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06/05/2022   15:28
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WELCOME ADDRESS

Dear Friends and Colleagues,

It is with great honour that we extend a céad míle fáilte (one hundred thousand welcomes) to you all and welcome you to NUI Galway for the Seventh International Conference on Mycobacterium bovis (M. bovis 2022). We would like to thank all of you for participating especially after the tumultuous events of the last two years.

As previously, this conference gathers together scientists, post-graduates, policy makers, veterinarians and industry stakeholders from around the world with the aim of sharing information that helps to provide practical solutions for the control and eradication of M. bovis. The previous conferences on Mycobacterium bovis took place in Dublin 1991, Dunedin 1995, Cambridge 2000, Dublin 2005, Wellington 2009 and Cardiff 2014.

Thanks to the variety of speakers, the programme covers a wide range of topics related to Mycobacterium bovis including: One Health, national control strategies, immunology, diagnostics, social science, wildlife, and epidemiology. We hope that we have put together an interesting and relevant programme with input from a wide range of countries and disease control programmes.

The conference also provides opportunities for colleagues to renew contacts, expand networks and socialise together. We encourage all attendees to interact with the speakers, your fellow delegates, and the sponsors during the conference in order to build relationships and collaborations for the future.

We would like to thank our speakers, delegates, NUI Galway, Abbey Conference & Events, volunteers, and our generous sponsors for their continued support of the conference. Without all of you, this conference would not be possible.

A selection of papers based on presentations by the plenary speakers will be peer reviewed and published in a special open access collection of the Irish Veterinary Journal with publication planned for later this year.

Once again, thank you all for participating in M. bovis 2022. We hope that you find the experience both beneficial and enjoyable.

The Scientific and Organising Committees

June 2022
GENERAL INFORMATION

Speaker Preparation
If you are presenting during the conference please take your presentation to the AV technicians in the corresponding meeting rooms (our staff will be happy to help and show you the rooms).

Name Badges
Please make sure to wear your name badge at all times during the conference. If you have booked a Gala Dinner Ticket please bring your badge with you.

Mobile Phones
Please turn off all mobile phones during conference sessions.

Internet
There is free WIFI provided by Eduroam;
username: 9876001t
password: nfqtj7387 (case sensitive)

Conference Information
If you have any general enquiries regarding the conference please see the staff at the registration desk.

Photography
Some photography will be taking place at the conference, if you do not wish to be photographed, please speak to a member of conference staff or the photographer.

Members of the Scientific Committee
Eamonn Gormley (Chair) – University College Dublin
Daniel Collins – University College Dublin
Margaret Good – Department of Agriculture, Food & the Marine (retired)
Stephen Gordon – University College Dublin
Kevin Kenny – Department of Agriculture, Food & the Marine
Simon More – University College Dublin
Eoin Ryan – Department of Agriculture, Food & the Marine
Michael Sheridan – Department of Agriculture, Food & the Marine (retired)

Members of the Organising Committee
Daniel Collins (Chair) – University College Dublin
Anthony Duignan – Department of Agriculture, Food & the Marine (retired)
Noreen Galvin – Department of Agriculture, Food & the Marine
Rosanne Greene – Department of Agriculture, Food & the Marine
Margaret Good – Department of Agriculture, Food & the Marine (retired)
Mary Hynes – Department of Agriculture, Food & the Marine
Donal Mooney – Department of Agriculture, Food & the Marine
Conor O’Mahony – Department of Agriculture, Food & the Marine

EXHIBITION FLOOR PLAN

MAIN LECTURE THEATRE
Bailey Allen Hall
See Campus Map on P8

Poster Viewing Area

To Registration & Break Out Rooms

Poster Viewing Area
Tuesday, 7th June

Welcome Reception & Barbeque at the NUI College “Sult Bar”
18:00 – 20:00

Thursday, 9th June

Gala Dinner at the Galmont Hotel
(Tickets required - please don’t forget your badge for entry)

The gala dinner will start with a welcome reception on the terrace of the hotel (weather permitting) followed by a 3 course dinner.

There will then be some Irish dancing and a Céilí (Irish dancing) and we hope you will all participate.

The dress code is smart casual.
Prof. Georgios Banos

Prof Banos graduated from the Faculty of Agriculture at the Aristotle University of Thessaloniki, Greece (emphasis on Livestock Production), before completing his MSc at the University of New Hampshire, USA and PhD at the University of Wisconsin-Madison, USA, in 1989, with a focus on the genetic improvement of farm animals. After a two-year post-doctoral stint at the Centre for the Genetic Improvement of Livestock at the University of Guelph in Canada, he accepted an offer to lead the newly established Interbull Centre, hosted by the Swedish University of Agricultural Sciences in Uppsala, Sweden, with the mandate to develop and deliver international genetic evaluation services to the global bovine sector, and with stakeholders in more than 30 countries worldwide. In the process, Prof Banos completed a Master of Business Administration degree at the University of Warwick in the UK. In 2000, he returned full time to the academia, as a Professor at the Faculty of Veterinary Medicine at the Aristotle University of Thessaloniki, Greece, where he conducted research and taught genetics of livestock disease resistance. For the next 12 years, he collaborated closely with Scotland’s Rural College (SRUC) in Edinburgh as a Visiting Professor. In 2012, he moved to Edinburgh to take on his current role, which is also linked to an Honorary Professorship with the University of Edinburgh. He continues conducting research on the genetics of farm animal disease resistance and performance, supervising PhD students, and teaching at the undergraduate and graduate levels. He has been keen on investigating the genetic background of animal resistance to bovine tuberculosis (bTB) and managed the research project that led to the launch of the national genetic evaluation for bTB in the UK.

Dr. Maria Laura Boschiroli

Dr Maria Laura Boschiroli is Research Director, head of the Bovine Tuberculosis National Reference Laboratory- OIE Bovine Tuberculosis Reference Laboratory at Anses (French Agency for Food, Environmental and Occupational Health & Safety). Laura completed her B.Sc and PhD on molecular microbiology at the Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Argentina. Her area of expertise includes molecular-genomic epidemiology, validation and introduction of new tests for the French diagnostic scheme for TB surveillance on livestock and wildlife, control of TB diagnostic reagents. She also provides advice to the World Organisation for Animal Health and the French authorities on the national TB control programme.

https://www.anses.fr/en

Dr. Lucía de Juan

Dr. Lucía de Juan is the Director at VISAVET Health Surveillance Centre, Director European at Union Reference Laboratory for Bovine Tuberculosis and an Associate Professor at the Vet School in the Universidad Complutense de Madrid. Lucía graduated in Veterinary Medicine (1997) and obtained a PhD in Veterinary Sciences (2005) from the University Complutense de Madrid. Since 1998 she has been working in the Animal Health Department of the Veterinary School. After the establishment of the VISAVET Health Surveillance Centre in 2008, she has been the Head of the Mycobacteria Unit until 2014. Currently, she is professor in the Vet School (UCM) and director of the VISAVET Centre and the European Union Reference Laboratory for Bovine Tuberculosis. She is an advisor for the Spanish Ministry of Agriculture, Food and the Environment regarding the eradication programme for bovine tuberculosis. As a result of her research career, Dr. de Juan has published more than 80 papers in international publications and she has also participated in national and international congresses with more than 250 contributions.


Dr. Sewellyn Davey

Sewellyn Davey is a retired Veterinary Scientist with extensive experience in the diagnosis and control of bovine brucellosis and tuberculosis. After majoring in Microbiology and Zoology for a Bachelor of Science degree in 1975, she graduated with a Bachelor of Veterinary Science in 1980 from the Onderstepoort Veterinary Faculty of the university of Pretoria. Early in her career, she was stationed at first at Ermelo, Mpumalanga, and later in Kroonstad, Free State. As a laboratory vet in these regional laboratories, she concentrated on disease investigation and diagnosis and in 1982 headed up the serology section in the Kroonstad Laboratory.

In 1987 Sewellyn was appointed State Veterinarian for Animal Health in Malmesbury in the Western Cape. Disease control was her mandate. In 2020 she retired from government service. She then registered with the South African Veterinary Council and is a private consultant for bovine brucellosis, MAP and bovine TB. This in order to assist her colleagues with the diagnosis, management and control of these diseases.

Sewellyn has consulted in South Africa and abroad. She served on the OIE ad hoc committee tasked with the rewriting of the Terrestrial Code chapters on Brucellosis and Tuberculosis. From 2016 until 2020 she was chairperson of the Ministerial Technical (Min Tech) Working Group on bovine brucellosis, and member of the Min Tech working group on bovine tuberculosis.

She relies heavily on academic and research advances to inform her laboratory and field work. This has improved her diagnoses of these three complicated intracellular diseases and promoted better disease control.
PLenary Speakers

Dr. Gareth Enticott

Dr. Gareth Enticott is a Reader in Human Geography at Cardiff University. His research focuses on biosecurity and animal disease surveillance and management. Dr. Enticott is an expert in the ongoing controversy in the UK surrounding bovine Tuberculosis in cattle and badgers and has advised the UK government on the role of social research in helping the management of the disease. His research has also focused on the management of bovine Tuberculosis in New Zealand. Specifically, his research has focused on farmers’ behaviour; farmers’ beliefs about disease transmission; and the impact of government attempts to change farmers’ biosecurity behaviour. He has also examined reforms to the veterinary profession and their effects on disease management including the use of diagnostics, and the migration of veterinary surgeons to the UK and New Zealand.

https://www.cardiff.ac.uk/people/view/363232-enticott-gareth

Dr. Ron Glanville

Ron Glanville has had a career of over 44 years working in animal health in Australia, including the positions of Chief Biosecurity Officer, Chief Veterinary Officer and Chief Inspector of Stock for the State of Queensland. Career highlights include: a key role in finalising bovine tuberculosis eradication; leading Queensland’s response to the 2007 equine influenza outbreak, as well as around 30 other emergency responses; and implementing the national livestock identification system. Ron also has had extensive experience working on national committees established to coordinate programs across the country.

In relation to bovine tuberculosis eradication, Ron was a field officer early in his career, progressing to a regional veterinary manager during a critical eradication phase in the north-west of Queensland, then later managed the program at the State level. For 15 years Ron held the statutory position of Chief Inspector of Stock, which was responsible for regulatory decision making for programs such as TB eradication. He also represented Queensland nationally to negotiate and establish the program’s overall strategic direction.

Since 2011 Ron has established a successful consulting business providing quality advice to industry and governments in the area of biosecurity, including strategic advice, program reviews, facilitation & training, emergency preparedness and response support. In 2020 Ron received the David Banks Australian Biosecurity Lifetime Achievement Award.

