management system data from Ireland and provided measures of indirect contacts. We collaborated with EuFMDiS modellers and DAFM stakeholders to parameterise a national FMD transmission model for Ireland. The Irish model is used by the NDCC as part of a Europe wide project using FMD transmission simulations to explore various control options and resource usage. A project entitled "Impact of on-farm biosecurity level in pig herds on the spread and control of foot-and-mouth disease," based upon the Irish FMD model was recently presented by EuFMD collaborators at the Open Session of EuFMD and can be found at **https://open.spotify.com/episode/6fTNB3HeuPt3MU4w7gPtNP**.

Livestock disease resilience

Livestock disease resilience: from individual to herd level

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Animal 15, (Suppl. 1), 100286 (2021)

Infectious diseases are a major threat to the sustainable production of high-producing animals. Control efforts, such as vaccination or breeding approaches often target improvements to individual resilience to infections, i.e., they strengthen an animal's ability to cope with infection, rather than preventing infection *per se*. There is increasing evidence for the contribution of non-clinical carriers (animals that become infected and are infectious but do not develop clinical signs) to the overall health and production of livestock populations for a wide range of infectious diseases. Therefore, we strongly advocate a shift of focus from increasing the disease resilience of individual animals to herd disease resilience as the appropriate target for sustainable disease control in livestock. Herd disease resilience not only captures the direct effects of vaccination or host genetics on the health and production performance of individuals but also the indirect effects on the environmental pathogen load that herd members are exposed to. For diseases primarily caused by infectious pathogens shed by herd members, these indirect effects on herd resilience are mediated both by individual susceptibility to infection and by characteristics (magnitude of infectiousness, duration of infectious period) that influence pathogen shedding from infected individuals. We review what is currently known about how vaccination and selective breeding affect herd disease resilience and its underlying components, and outline the changes required for improvement. To this purpose, we also seek to clarify and harmonise the terminology used in the different animal science disciplines to facilitate future collaborative approaches to infectious disease control in livestock.

National pig population model

The development of a national pig population model for commercial Irish pig herds

Collins, Á. et al.
DAFM & UCD CVERA

This project was initially undertaken with the aim to develop a pig population model to accurately estimate the number of pigs (piglets, weaners, finishers and breeding adults) in commercial Irish pig herds for each calendar year quarter. Outputs of such a model could be used to verify pig population data recorded by farmers in the DAFM antimicrobial usage database. During the project, a number of data issues were identified, and a series of recommendations were made with respect to national pig data systems. Verification and validation checks were recommended to ensure data are recorded accurately, comprehensively and in real time.

Nuclear contingency planning

Nuclear contingency planning

McGrath, G. et al.
UCD CVERA

CVERA, in conjunction with the EPA, Met Éireann and the Department of Agriculture, Food and the Marine, will create 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.

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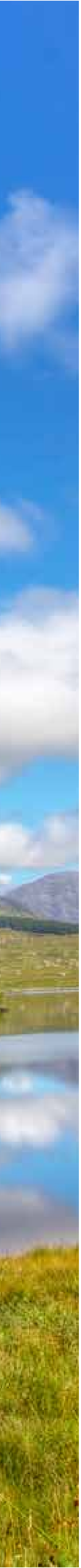

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Covid-19

Parameter estimation in support of national COVID-19 modelling

Inferred duration of infectious period of SARS-CoV-2: rapid scoping review and analysis of available evidence for asymptomatic and symptomatic COVID-19 cases

Byrne, A.W.[1], McEvoy, D.[2], Collins, Á.B.[3, 4], Hunt, K.[5], Casey, M.[3], Barber, A.[3], Butler, F.[5], Griffin, J.[4], Lane, E.A.[3, 4], McAloon, C.[6], O'Brien, K.[7], Wall, P.[2], Walsh, K.A.[7], More, S.J.[3]

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BMJ Open 10, e039856 (2020)

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a new coronavirus, emerged in China in late 2019. The virus causes COVID-19, a disease characterised by variable, mainly respiratory, symptoms across cohorts, from asymptomatic cases through to mild (e.g., dry cough and fever) and severe cases (e.g., pneumonia). The severity of symptoms, and their clinical outcome, have been reported to vary by age class and whether patients have underlying comorbidities. The case fatality rate increases with age and is highest for those above 70 years. There are several cases of asymptomatic test-positive patients reported in the emerging literature. Furthermore, asymptomatic (and pre-symptomatic) cases have been shown to be infectious, and secondary cases have been reported. However, the duration of this infectious period is difficult to measure accurately, and the time course of the natural history of infection generally must be inferred indirectly, via contact tracing of cases, serial repeated diagnostic virological studies and/or through modelling approaches. Symptomatic cases can experience an infectious pre-symptomatic period before the onset of symptoms, therefore understanding the whole infectious period for this cohort requires estimating the duration of both periods. It is essential to rapidly gain insight into this key variable impacting our understanding of COVID-19 epidemiology. Anderson et al point out one of the 'key unknowns' is the infectious period for COVID-19, which they suggest may be 10 days but subject to great uncertainty. Here we gathered data from published research from peer-reviewed and preprints from 1 December to 1 April 2020 to characterise the variation in the infectious duration inferred from the three lines of evidence. We also provide a narrative review of the viral dynamic literature. Our focus was on duration; relative infectiousness has been dealt with elsewhere. The aim of this review was to provide an overview and critical appraisal of published and preprint articles and reports that assess or quantify the inferred duration of the infectious period in order to best parameterise COVID-19 epidemiological transmission models.

Pre-symptomatic transmission of SARS-CoV-2 infection: a secondary analysis using published data

Casey-Bryars, M.[1], Griffin, J.[1], McAloon, C.G.[2], Byrne, A.W.[3], Madden, J.M.[1], McEvoy, D.[5], Collins, Á.B.[1, 4], Hunt, K.[6], Barber, A.[1], Butler, F.[6], Lane, E.A.[4], O'Brien, K.[7], Wall, P.[5], Walsh, K.A.[7], More, S.J.[1]

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BMJ Open 11, e041240 (2021)

There is currently a pandemic of COVID-19, a recently emerged and rapidly spreading infectious disease that is caused by the novel coronavirus, SARS-CoV-2. There are large direct impacts of COVID-19 among known cases. As of 19 April 2021, the WHO has reported 140, 886 773 confirmed cases and 3 012 251 deaths due to COVID-19. In China, 14% and 5% of cases were classified as severe and critical, respectively. There are also major indirect impacts of COVID-19 and its control measures on other aspects of healthcare and on the economy. In addition to vaccination, primary control measures entail reducing transmission from infectious individuals. These include case isolation, contact tracing and quarantine, physical distancing, hygiene and ventilation measures. Infectious people are identified when they report symptoms, and are tested for SARS-CoV-2. Infectious people without symptoms may be identified when an active surveillance programme is in place. In the absence of active surveillance, infectious people without symptoms may not be quarantined, and therefore may have more contacts with susceptible people resulting in increased SARS-CoV-2 transmission. Therefore, quantifying the transmission potential before or in the absence of symptoms will inform disease control measures and predictions of epidemic progression. Characteristics of pre-symptomatic and asymptomatic transmission are potentially different, and separate approaches may be required to understand them. In this paper, we capitalise on the considerable information about pre-symptomatic transmission that can be inferred from contact tracing studies. Therefore, we focus on transmission from people before they develop symptoms rather than from people who never develop symptoms. This addresses the urgent need for more data on the extent of pre-symptomatic transmission which has been highlighted by those developing models to inform policies. Reports of pre-symptomatic transmission emerged as detailed contact tracing was conducted during early outbreaks of COVID-19. Further, both viral genome and live virus have been detected in upper respiratory samples prior to symptom onset. These findings are supported by quantitative studies based on contact tracing, with reports of serial intervals or generation times similar in duration or shorter than incubation periods in some situations, and even cases of symptoms manifesting in the infectee prior to the infector. Several studies have quantified the proportion and timing of pre-symptomatic transmission, using a variety of datasets and methodologies. Here, we compare pre-symptomatic transmission across a range of different contexts using a consistent methodology. We build on our rapid review of SARS-CoV-2 serial interval and generation time and rapid systematic review and meta-analysis of incubation period with a secondary analysis of published data to estimate the proportion and timing of pre-symptomatic transmission of COVID-19.

Rapid review of available evidence on the serial interval and generation time of COVID-19

Griffin, J.[1], Casey, M.[1], Collins, Á.B.[1, 2], Hunt, K.[3], McEvoy, D.[4], Byrne, A.W.[5], McAloon, C.G.[6], Barber, A.[1], Lane, E.A.[1, 2], More, S.J.[1]

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BMJ Open 10, e040263 (2020)

In response to the COVID-19 outbreak, the Irish Epidemiological Modelling Advisory Group (IEMAG) for COVID-19 was established to assist the Irish National Public Health Emergency Team in their decision-making during the pandemic. A subcommittee from IEMAG was tasked with researching the various parameters, leading to the development of a series of synthesis documents relevant to the parameterisation of a COVID-19 transmission model for Ireland. The serial interval is the time between symptom onsets in an infector–infectee pair, that is, the interval between the onset of symptoms in an infectee and its presumed infector. This can be a negative number if the onset of symptoms in the infectee occurs prior to the onset of symptoms in the infector. The generation time, also known as the generation interval, is the time between infection events in an infector–infectee pair. The serial interval and the generation time are key parameters for assessing the dynamics of an infectious disease, and the generation time, or its proxy the serial interval, is an essential quantity for estimating the reproduction number. A number of scientific papers reported information pertaining to the serial interval and/or generation time for COVID-19. In the context of national control efforts in Ireland, our objective was to conduct a rapid review of available evidence to advise the IEMAG on appropriate parameter values for serial interval and generation time in national COVID-19 transmission models and on methodological issues relating to those parameters. This information may also be of use to developers of models and those involved in the implementation of control programmes in other countries.

Incubation period of COVID-19: a rapid systematic review and meta-analysis of observational research

McAloon, C.G.[1], Collins, Á.B.[2, 3], Hunt, K.[4], Barber, A.[2], Byrne, A.W.[5], Butler, F.[4], Casey, M.[2], Griffin, J.[2], Lane, E.[2, 3], McEvoy, D.[6], Wall, P.[6], Green, M.J.[7], O'Grady, L.[1, 7], More, S.J.[2]

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BMJ Open 10, e039652 (2020)

Reliable estimates of the incubation period are important for decision-making around the control of infectious diseases in human populations. Knowledge of the incubation period can be used directly to inform decision-making around infectious disease control. For example, the maximum incubation period can be used to inform the duration of quarantine, or active monitoring periods of people who have been at high risk of exposure. Estimates of the duration of the incubation period, coupled with estimates of the latent period, serial interval or generation times, may help infer the duration of the pre-symptomatic infectious period, which is important in understanding both the transmission of infection and opportunities for control. Finally, decision-making in the midst of a pandemic often relies on predicted events, such as daily number of new infections, from mathematical models. Such models depend on key input parameters relevant to the transmission of the specific infectious disease. It is important that input parameters into such models are as robust as possible. Given that some models fit data to many parameters, only some of which are specifically of interest but all of which are interdependent, output estimates may be compared with the robust estimates as part of the validation of the model. Earlier work has shown that for models of respiratory infections, statements regarding incubation periods are often poorly referenced, inconsistent or based on limited data. To date, many COVID-19 models have used input values from a single study. The decision on which study to use may vary from model to model. Recently, a systematic review of the epidemiological characteristics of COVID-19 reported that estimates of the central tendency of the incubation period ranged from 4 to 6 days. However, to the authors' knowledge, no studies have yet sought to estimate the incubation period through a meta-analysis of data available to date. Furthermore, it is important to note that incubation periods are expected to vary across individuals within the population. For this reason, it is critically important to understand the variation in incubation periods (ie, the distribution) within the population. However, a single measure of central tendency (ie, mean or median) cannot adequately represent this variation. To address this, studies often fit mathematical distributions to incubation period data. We hypothesised that a pooled estimate of the distribution of incubation periods could be obtained through a meta-analysis of data published to date. Therefore, the aim of this study was to conduct a rapid systematic review and meta-analysis of estimates of the incubation periods of COVID-19, defined as the period of time (in days) from virus exposure to the onset of symptoms. Specifically, we aimed to find a pooled estimate for the parameters of an appropriate distribution that could be subsequently used as an input in modelling studies and that might help quantify uncertainty around the key percentiles of the distribution as an aid to decision-making.

Estimation of the serial interval and proportion of pre-symptomatic transmission events of COVID-19 in Ireland using contact tracing data

McAloon, C.G.[1], Wall, P.[2], Griffin, J.[3], Casey, M.[3], Barber, A.[3], Codd, M.[2], Gormley, E.[1], Butler, F.[4], Messam, L.L.McV.[1], Walsh, C.[5], Teljeur, C.[6], Smyth, B.[7], Nolan, P.[8], Green, M.J.[9], O'Grady, L.[1, 9], Culhane, K.[10], Buckley, C.[11, 12], Carroll, C.[11], Doyle, S.[11], Martin, J.[11], More, S.J.[1, 3]

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BMC Public Health 21, 805 (2021)

The serial interval is the period of time between the onset of symptoms in an infector and an infectee and is an important parameter which can impact on the estimation of the reproduction number. Whilst several parameters influencing infection transmission are expected to be consistent across populations, the serial interval can vary across and within populations over time. Therefore, local estimates are preferable for use in epidemiological models developed at a regional level. We used data collected as part of the national contact tracing process in Ireland to estimate the serial interval of SARS-CoV-2 infection in the Irish population, and to estimate the proportion of transmission events that occurred prior to the onset of symptoms. After data cleaning, the final dataset consisted of 471 infected close contacts from 471 primary cases. The median serial interval was 4 days, mean serial interval was 4.0 (95% confidence intervals 3.7, 4.3) days, whilst the 25th and 75th percentiles were 2 and 6 days respectively. We found that intervals were lower when the primary or secondary case were in the older age cohort (greater than 64 years). Simulating from an incubation period distribution from international literature, we estimated that 67% of transmission events had greater than 50% probability of occurring prior to the onset of symptoms in the infector. Whilst our analysis was based on a large sample size, data were collected for the primary purpose of interrupting transmission chains. Similar to other studies estimating the serial interval, our analysis is restricted to transmission pairs where the infector is known with some degree of certainty. Such pairs may represent more intense contacts with infected individuals than might occur in the overall population. It is therefore possible that our analysis is biased towards shorter serial intervals than the overall population.