Prof. Stephen Gordon

Stephen Gordon obtained his BSc from NUI Galway, Ireland (1990), PhD from the University of Leicester, UK (1995) and pursued postdoctoral research at the Institut Pasteur, Paris as a Wellcome Trust Fellow (1995-99). He was a team leader in the TB Research Group, Veterinary Laboratories Agency, Weybridge (UK) from 1999-2007, and took up his current position in University College Dublin in 2008. His research focuses on understanding the molecular basis for virulence in mycobacterial pathogens and is funded by Science Foundation Ireland, the Dept. of Agriculture Food and Marine, Wellcome Trust, BBSRC and EU H2020.


Prof. Christian Gortázar

Prof. Christian Gortázar is the Head of the Health & Biotechnology (SaBio) group at IREC in Spain. Christian (San Sebastián, 1967) received a Degree in Veterinary Sciences at Universidad de Zaragoza, in 1990, and a PhD at the same University in 1997. Since 1999, he is Professor at IREC, a multidisciplinary research institute dealing with conservation and management of wildlife and their habitats (www.IREC.com). His lecturing on wildlife diseases is part of IREC's MSc and PhD programs, where he has mentored >20 successful international PhD students. He has acted as principal researcher in numerous grants and contracts on wildlife epidemiology and disease control. Co-author of >350 scientific publications, his research interests include viral, bacterial and parasitic diseases of wildlife, with emphasis on the epidemiology and control of relevant infections shared with livestock and humans, such as tuberculosis.


Prof. Vivek Kapur

Vivek Kapur is Professor of Microbiology and Infectious Diseases in the Department of Animal Science and Huk Distinguished Chair in Global Health. He is also Associate Director for strategic initiatives at the Huk Institutes of the Life Sciences at Penn State. He is also appointed as Professor of Infectious Diseases and Global Health at the Nelson Mandela African Institute of Science and Technology in Tanzania.

As an early adopter in the field of microbial genomics, Prof. Kapur’s research team has led the complete genome sequencing of some of the most important pathogens that cause diseases in animals and humans and conducted related investigations in infectious diseases and genomics. These studies have led to key insights on the evolution, physiology, and mechanisms of pathogenesis of these organisms, as well as the identification of numerous targets for diagnostic test development and vaccines. His current research effort focuses on the development, assessment, and implementation of strategies to accelerate control of tuberculosis and other zoonotic infections in low and middle-income countries.

Prof. Kapur trained in veterinary medicine at the University of Agricultural Sciences in Bangalore, India, received a Ph.D. in Veterinary Sciences from Penn State, and conducted post-doctoral research at the Baylor College of Medicine in Houston. He has previously held faculty and leadership positions at Baylor College of Medicine, the University of Minnesota College of Veterinary Medicine and Medical School, where he served as Director of the Biomedical Genomics Center.
In August 2019, Christine was appointed the role of Visiting Professor of Practice at Harper Adams University. Christine comes from a farming family in the Borders of Scotland, with a background in livestock genetics for a number of years in Scotland and the north of England prior to joining the Animal Health Agency (now part of Animal and Plant Health Agency). Christine worked in private practice with specific interest in research, meat processing and emerging diseases such as Schmallenberg and Porcine Epidemic Diarrhoea. She policy team, and also previously surveillance including detection and response to new disease control approaches. Prior to moving to Australia, Christine led Defra’s Animal Traceability and Public Health policy team, and also previously surveillance including detection and response to new and emerging diseases such as Schmallenberg and Porcine Epidemic Diarrhoea. She is an experienced veterinarian. Before joining the UK government services in 2008, Christine worked in private practice with specific interest in research, meat processing and livestock genetics for a number of years in Scotland and the north of England prior to joining the Animal Health Agency (now part of Animal and Plant Health Agency) as a Divisional Veterinary Manager in Scotland. Christine comes from a farming family in the Borders of Scotland, with a background in beef cattle and sheep. In August 2019, Christine was appointed the role of Visiting Professor of Practice at Harper Adams University.
PLENARY SPEAKERS

Dr. Eoin Ryan

Eoin Ryan qualified with a veterinary degree from University College Dublin in 2002, having previously obtained an intercalated BSc(Hons) in pathology at the Royal Veterinary College, UK, in 2001. Following a spell in mixed practice, he completed a PhD in foot-and-mouth disease at the Pirbright Institute, UK and an MSc in veterinary epidemiology and public health with the Royal Veterinary College, UK. He has worked in the UN Food and Agriculture Organisation on the control of foot-and-mouth disease. He has also worked in various roles in the Department of Agriculture, Food and the Marine (DAFM), Ireland, including in the veterinary laboratory service and veterinary public health. He is currently head of Ruminant Animal Health Division in DAFM, where he leads veterinary policy on TB eradication.

Ms Jane Sinclair

Jane graduated from Massey University, Palmerston North, NZ in 1980. Staying on to complete a masters in Epidemiology before heading out into clinical practice. After 26 years in mixed clinical practice, she became weary of after-hours call out work and grovelling around calving cows in the middle of the night had lost its appeal. So, in 2006 Jane enrolled at the Epi Centre at Massey to refresh her epidemiology knowledge by completing another masters in Epidemiology. At the same time, she also started as a District Disease Control Manager with the Animal Health Board. As the level of disease has dropped in NZ her role has now developed a national focus as a member of the Epidemiology Team within the Disease Control Planning and Integration team, which forms the "engine room" of OSPIR.

Nicolas Valdivieso

After graduating as a veterinarian, Nicolas moved from Santiago de Chile, to the extreme north of the country to be part of a foundation that seeks to overcome poverty in rural areas. In the northern valleys and highlands, he worked as a field veterinarian with goats, sheep and cameldids, providing technical assistance and developing investment projects to improve the income and sustainability of small producers.

In 2007 he started to work for the Livestock and Agriculture Service (SAG), and then, in 2009 he obtained a scholarship from the World Bank for postgraduate studies. Nicolas studied a master program in animal production systems, along with a minor degree in public policy at Wageningen University, the Netherlands. Upon his return to Chile in 2011, Nicolas returns to the official veterinary service, but this time at the central level, to work in epidemiology focused in monitoring and controlling animal endemic diseases. In 2015, he took on the challenge of the bovine tuberculosis control and eradication program, where he has integrate the public policy and epidemiology knowledge to control the bTB in a Chilean context, where infected animals are not compensated. Regardless, he has managed to reach consensus and update the program regulation, as well as reach agreement with Universities to carry out applied research. The most relevant projects it has been a pilot program of vaccination with BCG in highly infected dairies herds. This pilot was launched in 2016 and it has shown significant results not only in reducing bTB incidence, but also improving production indicators.

At the beginning of 2021, Nicolas moved to the Aysén region, in Patagonia, to work again at the local level as regional head veterinarian at the SAG, where he has taken on challenges such as to achieve the regional status of free from bTB.

http://www.sag.gob.cl/

Dr Bouda Vosough Ahmadi

Dr Bouda Vosough Ahmadi is a vet and agricultural economist, specialized in economics of livestock health and welfare. His research interests include assessing and evaluating agricultural policies and in particular prevention and control policies of contagious animal diseases as well as animal welfare. He is currently working as a consultant in economics of livestock health to the European Commission for the Control of Foot-and-Mouth Disease (EuFMD) which is one of the units of the Food and Agriculture Organization (FAO) based in Rome. Previously he worked for about 10 years as a senior agricultural economist in the Policy Analysis Team of Scotland’s Rural College (SRUC) based in Edinburgh. His research was mainly focused on policy analysis and socioeconomic impact assessments using quantitative methods and economic models applied to livestock health and welfare. In 2016, he worked for one year at the European Commission’s Joint Research Centre (JRC) based in Seville, where his main role was project management and contributing to further development and usage of an EU-Wide Individual Farm Model for Common Agricultural Policy (IFM-CAP) analysis. He has authored and coauthored a number of interdisciplinary peer-reviewed articles and he is the board member of the International Society for Economics and Social Sciences of Animal Health (ISESSAH).

https://www.researchgate.net/profile/Bouda_Vosough_Ahmadi

Ms Jane Sinclair

Jane graduated from Massey University, Palmerston North, NZ in 1980. Staying on to complete a masters in Epidemiology before heading out into clinical practice. After 26 years in mixed clinical practice, she became weary of after-hours call out work and grovelling around calving cows in the middle of the night had lost its appeal. So, in 2006 Jane enrolled at the Epi Centre at Massey to refresh her epidemiology knowledge by completing another masters in Epidemiology. At the same time, she also started as a District Disease Control Manager with the Animal Health Board. As the level of disease has dropped in NZ her role has now developed a national focus as a member of the Epidemiology Team within the Disease Control Planning and Integration team, which forms the "engine room" of OSPIR.
### DAY 1 - 7th June 2022 (Tuesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Venue</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>12:00</td>
<td>Bailey Allen Hall</td>
<td>Registration</td>
</tr>
<tr>
<td>14:00</td>
<td>Main Lecture Theatre</td>
<td>Welcome address; Bailey Allen Hall Foyer; Bailey Allen Hall Foyer</td>
</tr>
<tr>
<td>14:30</td>
<td>Main Lecture Theatre</td>
<td>Prof. Mark Agar - Wicked problems and bovine tuberculosis</td>
</tr>
<tr>
<td>15:00</td>
<td>Main Lecture Theatre</td>
<td>Prof. Stephen Gordon - One health approaches to the analysis of Mycobacterium bovis</td>
</tr>
<tr>
<td>15:30</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>16:00</td>
<td>Main Lecture Theatre</td>
<td>Prof. Ron Glanville - Bovine TB control in New Zealand - the journey from an endemic to eradication</td>
</tr>
<tr>
<td>16:30</td>
<td>Main Lecture Theatre</td>
<td>Prof. Christine Middlemiss - Bovine TB control in the 21st century; UK experience</td>
</tr>
<tr>
<td>17:00</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
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<tr>
<td>17:45</td>
<td>College Bar</td>
<td>Welcome reception</td>
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</tbody>
</table>