Relative infectiousness of asymptomatic SARS-CoV-2 infected persons compared with symptomatic individuals: a rapid scoping review

McEvoy, D.[1], McAloon, C.[2], Collins, Á.[3], Hunt, K.[4], Butler, F.[4], Byrne, A.[5], Casey-Bryars, M.[3], Barber, A.[3], Griffin, J.[3], Lane, E.A.[3, 6], Wall, P.[7], More, S.J.[3]

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The first case of COVID-19 was first reported from Wuhan, China, in December 2019. The outbreak of COVID-19 was declared a Public Health Emergency of International Concern on 30 January 2020 and a pandemic was declared on 11 March 2020. Since then, many countries have sought to contain the spread of the virus through a range of measures aimed at limiting transmission within the population. At the outset of an epidemic, a key principle of control might be quarantining of individuals with clinical symptoms fitting a particular case definition. However, for many infectious diseases, a proportion of infected individuals may never present with clinical signs (ie, asymptomatic) yet still be infectious to others. The existence of this cohort of SARS-CoV-2 infected individuals is now well recognised. The transmission potential of such asymptomatic individuals is likely to be different from those who have clinical signs. On the one hand, they might shed lower quantities of the infectious agent; on the other hand, their potential for contacts might be greater. Being unaware that they are infected, asymptomatic people are less likely to follow quarantine guidelines designed to restrict transmission from infected individuals. Decision making in the midst of a pandemic often relies on predicted outcomes from infectious disease models. Such models may aid in public health decision making by predicting the number of new cases each day as well as possible trajectories of an outbreak given different management options. Estimates from these models may be sensitive to the way in which asymptomatic individuals are considered. In particular, it is important to understand the proportion of individuals who are infectious but remain asymptomatic, as well as understanding the transmission potential in that cohort, compared with symptomatic individuals, that is, the relative infectiousness. This study sought to determine the relative infectiousness of asymptomatic SARS-CoV-2 infected persons compared with symptomatic individuals, based on a scoping review of available literature. A scoping review rather than a systematic review was undertaken given the rapidly evolving and complex literature available on SARS-CoV-2 infection and the range of ways in which 'infectiousness' might be defined and measured.

Reflecting on One Health in action during the COVID-19 response

Häsler, B.[1], Bazeyo, W.[2], Byrne, A.W.[3], Hernandez-Jover, M.[4, 5], More, S.J.[6], Rüegg, S.R.[7], Schwarzmann, O.[8], Wilson, J.[9], Yawe, A.[2]

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Frontiers in Veterinary Science 7, 578649 (2020)

The COVID-19 pandemic, a singular disruptive event in recent human history, has required rapid, innovative, coordinated and collaborative approaches to manage and ameliorate its worst impacts. However, the threat remains, and learning from initial efforts may benefit the response management in the future. One Health approaches to managing health challenges through multi-stakeholder engagement are underscored by an enabling environment. Here we describe three case studies from state (New South Wales, Australia), national (Ireland), and international (sub-Saharan Africa) scales which illustrate different aspects of One Health in action in response to the COVID-19 pandemic. In Ireland, a One Health team was assembled to help parameterise complex mathematical and resource models. In New South Wales, state authorities engaged collaboratively with animal health veterinarians and epidemiologists to leverage disease outbreak knowledge, expertise and technical and support structures for application to the COVID-19 emergency. The African One Health University Network linked members from health institutions and universities from eight countries to provide a virtual platform knowledge exchange on COVID-19 to support the response. Themes common to successful experiences included a shared resource base, interdisciplinary engagement, communication network strategies, and looking global to address local need. The One Health approaches used, particularly shared responsibility and knowledge integration, are benefiting the management of this pandemic and future One Health global challenges.

Population mobility trends, deprivation index and the spatio-temporal spread of Coronavirus disease 2019 in Ireland

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International Journal of Environmental Research and Public Health 18, 6285 (2021)

Like most countries worldwide, the coronavirus disease (COVID-19) has adversely affected Ireland. The aim of this study was to (i) investigate the spatio-temporal trend of COVID-19 incidence; (ii) describe mobility trends as measured by aggregated mobile phone records; and (iii) investigate the association between deprivation index, population density and COVID-19 cases while accounting for spatial and temporal correlation. Standardised incidence ratios of cases were calculated and mapped at a high spatial resolution (electoral division level) over time. Trends in the percentage change in mobility compared to a pre-COVID-19 period were plotted to investigate the impact of lockdown restrictions. We implemented a hierarchical Bayesian spatio-temporal model (Besag, York and Mollié (BYM)), commonly used for disease mapping, to investigate the association between covariates and the number of cases. There have been three distinct "waves" of COVID-19 cases in Ireland to date. Lockdown restrictions led to a substantial reduction in human movement, particularly during the 1st and 3rd wave. Despite adjustment for population density (incidence ratio (IR) = 1.985 (1.915–2.058)) and the average number of persons per room (IR = 10.411 (5.264–22.533)), we found an association between deprivation index and COVID-19 incidence (IR = 1.210 (CI: 1.077–1.357) for the most deprived quintile compared to the least deprived). There is a large range of spatial heterogeneity in COVID-19 cases in Ireland. The methods presented can be used to explore locally intensive surveillance with the possibility of localised lockdown measures to curb the transmission of infection, while keeping other, low-incidence areas open. Our results suggest that prioritising densely populated deprived areas (that are at increased risk of comorbidities) during vaccination rollout may capture people that are at risk of infection and, potentially, also those at increased risk of hospitalisation.

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

McAloon, C.G.[1], Wall, P.[2], Butler, F.[3], Codd, M.[2], Gormley, E.[1], Walsh, C.[4], Duggan, J.[5], Murphy, T.B.[6], Nolan, P.[7], Smyth, B.[8], O'Brien, K.[9], Teljeur, C.[10], Green, M.J.[11], O'Grady, L.[1, 11], Culhane, K.[12], Buckley, C.[13], Carroll, C.[13], Doyle, S.[13], Martin, J.[13], More, S.J.[1, 14]

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BMC Public Health 21, 2238 (2021)

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

Further COVID-19 research

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

Barry, G. et al.

UCD School of Veterinary Medicine

This study was designed to evaluate the establishment of a testing programme for SARS-CoV-2 infection in a university setting and to assess some of the factors that impact participation among both staff and students. Testing was undertaken over a pilot period using a rapid antigen test and a questionnaire was administered to evaluate satisfaction and to understand reasons behind participation or lack thereof. There were differences between staff and students with respect to participation rates as well as intrinsic and extrinsic motivations for participation. The pilot testing programme was helpful in reducing overall anxiety associated with the potential impact of COVID-19, but achieving good participation was challenging. Differing messaging/incentivisation is needed to encourage participation in those different cohorts.

COVID-19 risk factor study (St James's Hospital)

McGrath, J. et al.

St James's Hospital, UCD School of Veterinary Medicine

Healthcare workers (HCW) are considered a high-risk group for COVID-19 infection during the current pandemic. This study will investigate confirmed SARS-CoV-2 infection among HCWs in St James' Hospital during 2020-21. The clinical presentation of HCWs with confirmed COVID-19 infection will be described, and risk factors associated for infection given contact with a confirmed case will be determined. The former work will be conducted as a case study and the latter using a nested case-control study design.