### DAY 2 - 8th June 2022 (Wednesday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Venue</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:00</td>
<td>Main Lecture Theatre</td>
<td>Dr. Eoin Ryan - The Irish Bovine Tuberculosis Eradication Programme: Combining Stakeholder Engagement and Research Driven Policy to Tackle Bovine TB</td>
</tr>
<tr>
<td>10:00</td>
<td>Main Lecture Theatre</td>
<td>Ms. Jamie Swart - Bovine TB control in South Africa - the journey from epidemic to eradication</td>
</tr>
<tr>
<td>10:30</td>
<td>Main Lecture Theatre</td>
<td>Prof. Christophe De Mean - Bovine TB control in the 21st century; the UK experience</td>
</tr>
<tr>
<td>11:00</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
</tr>
<tr>
<td>11:45</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>12:00</td>
<td>Exhibition Area / An Bhidain</td>
<td>Break - Lunch will be served in An Bhidain</td>
</tr>
<tr>
<td>14:30</td>
<td>Main Lecture Theatre</td>
<td>Dr. Behzad Givi - Challenges to the control of Mycobacterium bovis in livestock and wildlife populations in the South African context</td>
</tr>
<tr>
<td>15:00</td>
<td>Main Lecture Theatre</td>
<td>Prof. Gilles de Jean - The 6/18 eradication programme in Spain - the role of the EU reference laboratory</td>
</tr>
<tr>
<td>15:30</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
</tr>
<tr>
<td>16:00</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>16:30</td>
<td>Exhibition Area</td>
<td>Break - The View Breakout Room</td>
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<tr>
<td>17:00</td>
<td>Exhibition Area</td>
<td>Poster viewing session 1</td>
</tr>
</tbody>
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### DAY 3 - 9th June 2022 (Thursday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Venue</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:00</td>
<td>Main Lecture Theatre</td>
<td>Dr. Daniel J. O’Brien - The devil you know and the devil you don’t: current status and challenges of bovine tuberculosis eradication in the United States</td>
</tr>
<tr>
<td>10:00</td>
<td>Main Lecture Theatre</td>
<td>Dr. Ron Glanville - Australia’s Colourful Path to Tuberculosis Freedom</td>
</tr>
<tr>
<td>10:30</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
</tr>
<tr>
<td>11:00</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>11:15</td>
<td>Exhibition Area</td>
<td>Break - Lunch will be served in An Bhidain</td>
</tr>
<tr>
<td>14:00</td>
<td>Main Lecture Theatre</td>
<td>Dr. Mieke Koutsoudi - Bovine tuberculosis control a disease-free country. France: does the long and winding road really lead to eradication?</td>
</tr>
<tr>
<td>14:30</td>
<td>Main Lecture Theatre</td>
<td>Prof. Nicola Claridge - Is it possible to control bovine tuberculosis without compensation? Reviewing ten years of the Chilean program and its progress</td>
</tr>
<tr>
<td>15:00</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
</tr>
<tr>
<td>15:30</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>16:00</td>
<td>Exhibition Area</td>
<td>Break - The View Breakout Room</td>
</tr>
<tr>
<td>16:30</td>
<td>Exhibition Area</td>
<td>Poster viewing session 2</td>
</tr>
<tr>
<td>18:00</td>
<td>Galmont Hotel</td>
<td>Gala dinner (Ticketed Event)</td>
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</tbody>
</table>

### DAY 4 - 10th June 2022 (Friday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Venue</th>
<th>Session</th>
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</thead>
<tbody>
<tr>
<td>9:00</td>
<td>Main Lecture Theatre</td>
<td>Prof. Christian Gómez - Can we ever eradicate TB from wildlife - a look into the future</td>
</tr>
<tr>
<td>10:00</td>
<td>Main Lecture Theatre</td>
<td>Dr. James McCormack - Horizon scanning: what next for TB control in England?</td>
</tr>
<tr>
<td>10:45</td>
<td>Exhibition Area</td>
<td>Break</td>
</tr>
<tr>
<td>11:00</td>
<td>Main Lecture Theatre</td>
<td>Prof. Jonathan Roughley - Do we know the burden of bovine tuberculosis? Introduction and a request from the Global Burden of Animal Diseases programme</td>
</tr>
<tr>
<td>11:30</td>
<td>Main Lecture Theatre</td>
<td>Prof. Nicola Claridge - Social determinants and the eradication of bovine tuberculosis: The role of Good Farmers and Well Men</td>
</tr>
<tr>
<td>12:15</td>
<td>Main Lecture Theatre</td>
<td>Panel discussion; chair, plenary speakers</td>
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</tbody>
</table>
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More information at thermofisher.com/bTB

Wicked Problems and Bovine Tuberculosis

Prof Vivek Kapur
Penn State University, United States

How might we control bovine tuberculosis in regions where test and slaughter of cattle is socially unacceptable, ecologically challenging, or economically unfeasible? What is the contribution of zoonotic TB to human TB in India, a country with both the largest number of dairy cattle and buffaloes and highest burden of human TB on the planet? What does the tuberculin test really measure? This presentation will share the approach we are taking to address these diverse questions and deal with bovine TB as a wicked problem for which orthogonal solutions are urgently needed. The presentation will also highlight some of the surprising and truly unexpected answers that we are finding, and emerging evidence-based strategies to accelerate the control of bovine TB.

One Health approaches to the analysis of Mycobacterium bovis

Professor Stephen Gordon
University College Dublin, Dublin, Ireland

The Mycobacterium tuberculosis complex (MTBC), the assembly of pathogens that cause tuberculosis (TB) in mammals, represents an ideal model in which to explore One Health concepts in infectious disease. This presentation will describe research comparing Mycobacterium bovis with the human-adapted pathogen Mycobacterium tuberculosis through such a One Health lens as a route to define the molecular basis for their distinct host tropism and evolutionary trajectories. Data from approaches such as genomics, transcriptomics and proteomics will be provided to show how genetic differences across M. bovis and M. tuberculosis translate to quantitative changes in pathogen gene expression and protein synthesis. Functional analyses will then be highlighted, using comparative studies of both pathogens in experimental cattle infections as well as in vitro macrophage infection models. Finally, we will discuss what these studies teach us about the virulence, evolution, and host adaptation of M. bovis and the application of such knowledge to TB control.

Challenges and opportunities of public-private partnerships in efforts to prevent, control and eradicate animal diseases

Dr Bouda Vosough Ahmadi
Animal Production and Health Division (NSA), Food and Agriculture Organisation (FAO), Rome, Italy

Animal disease risks and outbreaks can be characterised and controlled by institutional structures defining or influencing their rights, roles, and responsibilities. Institutional theory is shared across social sciences that provides vital context for evaluating the effectiveness of disease prevention and control interventions. Although prevention and control policies are often based on scientific approaches, however they may be socially or culturally limited because of institutional context. A wide range of institutions such as national governments and their agencies (i.e., public sector), communities of practice namely farmers, producers and manufacturers, veterinarians, laboratories, and consultants (i.e., private sector) as well as international organisations such as FAO, OIE, WHO, are often involved in animal disease prevention and control. In addition, other important contextual elements such as laws and codes of practice, customs and traditional cultures and beliefs as well as the market including insurance sector must be considered.

The mentioned institutions are involved and play roles in aspects of main policy instruments for disease prevention and control management. These policies include: i) Regulatory interventions: e.g., compensation for culled animals as happens in case of bTB; penalties for late or lack of reporting outbreaks of notifiable diseases; compulsory and/or optional vaccination; ii) Information, direct regulatory, market-based approaches (e.g., BVD eradication); iii) Other instruments such as the Coase theorem, the polluter pays principle, cost and responsibility sharing that is considered as a public-private partnership (PPP).

Innovative PPPs that bring together institutions such as businesses, governments and civil society actors are increasingly being promoted by international organisations such the UN for pooling much-needed financing and collaborations to strengthen animal disease prevention and control plans. However, actors and institutions from public and private sectors have diverging perspectives that may lead to under provision of disease control expenditure, less or no incentive to overcome transactions costs of monitoring and controlling diseases and not considering wider impacts of animal disease control plans. The main challenges and opportunities of applying the PPP concept to prevent and control animal diseases at global level have been established by drawing upon experiences gained from reviewing the past and ongoing projects facilitated under the global framework for the progressive control of transboundary animal diseases (GF-TADs) that are presented in this paper.
The contribution of selective breeding to controlling bovine tuberculosis

Prof Georgios Banos
Scotland’s Rural College (SRUC, Edinburgh, United Kingdom

Bovine tuberculosis (bTB) is one of the most persistent livestock health problems in many countries and is globally ranked in the top five most significant animal diseases for impact on public health and industry finances. Relevant costs emanate from involuntary culling of animals with a positive skin test, animal movement restrictions, and the cost of control and eradication programmes. Despite investment and control efforts, however, the incidence and prevalence of cases in parts of the UK persist. For example, the number of animals slaughtered in England and Wales due to bTB increased in 2021 by 4-8% compared to the previous year, warranting further efforts towards achieving the Officially Tuberculosis Free status goal.

Genetic selection aiming to identify and remove animals that are inherently susceptible to bTB from breeding has been proposed as a complementary measure to control the disease. The presence of genetic variation among individual animals in their capacity to respond to M. bovis exposure has been documented and quantified. Indeed, heritability estimates broadly ranging between 0.09 and 0.20 have been reported in various studies. Despite their moderate magnitude, these estimates suggest that host resistance of bTB is a trait amenable to improvement with selective breeding. Although relatively slow, genetic progress can be constant, cumulative and permanent, thereby complementing ongoing control measures. Importantly, no antagonistic correlations were found between bTB resistance and other important cattle traits suggesting that incorporating the former in breeding decisions would not impact adversely on productivity. On the contrary, a favourable genetic correlation of bTB resistance has been reported with the UK Profitable Lifetime Index, further corroborating the concept of selective breeding for bTB resistant animals. Indeed, simulation studies have clearly demonstrated the impact of genetic selection on reducing the probability of a bTB breakdown to occur, the percentage of secondary cases, and the duration of the breakdown should it actually occur. To this effect, a genetic evaluation of dairy cattle for bTB resistance was launched in the UK in 2017 and was followed by studies on beef cattle. Furthermore, research on the bovine genome conducted in different countries and cattle populations have identified multiple genomic markers and regions associated with animal bTB resistance and promoted the feasibility to increase the accuracy and efficiency of selective breeding with genomic selection. Several such regions harbour genes regulating immunological response and affecting overall animal fitness. Nevertheless, the combined outcomes of these studies suggest that host resistance to bTB is a complex, polygenic trait, with no single gene explaining alone the inherent differences among individual animals in different populations and datasets. Such results warrant the development of accurate genomic breeding values, capturing the collective effect of multiple genes, to underpin genomic selection programmes.

In addition to improving host resistance to bTB, scientists and practitioners have long considered the possibility to also reduce host infectivity as a supplementary strategy to disease control. Simulation studies have confirmed that bTB eradication could be accelerated if selective breeding considered both host resistance and infectivity traits. Ongoing studies are investigating the development of genetic predictions for infectivity. First results have encouragingly revealed the presence of genetic variation for infectivity with heritability estimates in the same range as for bTB resistance. This work is also focusing on the estimation of breeding values for bTB infectivity and correlation with bTB resistance and other important animal traits.

The majority of genetic research on bTB has been so far based on national surveillance data. Additional relevant information may increase the accuracy of genetic selection. To this effect, novel bTB predictions have been recently proposed based on mid-infrared milk spectral data combined with machine learning approaches.

In conclusion, genetic studies of bTB have generated knowledge and insights to support selective breeding as an additional measure towards controlling and eradicating the disease.

The Irish bTB Eradication Programme: Combining Stakeholder Engagement and Research-Driven Policy to Tackle Bovine TB

Dr Eoin Ryan
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A new Irish bovine tuberculosis (bTB) eradication strategy was launched in 2021, following several years of gradually increasing bTB levels associated with the expansion of the dairy sector since 2015. This strategy was informed by extensive discussions with stakeholders and a review of several aspects of bTB policy based on research. A stakeholder discussion body, the TB Forum, had been established in 2018 and this continues under the new strategy, supported by three working groups (scientific, financial and implementation). The strategy sets out actions to address cattle-to-cattle and badger-to-cattle bTB transmission, along with actions to improve farm biosecurity and empower farmers to make their own choices to reduce bTB risk.

Large scale vaccination of badgers has been rolled out under the new strategy, with over 20,000 km2 covered by the vaccination programme and approximately 7,000 badgers captured in vaccination areas in 2021. Badger culling continues in response to serious cattle bTB outbreaks epidemiologically linked to badgers. Vaccination efforts have been complemented by intensive communications campaigns, including an app enabling farmers to report the location of badger sets.

Cattle which test inconclusive to the tuberculin skin test have been re-tested using a gamma interferon blood test since April 2021, with 62% of these testing positive. These cattle are now being removed much earlier than would previously have been the case, reducing the potential for further spread. An enhanced oversight process has been put in place for herds experiencing extended or repeat bTB breakdowns. Whole genome sequencing is used to investigate links between breakdowns, with the results supporting operational decision making in case management. Communication including biosecurity advice, is co-designed with stakeholders, improving their effectiveness. A programme involving veterinary practitioners providing tailored biosecurity bTB advice to their clients was established in 2021 and is being rolled out nationally in 2022.

A core element of the new strategy is the continual improvement of policies in response to changing bTB risks. The role of research and data analysis has been critically important in underpinning the decisions taken under the new strategy. Levels of bTB in Ireland were lower in 2021 than in 2020, the first such year-on-year reduction since 2016, with herd incidence in 2021 at 4.33% and 20.931 reactors.

Bovine TB control in New Zealand – the journey from epidemic towards eradication

Ms Jane Sinclair
OSPRI, New Zealand

New Zealand has had bovine TB in the country since the settlers arrived in the mid 1800’s with their cattle from Europe bringing the disease with them. The introduction of the Australian brush tailed possum as a fur trade and its subsequent infection with bovine TB resulted in a very complicated disease dynamic within NZ. The emerging bTB epidemic in the 1980’s led to the formation of a not-for-profit organisation, the Animal Health Board in 1993 whose sole aim was to manage the disease nationally. Funding was a unique partnership between Government (central and local) and industry (dairy, beef and deer) and management was authorised through legislation where Mycobacterium bovis was deemed an “unwanted organism” in the Biosecurity Act 1993, and management strategized through a succession of National Pest Management Plans (NPMP). The three pillars of the management of the disease were: (i) Disease management with national surveillance through TB testing of domestic cattle and deer herds combined with slaughter house inspection of all carcases, and intense management of infected herds, (ii) movement control on stock from areas of high risk of possum infection and from infected herds, and (iii) eradication programme of possum population control. Through utilising these three pillars, NZ has seen a reduction in the number of infected herds from nearly 1700 as of 30th June 1995 to 26 as of 30th June 2019. Over the same period NZ had seen a reduction in the vector risk area (VRA) from 10 million to 6.5 million hectares.

Research had led to the belief that it was possible to eradicate the disease from possums in very large tracts of native bush and so in the latest NPMP 2016, three staged goals were adopted: TB freedom in herd by 2026, TB freedom in possums by 2040 and biological eradication of Mycobacterium bovis by 2055.

As the disease prevalence dropped dramatically this has thrown up challenges with the drop off in the Predictive Value of the diagnostic tests and the original TB testing programme considering only the proximity to infected possum populations. NZ has considerable nation-wide stock movements and so the role of translocation of disease via trading was becoming more problematic. Previously infected herds were known as “positive risk based testing” programme was considered where location, previous disease history and stock movements would all be considered. All of which relied heavily on good adoption of the very newly introduced National Animal Identification and Tracing (NAIT) system (2012).
Bovine TB control in the 21st century - the UK experience

Prof Christine Middlemiss
Chief Veterinary Officer of the United Kingdom (UK), United Kingdom

Bovine Tuberculosis (bTB) continues to be a challenging animal health problem in the UK, particularly in the South-West and West of England, and in parts of Wales, and Northern Ireland. Scotland is Officially bTB Free.

In the UK animal health and welfare policy is devolved and operates within a UK governance framework. Each UK nation has its own bTB eradication and control plans working towards the shared goal of UK have Officially bTB Free status. As such there is much in common and include a range of evidence-led interventions to tackle the disease in both cattle and wildlife.

Routine and targeted surveillance of cattle herds, movement restrictions on infected herds and rapid detection and removal of test-positive animals from those herds remain the foundation of our strategies, supported by statutory pre- and post-movement testing of cattle and slaughterhouse surveillance.

The strategies across the UK continue to adapt to make use of the latest scientific advances and epidemiological techniques. For example:

- World-leading BCG vaccination field trials in cattle began in 2021 in the UK, initially trialling a newly developed skin test that can detect infected among vaccinated cattle (a DIVA test). The DIVA skin test represents a significant scientific breakthrough and a major step forward in our battle against bovine TB. We have discussed future validation of this test and acceptance of BCG vaccination of cattle with the OIE to support the UK’s trade status. As such there is much in common and include a range of evidence-led interventions to tackle the disease in both cattle and wildlife.

- We continue to fund research to develop a molecularly defined (or synthetic) tuberculin (MDT) which would overcome the limitations of traditional tuberculins that form the basis of current global surveillance.

Challenges to the control of Mycobacterium bovis in livestock and wildlife populations in the South African context

Dr Sewellyn Davey
Western Cape Department Of Agriculture, South Africa

Bovine tuberculosis (bTB) was first diagnosed in cattle in South Africa in 1880 and proclaimed a controlled disease in 1911. Testing of cattle for bTB is voluntary and only outbreaks of disease are reported to the National Department of Agriculture for the prevalence of the disease in cattle is largely unknown. There is a Bovine Tuberculosis Scheme which is aimed at the control of bTB in cattle but the same measures of test and slaughter, and the quarantining of the property apply to wildlife as well. bTB was first diagnosed in wildlife in a greater kudu in the Eastern Cape in 1928 and has to date been found in 24 mammalian wildlife species. The African buffalo has become a maintenance host of the disease which is considered endemic in the Kruger National Park, the Hluhluwe-Imfolozi Park and the Madikwe Game Park.

Control of bTB at the wildlife-livestock interface is difficult because of spill over and spillback between species. Only buffalo are required by law to be tested before translocation, but bTB has been introduced to the Madikwe Game Park probably by the translocation of other infected wildlife species. There is no national control strategy for the control of bTB in wildlife. Indirect tests have been developed to test for bTB in eight species, 6 of which can be considered endangered. More research needs to be done in wildlife to develop an effective and efficient vaccine to combat the transmission of bTB within and between species. New policies need to be developed that are effective, affordable and encompassing to control the spread of bTB in both livestock and wildlife in South Africa.
STREAM 1 ABSTRACTS – ONE HEALTH - WEDNESDAY 8TH JUNE 2022

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Advancing One Health: Lessons learned from Zoonotic Tuberculosis (ZTB)

Dr Paula Fujimori1,2,3,4,5
1International Union Against Tuberculosis and Lung Disease and “Chairperson, Task Force and Writing Committee, Global Plan to End TB: 2023-2030”.
2Mycobacterium bovis (M. bovis) causes tuberculosis (TB) that is mostly clinically indistinguishable from that caused by human Mycobacterium tuberculosis (M. tb). In 2016, the global TB community developed the Zoonotic TB Roadmap, with the goal of helping to end the disease by 2030, in line with the United Nations Sustainable Development Goals.

The presentation will describe the collaboration to produce the Roadmap that involved the member-driven Zoonotic TB Subsection of the International Union Against Tuberculosis and Lung Disease (The Union), the World Health Organization, the World Organisation for Animal Health (OIE), and the Food and Agricultural Organization. The Roadmap formed the basis for the inclusion of both zoonotic and bovine TB in the United Nation's 2018 "Political declaration of the high-level meeting of the General Assembly on the fight against tuberculosis".

The presentation will describe how the lessons of ZTB can inform global One Health efforts. These include the need for: 1) stronger links between the human and animal health sectors, 2) how evidence-based research is fundamental; and 3) the role of popular media and affected communities to create awareness and demand for services. It will conclude with the progress to date of the Roadmap, from the global and national levels to an initiative that encourages mayors of local city government to drive changes in attitude and lead implementation of zoonotic services using a One Health approach.