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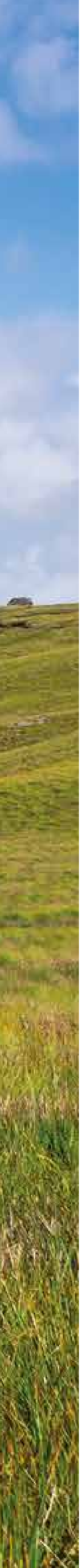
Scientific support



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.

CVERA provides scientific support to both *ad hoc* or ongoing activities, and to a range of national bodies including the Department of Agriculture, Food and the Marine, University College Dublin and Animal Health Ireland. Since March 2020, CVERA also contributed to the national COVID-19 response, primarily in support of the Irish Epidemiological Modelling Advisory Group (IEMAG). Our work draws on expertise within CVERA in epidemiology, statistics, geographic information systems, and database maintenance and interrogation.

The following provide a broad, non-exhaustive overview of scientific support provided by CVERA during 2020 and 2021.

Epidemiological support

Simon More

Department of Agriculture, Food and the Marine

- Member, Scientific Advisory Committee on Animal Health and Welfare
- Member, TB Forum
- Member, iNAP Animal Health Implementation Committee
- Member, Animal Health Surveillance Steering Group
- Member, CVERA management board
- Epidemiological support on a range of issues including:
    - National animal disease surveillance design, including a national bluetongue survey to substantiate freedom
    - Measurement of antimicrobial usage in farmed animals
    - Characterising animal movement: implications for national disease control

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 (VETS30170, VETS30290) and Medicine (MDSA10210)
    - Postgraduate, including Agricultural Science (AESC40020) and Dairy Herd Health (VETS40180)

- Postgraduate supervision or support
    - Finalised: Jonas Brock (PhD Leipzig University) [infectious bovine rhinotracheitis],
    - Ongoing: Ann Barber (PhD Wageningen University) [bovine tuberculosis], Annika van Roon (PhD Utrecht University) [tools for confidence of freedom from infection], Lisa Bradford (ECVPH) [epidemiology], Joana Pessoa (ECVPH) [epidemiology], Áine Collins (ECVPH) [epidemiology]

Irish Epidemiological Modelling Advisory Group (COVID-19)

- Member

Other

- Presentation to the Oireachtas Joint Committee on Agriculture, Food and the Marine
- Animal Health Ireland
    - Chair of the Technical Working Group, member of the Implementation Group, Johne's disease
    - Chair of the Technical Working Group, member of the Implementation Group, CellCheck programme
    - Provision of scientific support to AHI on issues relating to the BVD, Johne's disease, CellCheck and IBR programmes
- European Food Safety Authority
    - Chair of the Scientific Committee (SC)
    - Chair of the MUST-B (multiple stressors on honey bee colony health) working group
    - Member of African Swine Fever (ASF) working groups
- General scientific community
    - Editorial Advisory Board, *EFSA Journal*
    - Scientific Advisory Board, *Preventive Veterinary Medicine*
    - Deputy Editor, *Irish Veterinary Journal*
    - Independent referee for a number of international peer reviewed journals
    - Thesis examination (MVSc, PhD, *Doctor Medicinae Veterinariae*), several universities
    - Member, Scientific Committee, 7th International Conference on *Mycobacterium bovis* (*M. bovis* 2022)

Database and computer programming support

Jamie Tratalos

Department of Agriculture, Food and the Marine

- AIM Bovine Statistics Report 2020 & 2021
- Annual bluetongue freedom from disease analysis
- Provision of bovine movement datasets for use in a variety of projects
- Creation of herd and animal level TB datasets for use by CVERA staff
- Technical and analytical support to the DAFM abattoir surveillance group
- Mapping wild bird Avian Influenza surveillance results
- Production of FMD modelling standard operating procedures (SOP)

Other

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

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 DVO
    - TB quarterly maps
    - Area treated calculations are submitted on a regular basis in compliance with NPWS
    - Resources for regional offices and problem areas
    - WAU annual calculations
    - Density metric data
    - Badger survey appraisal layer
    - Forest harvesting setts
    - Raw Milk producing herds Vs reactor density
    - New setts in Kilkenny trial area
- GIS support for a range of studies, including:
    - Surveillance zone support
    - COVID-19 and population mobility
    - Highly Pathogenic Avian Influenza
    - Silvermines animal health
    - Dairy intensification maps
    - Fox location map
    - RVL catchment maps
    - *Anaplasma phagocytophilum* serosurvey (in collaboration with Teagasc/UCD)
    - Infectious Laryngotracheitis (ILM) maps

Animal Health Ireland

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

Other

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

Statistical support

Jamie Madden

Department of Agriculture, Food and the Marine

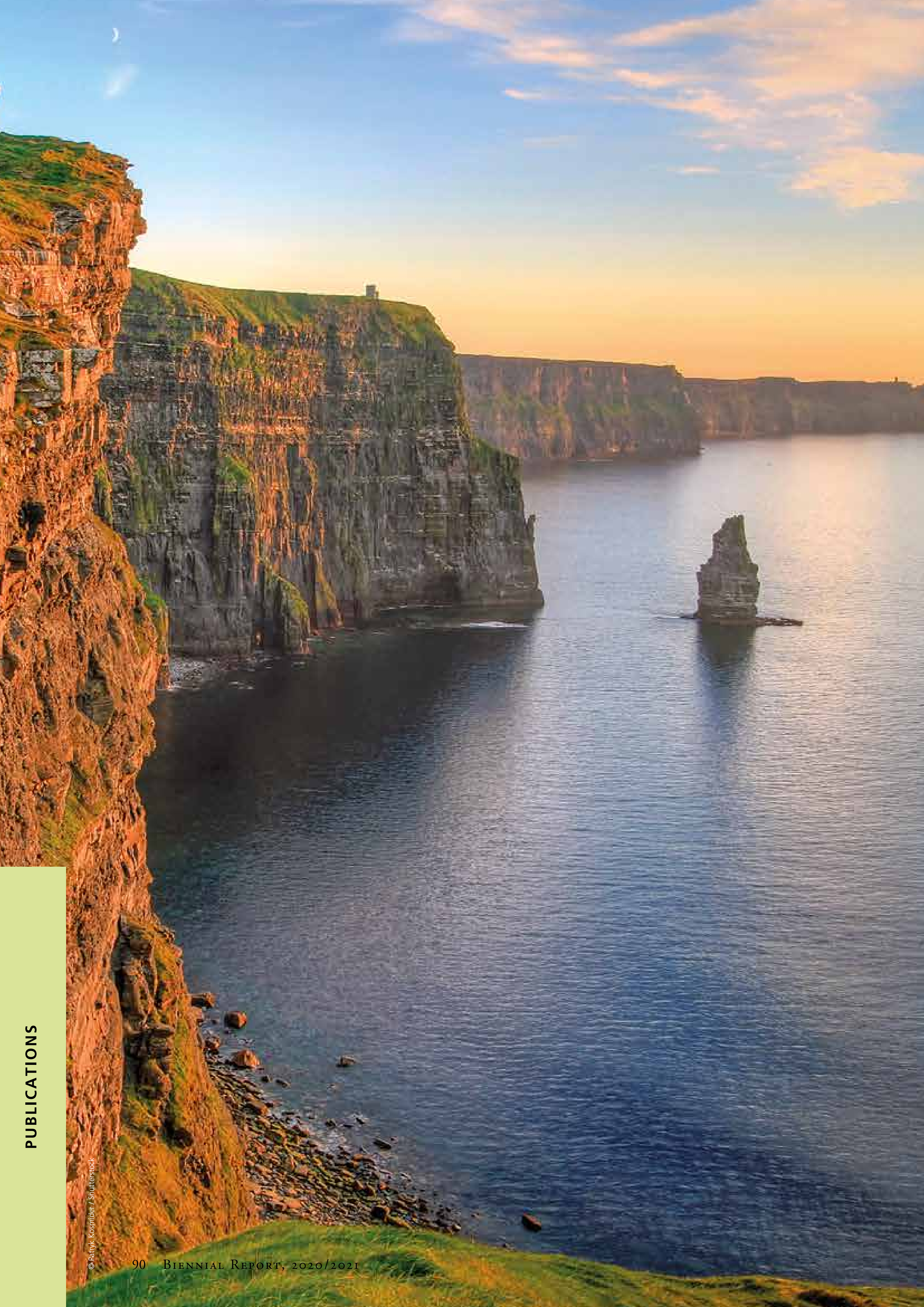
- Statistical and geospatial support for a range of projects.
- Processing and cleaning of raw bTB data for research purposes including development of a herd bTB breakdown file for use:
  - by DAFM's One Health Unit
  - for annual bTB incidence maps
  - variety of other bTB related projects