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Gene essentiality studies in Mycobacterium bovis offers novel insights into the genetic basis of virulence for the bovine pathogen

Dr Amanda J Gibson1,*, Ms Jennifer Stiens2, Dr Ian Passmore3, Dr Walwynny Faulkner4,5, Mr Josephous Miculob1, Dr Sam Willcock3, Dr Michael Coad6, Dr Stefan Berg6, Professor Dirk Werling1, Professor Brendan Wren7, Dr Irene Nobel7, Professor Bernardo Villarreal-Ramos8, Dr Sharon Kendall9
1Centre of Emerging Endemic and Exotic Disease, The Royal Veterinary College, Hatfield, UK; 2Institute of Structural and Molecular Biology, Biological Sciences, Birbeck, University of London, London, UK; 3London School of Hygiene and Tropical Medicine, London, UK, 4Centre of Excellence for Bovine Tuberculosis, IEBS, Aberystwyth University, Aberystwyth, UK; 5Systems Chemical Biology of Infection and Resistance Laboratory, The Francis Crick Institute, London, UK; 6Animal and Plant Health Agency, Surrey, UK

An understanding of the genetic basis of survival in members of the Mycobacterium tuberculosis complex is crucial for deciphering the biology of host-pathogen interactions. Over the last two-decades great progress has been made in defining the genes required for survival of the human-adapted Mycobacterium tuberculosis during infection, however equivalent studies in the animal-adapted Mycobacterium bovis are lacking. While large-scale efforts using whole genome sequencing have identified sequence polymorphisms between M. tuberculosis and M. bovis, whole genome essentiality screens have the potential to highlight if polymorphisms have an impact on gene function. We have been utilising whole genome transposon insertion sequencing (Tn-Seq) in both M. bovis AF2122/97 and M. tuberculosis H37Rv to uncover differences in gene essentiality between the two species. Additionally, we have been asking which genes are required for the survival of M. bovis during infection and performed the first whole genome essentiality screen of M. bovis in cattle. In this talk I will present our findings and highlight the novel virulence factors we have found in M. bovis. Our work further extends our knowledge of the genetic basis of survival in vivo in bacteria that cause tuberculosis. The outputs can be viewed through a one-health lens to inform the development of novel differential diagnostics and therapeutics for TB in both human and animal populations.
Bovine tuberculosis, caused by members of the Mycobacterium tuberculosis-complex, is spread across the world. It affects human and animal health, reduces the production of milk and meat and impacts the mental health and well-being of affected individuals and their families. There is a growing realization that collaborative efforts of multiple disciplines working locally, nationally, and globally are required to attain optimal health for people, animals and our environment - a so-called OneHealth approach. Calculating the global socio-economic costs and environmental impact of bovine tuberculosis is complex but should be given high priority to help galvanize a OneHealth approach to controlling this devastating disease.

It is well over 100 years ago since the early successes of a OneHealth approach to the control of tuberculosis bore fruit. Amongst these were the identification of Mycobacterium bovis and the demonstration that it could be transmitted from cattle to humans, most commonly through the consumption of milk. This led to the implementation of the pasteurization of milk in many countries. The tuberculin skin test was also developed during this golden era for microbiology along with BCG, one of the most commonly used human vaccines.

In 2016, the global TB community developed the Zoonotic TB Roadmap, with the goal of helping to end the global TB epidemic by 2030, in line with the United Nations Sustainable Development Goals. The Roadmap identified ten priority areas for addressing zoonotic tuberculosis. This talk will concentrate on reviewing progress made on some of the technical priorities outlined in the Roadmap such as improving diagnostics, developing vaccines and closing research gaps. In doing so, I will make the case that shared research in human and animal health can speed the development of new diagnostic tests for humans and livestock, and improve TB surveillance, control, and eradication programs.

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STAR-IDAZ International Research Consortium: Global coordination of animal disease research

Dr Johannes Charlier1,2, Maddy Newman1,2, Alex Morrow1

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STAR-IDAZ International Research Consortium (IRC), an international network of R&D programme owners/managers and international organisations around 50 countries, was established to coordinate research funding by addressing identified research needs, sharing results and delivering new and improved animal health strategies for priority animal health diseases/issues. Under the IRC, 28 partners from 19 countries moved to a higher level of commitment, dedicating a five-year budget of approximately $2.5 billion to contribute to IRC objectives. The STAR-IDAZ IRC is organized via scientific working groups, a scientific and executive committee, four regional networks and an EU-funded secretariat. These structures work together to encourage regional coordination and cooperation, bring programme owners and funders together to work with network partners, explore sharing for resources and identify international funding opportunities.

To achieve IRC goals, the working groups develop research roadmaps for a number of priority topics. These road maps are published on the STAR-IDAZ IRC website (www.star-idaz.net) and describe the building blocks and for each the key research questions and possible solutions routes to develop novel key scientific information, novel disease control tools or integration of new techniques. The roadmaps are based on ‘leads’ which are used to consider the Research Question (“What is the problem needing to be solved?”), Challenges (“What are the scientific and technological challenges/Knowledge gaps needing to be addressed”), Solution Routes (“What approaches could/should be taken?”), Dependencies (What needs to be done first) and State of the Art (Existing knowledge including success and failures). The details of current and planned research projects are mapped onto these roadmaps to determine the extent to which gaps are being addressed. This forms the basis of funding recommendations made to the IRC partners to encourage more focused and coordinated research on the priority gaps. Mycobacterium bovis roadmaps have been created to support development of new diagnostics, candidate vaccines as well as control strategies. These road maps now need further discussion with the global M. bovis research community for updating and validation.

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Is vaccinating badgers inferior to continued targeted culling? A non-inferiority study on the risk of Irish cattle herds developing bTB

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1DAFM, Dublin, Ireland, 2Veterinary College, University of Guelph, Guelph, Canada, 3Transboundary Epidemiology Analytics, Fort Collins, USA, 4University College Dublin School of Veterinary Medicine, Dublin, Ireland

Bovine tuberculosis (bTB) remains as a persistent disease in Ireland. Historically since 2005 in Ireland, targeted badger culling has been implemented as part of the bTB control/eradication program and has reduced badger densities in bTB endemic areas. Lowering badger densities in large areas of agricultural grassland has been shown previously to substantially reduce the risk of future cattle-herd bTB-breakdowns for up to ten years. Nonetheless, widespread implementation of badger-culling is not a sustainable practice as badgers are a legally protected species.

Vaccination of badgers with Bacille Calmette-Guérin (BCG) has been proposed as an alternative to prolonged or widespread badger culling. Thus, in 2011, a five-year non-inferiority study was implemented in seven counties in the ROI. This study was designed to contrast the bTB-cattle-herd-breakdown-risk in areas where intramuscular badger vaccination was conducted versus the bTB-cattle-herd-breakdown-risk in areas in the same county where badger culling was continued as the control treatment.

Our outcome of interest was a new-bTB cattle-herd breakdown event with a cumulative total of >2 standard interpretation skin-test reactors during the bTB epidemic.

Four and five years post commencement of badger vaccination, we contrasted the annual cattle-herd risks of our outcome for herds in the vaccination versus the targeted culling areas. The actual badger population in each study area and which are most of all culturally and ethically acceptable.

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Control of bovine tuberculosis in a high biodiversity developing country: feasible or fictional?

Prof Anita Michel1, Mrs Petronillah Sichewo1,2, Prof Eric Etter1,3

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Bovine tuberculosis caused by Mycobacterium bovis remains an impediment to livestock production in a number of countries around the world. However, low and middle income countries with a lack of adequate resources, the presence of a wildlife reservoir and impoverished farming communities are facing multifaceted challenges. In South Africa, one of the most biodiverse countries, bovine tuberculosis is maintained by domestic cattle in the commercial and subsistence farming sectors as well as by African buffalo from which it has spread to at least 20 other wildlife species species which are rare or endangered. Wildlife is not only abundant in national parks and other public game reserves but many wildlife species including the “Big Five” are owned in even higher numbers by private game farmers for commercial purposes. The sale and translocation of wildlife of unknown bovine tuberculosis status constitutes a high risk for disease dissemination. Diagnosis and control of bovine tuberculosis in African buffalo and to a certain extent in traditionally farmed communal cattle is expensive, increasingly ineffective, impractical and may be considered unethical. Therefore it is imperative for the national bovine tuberculosis control programme to consider additional alternative control strategies such as vaccination which are more affordable, practical and effective in the long term and which are most of all culturally and ethically acceptable.

STREAM 2 ABSTRACTS – NATIONAL CONTROL STRATEGIES - WEDNESDAY 8TH JUNE 2022

www.mbovis2022.com  NUI Galway, Ireland  7-10 June 2022
Field Veterinary Experiences of Bovine Tuberculosis Control in Fiji – Challenges, Progress, Recommendations for the Future

Dr Aoife Reid1, Dr Keresi Lomata1, Paul Colville1, Dr Sripad Sosale1
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Objective:
Raise awareness of Fiji’s bovine tuberculosis and brucellosis eradication campaign (BTEC) internationally. Challenges, progress and recommendations for bovine tuberculosis control in a developing country will be highlighted.

Key results/findings:
Fiji comprises of approximately 330 islands. BTEC began in Fiji in the 1980s and exists today through government funding and stakeholder support. Caudal skin fold testing is performed by locally trained BTEC testers with positive reactors removed for slaughter. Testing focuses on endemic infected dairy farming areas on Viti Levu, the main island. Beef, village and small holder farms are incorporated when possible. The 2020 national agricultural census estimated a cattle population of over 119,000. Many cattle across Fiji remain untested due to remote locations and logistical constraints. In 2014, improved test interpretation and staff training led to a tenfold increase in reactors. In late 2018, some large dairy farms in the centre of a chronically infected area agreed to re-engage with BTEC after years of non-participation; hundreds of reactors were detected with many condemned with generalised tuberculosis on meat inspection. The economic impact of BTEC on the dairy industry was severe, with a significant drop in milk production due to culling of reactors. Sustained collaboration from dairy industry leaders, MOA, Biosecurity Authority of Fiji (BAF), Fiji meat industry board (FMIB) and other stakeholders has been essential in dealing with the fallout. BAF and MOA now collaborate to enforce testing and monitor cattle movements. In 2018, an improved compensation scheme was implemented by MOA and FMIB, streamlining reactor removal and compensation payments. A new BTEC database was launched in 2019, enabling compilation of testing data centrally, to assist with recording, test scheduling, monitoring and evaluation. Fiji’s BTEC still faces challenges. The lack of a national herd and cattle registration system means the true cattle and herd population remains unknown. Limited farm facilities hamper the efficiency of testing and application of alternative testing methods. BTEC-specific legislation is warranted to ensure ongoing compliance. Increased monitoring and training of abattoir staff is needed for disease surveillance. Extending surveillance to other regions and to small holders across Fiji is required. Continuing stakeholder communication and support will be integral to the success of the program.

Significance/Impact of study:
Substantial progress has been made despite the need for improvements. The challenges faced at field and government level in Fiji are relevant to other developing countries, where shared experiences can be documented and learned from.

The epidemiological role of ‘no specific infection’ herds in bovine tuberculosis in Ireland

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1DAFM CVRL, Celbridge, Ireland, 2UCD, Dublin 4, Ireland, 2School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland

One complicating factor in the eradication of bovine tuberculosis (bTB) is the existence of herds within which cattle react to the intradermal skin-test but where lesions or other evidence of infection are not confirmed on abattoir inspection. Such herds are termed ‘no specific infection’ (NSI) herds and subsequent to the removal of reactors, these herds do not consistently return to a ‘clear’, skin-test negative status. As is anticipated that the proportion of these herds will increase as the overall incidence of bTB declines in countries such as Ireland, a greater understanding of the nature and dynamics of infection/disease within such herds will be essential.

This study investigated the potential epidemiological significance of NSI herds within the National herd. Key research objectives were to: formulate clear criteria as to what constitutes a NSI herd; and then use detailed post-mortem examination to determine the true infection status of reactors in such herds.

Rigorous criteria as to what constitutes a NSI herd were established following expert consultation within DAFM bTB policy, laboratory and regional veterinary services.

Following application of initial criteria to a database containing tuberculin test details of the National herd, 81 herds were initially identified. As the further selection criteria were applied, the vast majority (>92%) were excluded leaving six suspect herds. Many herds were excluded on the basis of having been located in a high-risk geographical region or by confirmation of recent or subsequent bTB infection. Detailed post-mortem examination of 8 animals from two of these herds revealed no grossly visible tuberculous lesions and Mycobacterium bovis was not cultured from a range of pooled tissues.

These preliminary findings suggest the number and epidemiological significance of NSI herds is somewhat limited. Even herds that met the rigorous selection criteria applied in this study disclosed relatively small numbers of reactors on sequential skin-testing. It is possible that in many such herds bTB is in a latent or early stage of development, where lesions are microscopic or absent, and bacterial loads small. Alternative test and disease management strategies are required to deal with such herds.

Using computer simulation models to assess potential impacts of changes to primary bovine tuberculosis surveillance testing of cattle in England

Dr. Colin Birch1, Mr. Richard Budgery1, Mr. Tom Doherty2, Dr. Oliver Tearne1, Professor Rowland Kao1, Dr. Mark Arnold1, Professor Graham Smith1
1Animal and Plant Health Agency, Weybridge and York, United Kingdom, 2University of Edinburgh, Edinburgh, United Kingdom

Objective
Currently three computer models of bovine tuberculosis (bTB) epidemiology and control are available at the Animal and Plant Health Agency (APHA) to inform bTB control strategies in England. The APHA baderg / cattle model was developed from an individual badger-based model resolved in virtual regions of up to 1000 km². The others represent the farm and cattle population of Great Britain (GB), with abstract representation of infection from badgers: BoTMET models at farm level resolution, while BTEC models at individual cattle level, fitting parameter estimates by approximate Bayesian computation (ABC), which allows estimation of model uncertainty.

The recent Godfray Review of bTB strategy in England recommended consideration of changes to surveillance testing. One option was, in areas with high bTB incidence, to use the more sensitive but less specific Single Intradermal Cervical Test (SICCT) as the primary screening test for cattle herds in place of the current Single Intradermal Comparative Cervical Test (SICT). The objective of this study was to use the models described above to estimate the net effects of this change and their dynamics.

Key Results
The models, particularly TBMI, require precise specification of the alternative surveillance options. The specificity of the SICT in GB is uncertain, and will vary regionally, but all models were run with an initial scenario set at a presumed high SICT specificity (99%). This change in surveillance testing was predicted to reduce the numbers of both true positive reactors and undetected infected cattle substantially more than the number of confirmed herd breakdowns; the decrease in the number of true positive reactors would roughly match the increase in the number of false positive reactors, after a short lag in which there would be an increase in total reactors. However, when model parameters were set at lower SICT specificities (i.e. <95%), which may be observed in some areas, all three models concurred in predicting large increases in the numbers of total reactors and total herd breakdowns.

Significance
Scenario definition is challenging and time-consuming, but this work revealed choices between alternative implementations of the various surveillance policy options. The consistency among the predictions of three separate models with contrasting assumptions and logic was reassuring, although differences between the presentations of their outputs complicated comparison. The model outputs suggested more understanding is required of SICT specificity and the factors influencing it before SICT could be adopted for routine herd surveillance in England.

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The epidemiological role of ‘no specific infection’ herds in bovine tuberculosis in Ireland

Mr. Jimmy Wiseman1,2, Assoc. Prof. Joe Cassidy1, Prof. Eamonn Gormley2
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One complicating factor in the eradication of bovine tuberculosis (bTB) is the existence of herds within which cattle react to the intradermal skin-test but where lesions or other evidence of infection are not confirmed on abattoir inspection. Such herds are termed ‘no specific infection’ (NSI) herds and subsequent to the removal of reactors, these herds do not consistently return to a ‘clear’, skin-test negative status. As is anticipated that the proportion of these herds will increase as the overall incidence of bTB declines in countries such as Ireland, a greater understanding of the nature and dynamics of infection/disease within such herds will be essential.

This study investigated the potential epidemiological significance of NSI herds within the National herd. Key research objectives were to: formulate clear criteria as to what constitutes a NSI herd; and then use detailed post-mortem examination to determine the true infection status of reactors in such herds.

Rigorous criteria as to what constitutes a NSI herd were established following expert consultation within DAFM bTB policy, laboratory and regional veterinary services.

Following application of initial criteria to a database containing tuberculin test details of the National herd, 81 herds were initially identified. As the further selection criteria were applied, the vast majority (>92%) were excluded leaving six suspect herds. Many herds were excluded on the basis of having been located in a high-risk geographical region or by confirmation of recent or subsequent bTB infection. Detailed post-mortem examination of 8 animals from two of these herds revealed no grossly visible tuberculous lesions and Mycobacterium bovis was not cultured from a range of pooled tissues.

These preliminary findings suggest the number and epidemiological significance of NSI herds is somewhat limited. Even herds that met the rigorous selection criteria applied in this study disclosed relatively small numbers of reactors on sequential skin-testing. It is possible that in many such herds bTB is in a latent or early stage of development, where lesions are microscopic or absent, and bacterial loads small. Alternative test and disease management strategies are required to deal with such herds.
STREAM 3 ABSTRACTS – WILDLIFE 1 - WEDNESDAY 8TH JUNE 2022

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Vaccinating badgers in a post-cull landscape: insights from the field

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Objective:

In 2010 the Badger BCG vaccine was licensed for use in badgers in the UK to reduce the severity of Mycobacterium bovis infection, and hence the risks of onward transmission to cattle. Effort required to carry out vaccination in undisturbed badger populations is well documented. However, this information is unlikely to accurately reflect the experiences of extensively culled populations where badger density and social behaviour may be markedly different. We present an evidence based assessment of the likely effort required to vaccinate in badger populations which have recently been culled, drawing on data from vaccination operations in a previously culled area and the practical field experiences of expert badger trappers.

Key results / findings:

When trapping badgers for vaccination in areas that had previously been culled, experienced government field staff adapted their practices in response to the lower density, likely more mobile residural population. An increased reliance on remote trapping (trapping away from the sett rather than at the sett itself) was noted as well as acknowledgment of the increased need for skill and experience in interpreting field signs and trapping effectively in such populations.

Significance / Impact of study:

The findings of this study will help inform practical approaches for vaccination of previously culled badger populations.

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Use of Dual Path Platform VetTB test in the Test, Vaccinate or Remove wildlife intervention project in Northern Ireland

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Objectives

The DPP VetTB test (Chembio Diagnostic Systems, Medford, NY USA) is a single use, point of care, immune-chromatographic (lateral-flow) rapid test for the detection of antibodies to Mycobacterium tuberculosis and M. bovis in cervid serum. Two recombinant antigens (MPB83 and CF10/ESAT-6 fusion) proteins are immobilised on the test strip as separate bands (Band 1 and Band 2 respectively). A 5 year TVR project commenced in 2014 in a 100km2 area of Northern Ireland. It involved capturing badgers and vaccinating those that tested negative for bTB (BadgerBCG – BCG Danish 1331) and removal of those that tested bTB positive using the DPP VetTB test for cervids. Four diagnostic tests were used within the study (Interferon gamma assay (IFN-γ), culture (clinical samples and post mortem), DPP VetTB using whole blood and DPP VetTB using serum. Because of supply issues with BadgerBCG, BCG Sofia (SL222) was used in the final two years.

Key results and findings

Initial analyses showed the test performed as accurately as established laboratory tests for M. bovis and showed good inter rater reliability. It was not compromised by the use of whole blood rather than serum in the field. The parallel interpretation of Band 1 (MPB83) and Band 2 (CFP10/ESAT-6) was not the better than the use of Band 1 only. Bayesian latent class analysis based on Band 1 estimated DPP VetTB test with serum to have a sensitivity of 0.59 (95% CI 0.42-0.77) and specificity as 0.98 (95% CI 0.96-0.99). The same test with whole blood showed a higher sensitivity (0.69 (95% CI 0.49-0.88)) but lower specificity (0.97 (95% CI 0.96-0.99)). The change from BCG Danish to BCG Sofia significantly impacted on DPP VetTB serum test characteristics. In addition, there was weak evidence of increasing sensitivity of IFN-γ over time and differences in DPP VetTB test sensitivity between adults and cubs.

Significance/Impact of study

The results give confidence in the reliability and reproducibility of the DPP VetTB test in field conditions. Therefore the DPP VetTB test is suitable for trap side use as a diagnostic tool in badgers.

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What we have learnt about oral BCG vaccination of badgers

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Objective:

Over the last decade, an oral vaccine based on BCG against TB in badgers has been in development at APHA, along with national and international networks. The objective was to develop and license a safe, palatable, robust product conferring significant protection to targeted badger populations. The efficacy of the vaccine candidates was measured in a series of eight experimental studies using captive animals manually challenged by endobronchial M. bovis.

Key results

Overall, the oral vaccination by live BCG was significantly protective in badgers, based on the scored severity of lesions and the spread of infection in tissues. However, inconsistent outcomes were associated with attempts to offer baits for voluntary consumption, whereas direct delivery of live BCG to the mouth and back of the throat of anaesthetised badgers was effective. The dose of effectively delivered live BCG appeared like a major factor for inducing protection, and was associated with measurable immune responses.

Significance

This corpus of work has demonstrated the feasibility of bait-delivered oral vaccination of badgers, in spite of significant constraints as follows: 1) the relatively high doses of M. bovis administered directly to the lung at challenge place a very high barrier to the demonstration of significant vaccine efficacy, while unrepresentative of the infectious challenge to badgers exposed naturally to M. bovis in the wild; 2) compared to the dose of BCG used for injection, efficacious oral doses of BCG are at the upper limit of what can be produced through surface-pellicle growth, unless the vaccine is concentrated, increasing the cost and with unknown effects on protective efficacy. Protection achieved with BCG produced in a fermenter suggests this as an alternative viable method of producing high titres of BCG suitable for oral vaccination, which may be worked up to commercial scale; 3) the delivery of oral BCG to sites of immune induction using baits currently appears to introduce such variation as to render experimental studies variable and inconsistent. However, if the technical challenge of increasing and standardising the mucosal uptake of BCG following the consumption of palatable and environmentally robust baits could be resolved, the necessary efficacy data needed to support the claims of a licensed product could be generated.