University College Dublin

- Providing statistical, 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 Epidemiological Modelling Advisory Group (IEMAG). National group formed in 2020 to provide statistical and mathematical modelling support in response to the COVID-19 pandemic.
  - Member of the geospatial sub-group
  - Providing spatial-statistical, spatio-temporal mapping and support
- Member of the Irish Statistical Association



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Publications

During 2020 - 2021

Peer reviewed papers & book chapters

Ashford, R.T., Anderson, P., Waring, L., Davé, D., Smith, F., Delahay, R.J., Gormley, E., Chambers, M.A., Sawyer, J., Lesellier, S., 2020. Evaluation of the Dual Path Platform (DPP) VetTB assay for the detection of *Mycobacterium bovis* infection in badgers. *Preventive Veterinary Medicine* 180, 105005. **https://doi.org/10.1016/j.prevetmed.2020.105005**

Barrett, D., Clegg. T., McGrath, G., Guelbenzu, M., O'Sullivan, P., More, S.J., Graham, D.A., 2020. Herd-level factors associated with detection of calves persistently infected with bovine viral diarrhoea virus (BVDV) in Irish herds with negative herd status (NHS) during 2017. *Preventive Veterinary Medicine* 179, 104990. **https://doi.org/10.1016/j.prevetmed.2020.104990**

Biemans, F., Ben Romdhane, R., Gontier, P., Fourichon, C., Ramsbottom, G., More, S.J., Ezanno, P., 2021. Modelling transmission and control of *Mycobacterium avium* subspecies *paratuberculosis* within Irish dairy herds with compact spring calving. *Preventive Veterinary Medicine* 186, 105228. **https://doi.org/10.1016/j.prevetmed.2020.105228**

Boklund, A., Dhollander, S., Chesnhoiu Vasile, T., Abrahantes, J.C., Bøtner, A., Gogin, A., Gonzalez Villeta, L.C., Gortázar, C., More, S.J., Papanikolaou, A., Roberts, H., Stegeman, A., Ståhl, K., Thulke, H.H., Viltrop, A., Van der Stede, Y., Mortensen, S., 2020. Risk factors for African swine fever incursion in Romanian domestic farms during 2019. *Scientific Reports* 10, 10215. **https://doi.org/10.1038/s41598-020-66381-3**

Brock, J., Lange, M., More, S.J., Graham, D., Thulke, H.H., 2020. Reviewing age-structured epidemiological models of cattle diseases tailored to support management decisions: guidance for the future. *Preventive Veterinary Medicine* 174, 104814. **https://doi.org/10.1016/j.prevetmed.2019.104814**

Brock, J., Lange, M., Guelbenzu-Gonzalo, M., Meunier, N., Vaz, A.M., Tratalos, J.A., Dittrich, P., Gunn, M., More, S.J., Graham, D., Thulke, H.-H., 2020. Epidemiology of age-dependent prevalence of Bovine Herpes Virus Type 1 (BoHV-1) in dairy herds with and without vaccination. *Veterinary Research* 51, 124. **https://doi.org/10.1186/s13567-020-00842-5**

Brock, J., Lange, M., Tratalos, J.A., More, S.J., Graham, D.A., Guelbenzu-Gonzalo, M., Thulke, H.-H., 2021. Combining expert knowledge and machine-learning to classify herd types in livestock systems. *Scientific Reports* 11, 2989. **https://doi.org/10.1038/s41598-021-82373-3**

Brock, J., Lange, M., Tratalos, J.A., More, S.J., Guelbenzu-Gonzalo, M., Graham, D.A., Thulke, H.-H., 2021. A large-scale epidemiological model of BoHV-1 spread in the Irish cattle population to support decision-making in conformity with the European Animal Health Law. *Preventive Veterinary Medicine* 192, 105375. **https://doi.org/10.1016/j.prevetmed.2021.105375**

Byrne, A.W., Barrett, D., Breslin, P., Madden, J.M., O'Keeffe, J., Ryan, E., 2020. Post-mortem surveillance of bovine tuberculosis in Ireland: herd-level variation in the probability of herds disclosed with lesions at routine slaughter to have skin test reactors at follow-up test. *Veterinary Research Communications* 44, 131-136. **https://doi.org/10.1007/s11259-020-09777-w**

Byrne, A.W., Barrett, D., Breslin, P., Madden, J.M., O'Keeffe, J., Ryan, E., 2020. Bovine tuberculosis *(Mycobacterium bovis)* outbreak duration in cattle herds in Ireland: a retrospective observational study. *Pathogens* 9, 815. **https://doi.org/10.3390/pathogens9100815**

Byrne, A.W., Barrett, D., Breslin, P., Madden, J.M., O'Keeffe, J., Ryan, E., 2021. Future risk of bovine tuberculosis *(Mycobacterium bovis)* breakdown in cattle herds 2013-2018: a dominance analysis approach. *Microorganisms* 9, 1004. **https://doi.org/10.3390/microorganisms9051004**

Byrne, A.W., McEvoy, D., Collins, Á.B., Hunt, K., Casey, M., Barber, A., Butler, F., Griffin, J., Lane, E.A., McAloon, C., O'Brien, K., Wall, P., Walsh, K.A., More, S.J., 2020. Inferred duration of infectious period of SARS-CoV-2: rapid scoping review and analysis of available evidence for asymptomatic and symptomatic COVID-19 cases. *BMJ Open* 10, e039856. **https://doi.org/10.1136/bmjopen-2020-039856**

Byrne, A.W., Parnell, A., O'Keeffe, J., Madden, J.M., 2021. The challenge of estimating wildlife populations at scale: the case of the European badger *(Meles meles)* in Ireland. *European Journal of Wildlife Research* 67, 85. **https://doi.org/10.1007/s10344-021-01528-9**

Casey-Bryars, M., Griffin, J., McAloon, C.G., Byrne, A.W., Madden, J.M., McEvoy, D., Collins, Á.B., Hunt, K., Barber, A., Butler, F., Lane, E.A., O'Brien, K., Wall, P., Walsh, K.A., More, S.J., 2021. Pre-symptomatic transmission of SARS-CoV-2 infection: a secondary analysis using published data. *BMJ Open* 11, e041240. **https://doi.org/10.1136/bmjopen-2020-041240**