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How Important Is Age When Vaccinating Badgers? Satellite Tracking European Badgers Meles Meles Reveals the Optimal Age for BCG Vaccination

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Objective:

The satellite tracking study was originally designed to observe the effect of major roadworks on the ranging behaviour, movements and health status (including in relation to tuberculosis (TB) infection) of a population of wild Irish badgers Meles meles. Due to the global financial crisis, the roadworks were delayed for 3 years which allowed for an extended and detailed study of this badger population.

Key results / findings:

The study took place in a 40km² area of County Wicklow, Ireland. 144 badgers were cage trapped and vaccinated with Bacille Calmette-Guérin (BCG) at time of first capture. 80 badgers from 12 social groups were fitted with satellite
tracking collars. The trapping and satellite tracking of badgers ran for 7½ years generating over 103,000 GPS fixes. Analysis of the data from the satellite tracking and the detailed records on each badger trapped has revealed in-depth information on the movement patterns and strategies adopted by this medium density population of badgers. The data from the GPS collars and trapping records clearly showed three types of ranging strategies: traditional range, super-rangers, and dispersers. The age, distance, travelled, and social group interactions of the different types of ranged badgers were analysed.

The majority of badgers were traditional ranges (TRs) with a mean home range size of 1.74 km². 90% of the TRs made regular extra-territorial excursions (ETEs). On average, 22% of males became super-rangers (SRs) with a mean home range size of 3.93 km². The age range of these males was 2.5 years and they held their super-ranges for periods varying from 2–36 months. In addition, 19% of the badgers dispersed during the study, 57% of these were young adults with some only 12 months old. Dispersal is a highly complex process where the mean straight-line distance between natal and new social groups was 3.1 km but the mean full trajectory distance was 120 km.

**Significance/Impact of study:** The study revealed complex movement patterns based on age, sex, and ranging type. It highlighted the amount of social group interactions in this population and that there is an optimal age for BCG vaccination. This optimal age is based on vaccinating badgers before they start to engage in ranging behaviours that carry an increased risk of *Mycobacterium bovis* transmission. BCG vaccination of this cohort could break the *M. bovis* transmission cycle in this species.

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**Effect on ranging badger behaviour after selective removal of bovine tuberculosis test positive badgers in Northern Ireland**

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**Abstract**

Objective: Badgers are widely accepted as a reservoir of bovine tuberculosis (bTB) in the British Isles. Knowledge of their ranging behaviour is of importance as previous research has suggested that badger proactive culling interventions could potentially lead to social perturbation with a subsequent hypothesised perturbation effect reflected by increased levels of bTB in cattle due to increased contact rates. In 2014, for a five year wildlife intervention project was started in a 100 km² area with a relatively high badger density in County Down, Northern Ireland. The intervention was based on selective removal of bTB test positive badgers and vaccination of bTB test negative badgers (Test and Vaccinate or Remove; TVR). This approach involves a lower, and therefore more publically acceptable, level of badger removal compared to pro-active culling. The aim of the current study was to look at the effect of TVR intervention on badger ranging behaviour.

**Key results/findings:**

The ranging behaviour, based on calculation of home ranges, was measured by applying Global Positioning System (GPS) collars to a cohort of approximately 40 badgers every year. Both annual and monthly home ranges were calculated based on 95% and 50% fixed density kernels. Multi-variable linear mixed model analysis included confounding factors such as age and sex of badgers, year of GPS collar application, number of location points recorded, seasonal variation, badger density and culling intensity. We analysed the badger ranging behaviour based on home range estimates from 105 individual badgers over 21,200 collar-nights. The ranging behaviour was compared between the base line situation (home range sizes without intervention) and home range sizes after TVR intervention in order to evaluate whether intervention caused a significant difference. The TVR intervention led to 2-10% of badgers being estimated to be removed annually (compared to the majority of badgers in non-selective cull trials). The results indicate that there was no statistically significant difference in badger ranging behaviour with TVR intervention. Overall, the TVR selective culling approach was effective in the proportion of badgers culled being quiet when compared to more badgers being recorded in the study area as road traffic collision fatalities than culling through TVR intervention.

**Significance/Impact of study:**

The TVR approach is novel and has never been conducted elsewhere. The study findings are important for the development of future badger intervention strategies.
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Precision cut lung slices infection reveals type 1 interferon pathway is induced by Mycobacterium bovis but not M. tuberculosis

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Objective:
Mycobacterium bovis (Mb) responsible for bovine TB, and Mycobacterium tuberculosis (Mt) for human TB, are greater than 99.9% identical at the genetic level. It has been shown that the human pathogen, Mtbs, shows reduced ability to cause disease in cattle (PMID: 20049086); furthermore, epidemiological studies have shown that Mb is less able to cause disease in humans (PMID: 5297551). However, the genetic reason(s) why one is an animal pathogen and the other human pathogen is not known. If we were able to determine the basis for the ability of these pathogens to cause disease, we would be able to develop better control tools, such as vaccines and diagnostics, to control these diseases in both humans and animals.

Mb causes a chronic infection preferentially targeting the lung. The early steps after infection that influence the physiopathology of the disease are still poorly understood. We aim to get a deeper understanding of the physiopathology of Mb infection in the target species i.e. bovine and in the target organ, the lung. We compared the host tissue responses after Mb and Mt infection. Such comparative study of human and animal pathogens is a key example of the One Health concept that explores the interrelation of human and animal health.

Key findings:
We set up a protocol for ex vivo infection of bovine lungs (Precision-cut lung slices; PCLS) that helps deciphering early steps following infection in the natural environment. We performed in situ imaging of PCLS infected with a fluorescent Mb strain, and localized our bacilli in the alveolar compartment, in contact with pneumocytes, near or inside alveolar macrophages. We analyzed the global tissue signature following infection by two Mb strains (AF2122 and Mb3601) and two Mt strains (H37Rv and BTB1558). We performed a transcriptomic analysis using two different technologies, NanoString nCounter Analysis System and Fluidigm Biomark; and measured cytokines/chemokines in culture supernatant using Luminex. We performed a transcriptomic analysis using two different technologies, NanoString nCounter Analysis System and Fluidigm Biomark; and measured cytokines/chemokines in culture supernatant using Luminex. We performed a transcriptomic analysis using two different technologies, NanoString nCounter Analysis System and Fluidigm Biomark; and measured cytokines/chemokines in culture supernatant using Luminex.

Impact:
We aim to improve our comprehension of host-pathogen interactions ex vivo while reducing reliance on animal experiments, and contribute to future disease control strategies through a One Health approach.

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Joining the dots and filling in some gaps: The influence of vitamin D on γδ T cell function of potential relevance to bovine tuberculosis

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An incomplete understanding of bovine immunity contributes to our inability to eradicate bovine tuberculosis (bTB). Based on emerging data from our laboratory, we hypothesised that vitamin D concentrations may modulate innate cell function and thereby contribute to bTB susceptibility as well as the ability of cattle to counter infection. A significant proportion of cattle have insufficient levels of 25OHD in circulation, particularly during periods of low sunshine intensity and peak physiological pressure. Vitamin D has multiple well documented immunoregulatory roles and our in vitro and in vivo supplementation has shown that vitamin D significantly improves mycobacterial killing. γδ T cells link the innate and adaptive immune system and are classified based on expression of the Workshop cluster 1 (WC1) receptor. Our results showed that in vivo vitamin D supplementation regulates γδ T cell subset differentiation in calves. Furthermore, analysis of these cells from SICTT and IFN-γ ELISA positive cattle suggests that the WC1+ subset transcription is preferentially significantly altered relative to other leukocyte subsets. Temporal changes in vitamin D concentrations could play an important role in regulating anti-mycobacterial immunity by multiple immune cell subsets including γδ T cells which has widespread relevance for bTB resistance, responses to diagnostic tests and recurrent bTB.

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Evidence of immunomodulating effect of environmental mycobacteria in BCG vaccinated cattle

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Pre-exposure to non-tuberculous mycobacteria (NTM) have been implicated in a reduced efficacy of BCG vaccination and false positive bovine tuberculosis diagnosis. This is due to anamnestic responses to shared antigens between NTM and Mycobacterium tuberculosis complex. These cross reactive immune responses are believed to be due to Original Antigenic Sin phenomenon.

Our model investigated the effect of “persistent” pre-exposure to two commonly isolated NTM (M. malsburensyri and M. nonchromagenicum) in two age groups of cattle i.e. less than 6 months and greater than 6 months. Interferon-γ responses [in vitro (bovigam) and invivo (skin test)] to 5 NTM derived purified protein derivatives as well as humoral immune responses to PPD-A and PPD-B as well as to MTBC specific antigens were measured for several weeks before and after BCG vaccination. We hypothesized that the immune reactivity to NTM PPDs (PPD-M and PPD-N) will generate the strongest immune responses in animals sensitized with the corresponding NTMs whilst a milder response will be seen in response to other NTM PPDs to which they have not been exposed to.

Our observations were consistent with our expectations. It further indicated that all the treatment groups presented as strongly responsive to PPD-B by week 4 of the NTM exposure (despite not being responsive to PPD-B prior to the start and end of the experiment). This heightened PPD-B responsiveness in all treatment groups corresponded to approximately one week after the animals had NTM sensitization via multiple routes of exposure. Although our results do not clearly show specific immune responses due to an underlying persistent non-experimentally induced NTM exposure, the phenomenon of original antigenic sin was observed nonetheless towards shared antigens (MPB83 and MPB70) at the instance of NTM exposure. Furthermore, we observed that there was a decline in IFN-γ responses post BCG vaccination. In conclusion, persistent NTM exposure may confound M. bovis diagnosis if the animals were tested at the peak of the immune reactivity to NTM exposure. Furthermore, persistent NTM exposure suggests negative effects on the efficacy of BCG vaccination in cattle, hence, in NTM endemic areas, the role of shared mycobacterial antigens in bovine TB vaccination control strategy becomes significant from the very first day of a neonatal calf.
Direct PCR in Bovine Tissue Samples to Detect the Mycobacterium tuberculosis Complex: time for change
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Objective.
Real-Time PCR is considered a promising technique in the detection of Mycobacterium tuberculosis complex (MTBC) species in bovine tissue samples. It is a sensitive and specific method which yields results in a reduced period of time and is not subjected to the limitations of microbiological culture. The objective of this study was to evaluate the diagnostic performance of two Real-Time PCRs based on the IS6110 and mpb70 molecular targets in the detection and quantification of MTBC DNA.