Clarke A.M., More S.J., Maher J., Byrne A.W., Horan M., Barrett D., 2020. Development and application of a prioritisation tool for animal health surveillance activities in Ireland. *Frontiers in Veterinary Science* 7, 596867. **https://doi.org/10.3389/fvets.2020.596867**

Crispell, J., Cassidy, S., Kenny, K., McGrath, G., Warde, S., Cameron, H., Rossi, G., MacWhite, T., White, P.C.L., Lycett, S., Kao, R.R., Moriarty, J., Gordon, S.V., 2020. *Mycobacterium bovis* genomics reveals transmission of infection between cattle and deer in Ireland. *Microbial Genomics* 6, 8. **https://doi.org/10.1099/mgen.0.000388**

Doeschl-Wilson, A., Knap, P.W., Opriessnig, T., More, S.J., 2021. Livestock disease resilience: from individual to herd level. *Animal* 15, (Suppl. 1), 100286. **https://doi.org/10.1016/j.animal.2021.100286**

Gavey, L., Citer, L., More, S.J., Graham, D., 2021. The Irish Johne's control programme. *Frontiers in Veterinary Science* 8, 703843. **https://doi.org/10.3389/fvets.2021.703843**

Graham, D., More, S.J., O'Sullivan, P., Lane, E., Barrett, D., Lozano, J.-M., Thulke, H.-H., Verner, S., Guelbenzu, M., 2021. The Irish programme to eradicate bovine viral diarrhoea virus – organization, challenges and progress. *Frontiers in Veterinary Science* 8, 674557. **https://doi.org/10.3389/fvets.2021.674557**

Griffin, J., Casey, M., Collins, Á.B., Hunt, K., McEvoy, D., Byrne, A.W., McAloon, C.G., Barber, A., Lane, E.A., More, S.J., 2020. Rapid review of available evidence on the serial interval and generation time of COVID-19. *BMJ Open* 10, e040263. **https://doi.org/10.1136/bmjopen-2020-040263**

Häsler, B., Bazeyo, W., Byrne, A.W., Hernandez-Jover, M., More, S.J., Rüegg, S.R., Schwarzmann, O., Wilson, J., Yawe, A., 2020. Reflecting on One Health in action during the COVID-19 response. *Frontiers in Veterinary Science* 7, 578649. **https://doi.org/10.3389/fvets.2020.578649**

Humphries, R., Mulchrone, K., Tratalos, J., More, S.J., Hövel, P., 2021. A systematic framework of modelling epidemics on temporal networks. *Applied Network Science* 6, 23. **https://doi.org/10.1007/s41109-021-00363-w**

Jordan, A.G., Citer, L.R., McAloon, C.G., Graham, D.A., Sergeant, E.S.G., More, S.J., 2020. Johne's disease in Irish dairy herds: considerations for an effective national control programme. *Irish Veterinary Journal* 73, 18. **https://doi.org/10.1186/s13620-020-00166-y**

Kęsik-Maliszewska, J., Collins, Á.B., Rola, J., Blanco-Penedo, I., Larska, M., 2021. Schmallenberg virus in Poland endemic or re-emerging? A six-year serosurvey. *Transboundary and Emerging Diseases* 68, 2188-2198. **https://doi.org/10.1111/tbed.13870**

Madden, J.M., McGrath, G., Sweeney, J., Murray, G., Tratalos, J.A., More, S.J., 2021. Spatio-temporal models of bovine tuberculosis in the Irish cattle population, 2012-2019. *Spatial and Spatio-temporal Epidemiology* 39, 100441. **https://doi.org/10.1016/j.sste.2021.100441**

Madden, J.M., More, S.J., Teljeur, C., Gleeson, J., Walsh, C., McGrath, G., 2021. Population mobility trends, deprivation index and the spatio-temporal spread of Coronavirus disease 2019 in Ireland. *International Journal of Environmental Research and Public Health* 18, 6285. **https://doi.org/10.3390/ijerph18126285**

Martin, H., Manzanilla, E.G., More, S.J., O'Neill, L., Bradford, L., McAloon, C.I., Collins, Á.B., McAloon, C.G., 2020. Current antimicrobial use in farm animals in the Republic of Ireland. *Irish Veterinary Journal* 73, 11. **https://doi.org/10.1186/s13620-020-00165-z**

Martin, S.W., O'Keeffe, J., Byrne, A.W., Rosen, L.E., White, P.W., McGrath, G., 2020. Is moving from targeted culling to BCG-vaccination of badgers *(Meles meles)* associated with an unacceptable increased incidence of cattle herd tuberculosis in the Republic of Ireland? A practical non-inferiority wildlife intervention study in the Republic of Ireland (2011-2017). *Preventive Veterinary Medicine* 179, 105004. **https://doi.org/10.1016/j.prevetmed.2020.105004**

McAloon, C.G., Collins, Á.B., Hunt, K., Barber, A., Byrne, A.W., Butler, F., Casey, M., Griffin, J., Lane, E., McEvoy, D., Wall, P., Green, M.J., O'Grady, L., More, S.J., 2020. Incubation period of COVID-19: a rapid systematic review and meta-analysis of observational research. *BMJ Open* 10, e039652. **https://doi.org/10.1136/bmjopen-2020-039652**

McAloon, C.G., O'Grady, L., Botaro, B., More, S.J., Doherty, M., Whyte, P., Nielsen, S.S., Citer, L., Kenny, K., Graham, D., Green, M., 2020. Individual and herd-level milk ELISA test status for Johne's disease in Ireland after correcting for non-disease-associated variables. *Journal of Dairy Science* 103, 9345-9354. **https://doi.org/10.3168/jds.2019-18018**

McAloon, C.G., Wall, P., Butler, F., Codd, M., Gormley, E., Walsh, C., Duggan, J., Murphy, T.B., Nolan, P., Smyth, B., O'Brien, K., Teljeur, C., Green, M.J., O'Grady, L., Culhane, K., Buckley, C., Carroll, C., Doyle, S., Martin, J., More, S.J., 2021. Numbers of close contacts of individuals infected with SARS-CoV-2 and their association with government intervention strategies. *BMC Public Health* 21, 2238. **https://doi.org/10.1186/s12889-021-12318-y**

McAloon, C.G., Wall, P., Griffin, J., Casey, M., Barber, A., Codd, M., Gormley, E., Butler, F., Messam, L.L.McV., Walsh, C., Teljeur, C., Smyth, B., Nolan, P., Green, M.J., O'Grady, L., Culhane, K., Buckley, C., Carroll, C., Doyle, S., Martin, J., More, S.J., 2021. Estimation of the serial interval and proportion of pre-symptomatic transmission events of COVID-19 in Ireland using contact tracing data. *BMC Public Health* 21, 805. **https://doi.org/10.1186/s12889-021-10868-9**

McAloon, C.I., McCoy, F., More, S.J., 2021. Short Communication: Trends in estimated intramammary antimicrobial usage in the Irish dairy industry from 2003 to 2019. *JDS Communications* 2, 271-276. **https://doi.org/10.3168/jdsc.2021-0081**

McEvoy, D., McAloon, C., Collins, Á., Hunt, K., Butler, F., Byrne, A., Casey-Bryars, M., Barber, A., Griffin, J., Lane, E.A., Wall, P., More, S.J., 2021. Relative infectiousness of asymptomatic SARS-CoV-2 infected persons compared with symptomatic individuals: a rapid scoping review. *BMJ Open* 11, e042354. **https://doi.org/10.1136/bmjopen-2020-042354**

McFarland, L., Macken-Walsh, Á., Claydon, G., Casey, M., Douglass, A., McGrath, G., McAloon, C.G., 2020. Irish dairy farmers' engagement with animal health surveillance services: Factors influencing sample submission. *Journal of Dairy Science* 103, 10614-10627. **https://doi.org/10.3168/jds.2019-17889**

McLoughlin, K.E., Correia, C.N., Browne, J.A., Magee, D.A., Nalpas, N.C., Rue-Albrecht, K., Whelan, A.O., Villarreal-Ramos, B., Vordermeier, H.M., Gormley, E., Gordon, S.V., MacHugh, D.E., 2021. RNA-Seq transcriptome analysis of peripheral blood from cattle infected with *Mycobacterium bovis* across an experimental time course. *Frontiers in Veterinary Science* 8, 662002. **https://doi.org/10.3389/fvets.2021.662002**

Meunier, N.V., McKenzie, K., Graham, D.A., More, S.J., 2020. Stakeholder perceptions of non-regulatory bovine health issues in Ireland: past and future perspectives. *Irish Veterinary Journal* 73, 25. **https://doi.org/10.1186/s13620-020-00178-8**

Middleton, S., Steinbach, S., Coad, M., McGill, K., Brady, C., Duignan, A., Wiseman, J., Gormley, E., Jones, G.J., Vordermeier, H.M., 2021. A molecularly defined skin test reagent for the diagnosis of bovine tuberculosis compatible with vaccination against Johne's Disease. *Scientific Reports* 11, 2929. **https://doi.org/10.1038/s41598-021-82434-7**

More, S.J., 2020. European perspectives on efforts to reduce antimicrobial usage in food animal production. *Irish Veterinary Journal* 73, 2. **https://doi.org/10.1186/s13620-019-0154-4**

More, S.J., Marchewka, J., Hanlon, A., Balzani, A., Boyle, L., 2021. An evaluation of four private animal health and welfare standards and associated quality assurance programmes for dairy cow production. *Food Policy* 105, 102169. **http://doi.org/10.1016/j.foodpol.2021.102169**

Sleeman, D.P., Collins, D.M., O'Keeffe, J.J., Mackey, M., 2021. Emergence counts of badgers *(Meles meles)* in lowland Co. Wicklow. *Irish Naturalists' Journal* 37, 150-154. **https://irishnaturalistsjournal.org/**

Sleeman, D.P., Mackey, M., O'Keeffe, J., Collins, D.M., 2021. Two-tier badgers' *(Meles meles)* territories in lowland Wicklow, *Ireland. Irish Naturalists' Journal* 38, 1-4. **https://irishnaturalistsjournal.org/**

Tratalos, J.A., Madden, J.M., McGrath, G., Graham, D.A., Collins, Á.B., More, S.J., 2020. Spatial and network characteristics of Irish cattle movements. *Preventive Veterinary Medicine* 183, 105095. **https://doi.org/10.1016/j.prevetmed.2020.105095**

van Roon, A.M., Mercat, M., van Schaik, G., Nielen, M., Graham, D.A., More, S.J., Guelbenzu-Gonzalo, M., Fourichon, C., Madouasse, A., Santman-Berends, I.M.G.A., 2020. Quantification of risk factors for bovine viral diarrhea virus in cattle herds: A systematic search and meta-analysis of observational studies. *Journal of Dairy Science* 103, 9446-9463. **https://doi.org/10.3168/jds.2020-18193**

van Roon, A.M., Rapaliute, E., Koleci, X., Muñoz, V., Mercat, M., Faverjon, C., Santman-Berends, I.M.G.A., Nielen, M., More, S.J., Graham, D., Guelbenzu-Gonzalo, M., Madouasse, A., Fourichon, C., van Schaik, G., 2021. Key learnings during the development of a generic data collection tool to support assessment of freedom of infection in cattle herds. *Frontiers in Veterinary Science* 8, 656336. **https://doi.org/10.3389/fvets.2021.656336**

van Roon, A.M., Santman-Berends, I.M.G.A., Graham, D., More, S.J., Nielen, M., van Duijn, L., Mercat, M., Fourichon, C., Madouasse, A., Gethmann, J., Sauter-Louis, C., Frössling, J., Lindberg, A., Correia-Gomes, C., Gunn, G.J., Henry, M.K., van Schaik, G., 2020. A description and qualitative comparison of the elements of heterogeneous bovine viral diarrhea control programs that influence confidence of freedom. *Journal of Dairy Science* 103, 4654-4671. **https://doi.org/10.3168/jds.2019-16915**

Yatabe, T., Martínez-López, B., Díaz Cao, J.M., Geoghegan, F., Ruane, N.M., Morrissey, T., McManus, C., Hill, A.E., More, S.J., 2020. Data-driven network modelling as a framework to evaluate the transmission of piscine myocarditis virus (PMCV) in the Irish farmed Atlantic salmon population and the impact of different mitigation measures. *Frontiers in Veterinary Science* 7, 385. **https://doi.org/10.3389/fvets.2020.00385**

Scientific opinions

S.J. More [UCD CVERA] with members of the Panel on Animal Health and Welfare (AHAW), the Scientific Committee (SC) of the European Food Safety Authority [EFSA], and working groups on MUST-B (risk assessment of multiple stressors in honeybees) and African Swine Fever.

European Food Safety Authority (EFSA), Boklund, A., Bøtner, A., Chesnoiu, V.T., Depner, K., Desmecht, D., Guberti, V., Helyes, G., Korytarova, D., Linden, A., Miteva, A., More, S., Olsevskis, E., Ostojic, S., Roberts, H., Spiridon, Ståhl, K., Thulke, H.-H., Vilija, G., Viltrop, A., Wallo, R., Wozniakowski, G., Abrahantes, J.C., Dhollander, S., Gogin, A., Ivanciu, C., Papanikolaou, A., González Villeta, L.C., Gortázar Schmidt, C., 2020. Epidemiological analyses of African swine fever in the European Union (November 2018 to October 2019). *EFSA Journal* 18 (1), 5996. **https://doi.org/10.2903/j.efsa.2020.5996**

European Food Safety Authority (EFSA), Nielsen, S.S., Alvarez, J., Bicout, D.J., Calistri, P., Depner, K., Drewe, J.A., Garin-Bastuji, B., Gonzales Rojas, J.L., Gortazar Schmidt, C., Herskin, M., Michel, V., Miranda Chueca, M.A., Pasquali, P., Roberts, H.C., Sihvonen, L.H., Spoolder, H., Stahl, K., Velarde, A., Winckler, C., Abrahantes, J.C., Dhollander, S., Ivanciu, C., Papanikolaou, A., Van der Stede, Y., Blome, S., Guberti, V., Loi, F., More, S., Olsevskis, E., Thulke, H.H., Viltrop, A., 2021. ASF Exit Strategy: Providing cumulative evidence of absence of African swine fever virus circulation in wild boar populations using standard surveillance measures. *EFSA Journal* 19 (3), 6419. **https://doi.org/10.2903/j.efsa.2021.6419**

EFSA AHAW Panel (EFSA Panel on Animal Health and Welfare), Nielsen, S.S., Alvarez, J., Bicout, D.J., Calistri, P., Canali, E., Drewe, J.A., Garin-Bastuji, B., Gonzales Rojas, J.L., Herskin, M., Michel, V., Miranda Chueca, M.A., Michel, V., Padalino, B., Pasquali, P., Roberts, H.C., Sihvonen, L.H., Spoolder, H., Stahl, K., Velarde, A., Viltrop, A., Winckler, C., Blome, S., More, S., Gervelmeyer, A., Antoniou, S.-E., Gortazar Schmidt, C., 2021. African swine fever and outdoor farming of pigs. *EFSA Journal* 19 (6), 6639. **https://doi.org/10.2903/j.efsa.2021.6639**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Halldorsson, T.I., Hernández-Jerez, A., Bennekou, S.H., Koutsoumanis, K., Machera. K., Naegeli. H., Nielsen, S.S., Schlatter, J.R., Schrenk, D., Silano, V., Turck, D., Younes, M., Arnold, G., Dorne, L.-L., Maggiore, A., Pagani, S., Szentes, C., Terry, S., Tosi, S., Vrbos, D., Zamariola, G., Rortais, A., 2020. A systems-based approach to the environmental risk assessment of multiple stressors in honey bees. *EFSA Journal* 19 (5), 6607. **https://doi.org/10.2903/j.efsa.2021.6607**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Halldorsson, T.I., Hernández-Jerez, A., Bennekou, S.H., Koutsoumanis, K., Machera. K., Naegeli. H., Nielsen, S.S., Schlatter, J.R., Schrenk, D., Silano, V., Turck, D., Younes, M., Glandorf, B., Herman, L., Tebbe, C., Vlak, J., Aguilera, J., Schoonjans, R., Cocconcelli, P.S., 2020. Evaluation of existing guidelines for their adequacy for the microbial characterisation and environmental risk assessment of microorganisms obtained through synthetic biology. *EFSA Journal* 8 (8), 6263. **https://doi.org/10.2903/j.efsa.2020.6263**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Halldorsson, T., Hernández-Jerez, A., Hougaard Bennekou, S., Koutsoumanis, K., Lambré, C., Machera. K., Naegeli. H., Nielsen, S., Schlatter, J., Schrenk, D., Silano, V., Turck, D., Younes, M., Castenmiller, J., Chaudhry, Q., Cubadda, F., Franz, R., Gott, D., Mast, J., Mortensen, A., Oomen, A.G., Weigel, S., Barthelemy, E., Rincon, A., Tarazona, J., Schoonjans, R., 2021. Guidance on technical requirements for regulated food and feed product applications to establish the presence of small particles including nanoparticles. *EFSA Journal* 19 (8), 6769. **https://doi.org/10.2903/j.efsa.2021.6769**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Halldorsson, T., Hernández-Jerez, A., Hougaard Bennekou, S., Koutsoumanis, K., Lambré, C., Machera. K., Naegeli. H., Nielsen, S., Schlatter, J., Schrenk, D., Silano, V., Turck, D., Younes, M., Castenmiller, J., Chaudhry, Q., Cubadda, F., Franz, R., Gott, D., Mast, J., Mortensen, A., Oomen, A.G., Weigel, S., Barthelemy, E., Rincon, A., Tarazona, J., Schoonjans, R., 2021. Guidance on risk assessment of nanomaterials to be applied in the food and feed chain: Part 1, human and animal health. *EFSA Journal* 19 (8), 6768. **https://doi.org/10.2903/j.efsa.2021.6768**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Halldorsson, T.I., Hougaard Bennekou, S., Koutsoumanis, K., Machera. K., Naegeli. H., Nielsen, S., Schlatter, J., Schrenk, D., Silano, V., Turck, D., Younes, M., Aggett, P., Castenmiller, J., Giarola, A., de Sesmaison-Lecarré, A., Tarazona, J., Verhagen, H., Hernández-Jerez, A., 2020. Statement on the derivation of Health-Based Guidance Values (HBGVs) for regulated products that are also nutrients. *EFSA Journal* 19 (3), 6479. **https://doi.org/10.2903/j.efsa.2021.6479**

EFSA Scientific Committee, More, S.J., Bampidis, V., Benford, D., Bragard, C., Hernandez-Jerez, A., Bennekou, S.H., Halldorsson, T.I., Koutsoumanis, K.P., Lambré, C., Machera, K., Naegeli, H., Nielsen, S.S., Schlatter, J.R., Schrenk, D., Silano, V., Turck, D., Younes, M., Benfenati, E., Crépet, A., Te Biesebeek, J.D., Testai, E., Dujardin, B., Dorne, J.L.C.M., Hogstrand, C., 2021. Guidance document on scientific criteria for grouping chemicals into assessment groups for human risk assessment of combined exposure to multiple chemicals. *EFSA Journal* 19 (12), 7033. **https://doi.org/10.2903/j.efsa.2021.7033**

EFSA Scientific Committee, More, S., Bambidis, V., Benford, D., Bragard, C., Hernandez-Jerez, A., Bennekou, S.H., Koutsoumanis, K., Machera. K., Naegeli. H., Nielsen, S.S., Schlatter, J.R., Schrenk, D., Silano, V., Turck, D., Younes, M., Fletcher, T., Greiner, M., Ntzani, E., Pearce, N., Vinceti, M., Ciccolallo, L., Georgiadis, M., Gervelmeyer, A., Halldorsson, T.I., 2020. Draft for internal testing Scientific Committee guidance on appraising and integrating evidence from epidemiological studies for use in EFSA's scientific assessments. *EFSA Journal* 8 (8), 6221. **https://doi.org/10.2903/j.efsa.2020.6221**

EFSA Scientific Committee, More, S.J., Bambidis, V., Bragard, C., Halldorsson, T.I., Hernández-Jerez, A., Hougaard Bennekou, S., Koutsoumanis, K., Lambré, C., Machera. K., Naegeli. H., Nielsen, S.S., Schlatter, J., Schrenk, D., Turck, D., Younes, M., Aquilina, G., Bignami, M., Bolognesi, C., Crebelli, R., Gürtler, R., Marcon, F., Nielsen, E., Vleminckx, C., Carfì, M., Martino, C., Maurici, D., Parra Morte, J., Rossi, M., Benford, D., 2021. Guidance on aneugenicity assessment. *EFSA Journal* 19 (8), 6770. **https://doi.org/10.2903/j.efsa.2021.6770**

EFSA Scientific Committee, More, S., Benford, D., Bennekou, S.H., Bampidis, V., Bragard, C., Halldorsson, T., Hernandez-Jerez, A., Koutsoumanis, K., Lambré, C., Machera, K., Mullins, E., Nielsen, S.S., Schlatter, J., Schrenk, D., Turck, D., Tarazona, J., Younes, M., 2021. Opinion on the impact of non-monotonic dose responses on EFSA's human health risk assessments. *EFSA Journal* 19 (10), 6877. **https://doi.org/10.2903/j.efsa.2021.6877**

More, S.J., Auteri, D., Rortais, A., Pagani, S., 2021. EFSA is working to protect bees and shape the future of environmental risk assessment. *EFSA Journal* 19 (1), e190101. **https://doi.org/10.2903/j.efsa.2021.e190101**

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