Key results/findings.
Nine hundred and eighty-five (IS6110) and 200 (mpb70) bovine tissue samples were processed and analysed in parallel through microbiological culture and Real-Time PCR. When compared to culture, diagnostic sensitivity was 96.78% (95% CI: 94.46% - 98.15%) for the IS6110 PCR and 89.19% (95% CI: 79.80% - 95.22%) for the mpb70 PCR, whereas diagnostic specificity was 99.02% (95% CI: 97.88% - 99.55%) and 96.03% (95% CI: 90.98% - 98.70%), respectively. Minor cross-reactivity was detected for the IS6110 PCR against a reduced number of Mycobacterium avium subsp. hominissuis isolates. Diagnostic Performance of the IS6110 PCR was moderate and very high in samples with non-visible and visible lesions, respectively.

Significance/Impact of study.
The Real-Time PCRs presented here show high diagnostic performance when compared to culture, indicating that they are suitable as first-line techniques in the detection of MTBC species in bovine tissue samples. The single-copy nature of the mpb70 makes it also an appealing quantification technique with multiple applications. The high performance of the IS6110 PCR in samples with visible lesions makes this method an alternative to culture in this type of samples.

Flexible extended gamma and antibody testing - expanding the BTB surveillance toolkit in Wales
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Since 2018, two additional TB tests, the flexible extended interferon-gamma test (FLEXI-IFNG) and the IDEXX antibody test (IAT) have been selectively deployed across all TB Areas of Wales to support the tuberculin skin test and supplementary IFNG test as part of TB control measures for cattle.

The FLEXI-IFNG test contains an additional peptide cocktail antigen (ESAT6/CFP10) specific for M. bovis that has been used in the TB test portfolio at APHA since October 2006. The absence of ESAT6/CFP10 antigens in M. avium complex mycobacteria (MAC) means that M. bovis infection may be identified in the FLEXI-IFNG test by a positive peptide response where MAC-driven increases in PRDA responses confound the comparative PPD component of the test. The FLEXI-IFNG test, a flexible interpretation of the original extended IFNG test, was therefore deployed for targeted use on groups of cattle suspected of MAC/M. bovis coinfection.

The IAT test measures antibody responses to two immunodominant antigens, MPB83 and MPB70. The test has been deployed largely as a third line test (i.e. behind skin and IFNG) for negative skin- and IFNG- testing cattle. Parallel application of the above tests with the skin test allows for the additional identification of M. bovis infection in persistent or chronic infected herds where clearing TB can be challenging. Here we investigate the application of the FLEXI-IFNG and IAT tests between 2018 and 2020 on 242 such herds across the five different Welsh TB Areas.

We describe the test outcomes in herds receiving both tests (n=111), herds receiving the IAT only (n=45 herds) and herds receiving the FLEXI-IFNG only (n=86 herds) and assess the potential of these tests for added value of infection detection. We also consider FLEXI-IFNG and IAT test outcomes within each group in comparison with the risk posed by prior skin test PPDB responses.
154 of these animals were repeatedly tested for the presence of Mycobacterium bovis in blood and faeces using viral phage testing and qPCR. 125 of them (81%) had at least one phage positive test. 34 had at least one positive qPCR test on faeces, indicating shedding.

Animals which were shown to be shedding were either culled or isolated to prevent transmission. High risk animals were prioritised for culling, but with economic performance permitting mauling decisions. All potential risks of transmission were identified and controlled by management and husbandry.

After three years of the control programme, the herd is now Officially TB Free and has had no SICCT reactors in the last 4 routine skin tests.

Impact
This study demonstrates the potential for controlling and eradicating M. bovis from persistently infected herds where endemic infection circulates within the herd and cannot be identified or controlled by the statutory control programmes that rely on the SICCT to identify infected animals.

The control programme allows the economical and meticilous removal of infection from the herd, and minimises the risk of re-introduction by minimising environmental contamination.

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Diagnosis and surveillance of acute clinical Mycobacterium bovis tuberculosis in captive cheetah following suspected predation of an infected badger

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Objective:
Discuss the management, diagnosis, surveillance and challenges of potential cases of tuberculosis in a captive setting where this is known contact of animals with confirmed wildlife vectors infected with Mycobacterium bovis. To challenge previously published incubation times with regard to tuberculosis infection in cheetah.

Key findings:
On the 11th May 2015 a juvenile male 5kg badger (Meles meles) was found dead in a cheetah (Acinonyx jubatus) enclosure with three of six adults found at the carcass. On post-mortem examination there was a single penetrating injury to the right lateral thorax consistent with a bite wound, bilateral granulomatous pneumonia, granulomatous nephritis, emaciation and anorexia. Lung, kidney, mediastinal and mesenteric lymph nodes demonstrated acid fast organisms which were later confirmed as Mycobacterium bovis spoligotype Z2a. The six cheetahs were anaesthetised on the 20th May for health checks and tuberculosis work ups which consisted of clinical examination, thoracic and abdominal radiographs, biochemistry and haematology, lung wash and culture, lung wash MZN cytology, serological testing (PPD, Chembio), IGRAs (Biobest Laboratories Ltd), and SICCT. All the cheetahs were considered to have normal results with no evidence of tuberculosis detectable. The initial strategy was to wait approximately 6 months and retest using the same protocols.

The first clinical case cheetah was euthanased on the 20th November 2015, 6 months and 9 days after the suspected primary contact. The animal had lost 14kg in the preceding 6 weeks and suffered from haemorrhagic diarrhoea and ataxia. CT scan revealed severe pyogranulomatous cavity pneumonia, granulomatous enteritis, and granulomatous lymphadenitis. These were subsequently culture confirmed as M. bovis sp21a. The remaining cheetahs underwent health checks as planned on the 1st December. A second cheetah was euthanased on the 9th December 2015 following a weak positive IGRAs and was found to have a bilateral granulomatous cavity pneumonia confirmed as culture positive M. abscessus. The primary clinical veterinarian moved to another collection and subsequent deaths occurred but no spoliogopyting were reported. Details of the management of the remaining animals are discussed in the presentation.

Significance of study:
The incubation period in the primary case was just over 6 months. This case series demonstrates the challenges of diagnosing multiple Mycobacterium species infections with little or no validated tests available.
An Incentive Program to Increase Testing of Wild White-tailed Deer for Bovine Tuberculosis

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Bovine tuberculosis (bTB), caused by Mycobacterium bovis, is enzootic in free-ranging white-tailed deer (Odocoileus virginianus) in eastern Lower Michigan, USA. Some cattle producers have alleged that surveillance by the Michigan Department of Natural Resources (MDNR) systematically underestimates bTB prevalence in wild deer because testing is voluntary, not all landowners participate, and some hunters deliberately hide lesioned animals. This has been cited as a possible explanation for the patchy spatial distribution of the disease, and for the dissonance between locations of cattle herd breakdowns and areas of high prevalence in deer. The Michigan Department of Agriculture and Rural Development suggested that monetary payments to hunters for bTB-positive deer could increase hunter participation, testing for the disease, and better define its extent. Consequently, in 2011 and 2012, US$200 was offered to any licensed hunter who harvested a deer that cultured positive for M. bovis. Key results/findings: Over the two year course of the incentive program, 40 of 10,751 deer (0.4%) tested statewide cultured positive for M. bovis. After excluding deer taken via out-of-season shooting permits, 36 hunters were eligible for, and offered, the incentive payment. Of those, 16 (44%) accepted, 10 (67%) in 2011 and 6 (29%) in 2012. Over the period of the incentive program, there was no significant change in the number of deer tested for bTB in either the core outbreak area or the broader absentee area. The rate of hunters submitting deer for bTB testing for the first time (29%) was not significantly different than long term averages (20-30%), nor were significant differences in antlerless deer harvest, number of hunters, nor time spent hunting noted. There was no association between acceptance of the incentive payment and the identification of bTB-positive deer for the first time in either new townships (93 km²) or sections (2.6 km²). Because deer density reductions, and so bTB control efforts, are dependent upon hunter cooperation, caution is warranted when trialing measures to which hunter reaction may be unpredictable. Despite their presumed attractiveness, monetary payments for infected deer were rejected by a majority of hunters. Possible reasons for the program’s failure are discussed, including the perception of incentives as a ‘bounty’ on a charismatic and economically valuable species.

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Are deer a wildlife maintenance host of TB in Ireland?

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Objective:
To explain patterns in cattle herd TB breakdown density, at the county-level, across Ireland, using the density of known maintenance host species, i.e. cattle, badgers and deer between 2000 and 2018.

Key results/findings:
The density of all three potential TB maintenance hosts (cattle, badgers and deer) showed positive correlations with cattle herd TB breakdown density at the county level.

There was a negative correlation of year with cattle herd TB breakdown density. If County Wicklow data were excluded from the analysis, there was no longer a positive correlation between deer density and cattle herd TB breakdown density. Density estimates indicate that sika herds in County Wicklow may currently be capable of maintaining TB.

Significance/Impact of study:
The positive correlations between the densities of all three potential TB maintenance hosts and cattle herd TB breakdown density demonstrates that as the densities of these potential host species (cattle, badgers and deer) increase, so does the number of cattle herd TB breakdowns.

The negative correlation between the cattle herd TB breakdown density and year demonstrates that cattle herd TB breakdowns have been decreasing nationally during the study period (2000 – 2018). This indicates that current TB reduction policies are proving effective.

The lack of a positive correlation between deer density and cattle herd TB breakdown density, for a dataset lacking any information on County Wicklow, indicates that there is a special relationship with deer and TB in County Wicklow.

The sika density in County Wicklow in 2017 (24.8 animals km-2) was above the regional density threshold values identified for TB maintenance in red deer in mainland Europe (5.6 animals km-2) (Fink et al. 2015), white-tailed deer in North America (4.5 to 8.8 animals km-2) (Michigan Department of Natural Resources 2016) and Fallow Deer in south-west England (15 animals km-2) (Ward et al. 2008). While sika remain at high densities in County Wicklow, they would appear to be an additional complication to the management of TB in that county.

If deer densities were to rise above the threshold values for TB maintenance in other counties, deer may also pose problems for TB management in those counties.

2014

Successful eradication of bovine tuberculosis from a wildlife reservoir in Manitoba, Canada

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Historically, bovine tuberculosis (bTB) was known to occur in one of two wildlife reservoirs in Canada; wood bison in and around Wood Buffalo National Park and in elk and white-tailed deer in and around Riding Mountain National Park. Only the latter reservoir, located in southern Manitoba, has been associated with known spillover to surrounding cattle herds. A coordinated effort to successfully eradicate Mycobacterium bovis from this area (formally established as the Riding Mountain Eradication Area [RMEA]) between 2000 and 2019 by wildlife and agricultural government agencies, local beef producers and First Nations will be described. More than 18,000 elk and white-tailed deer and more than 240,000 domestic livestock from herds in the vicinity of the Park were assessed to identify and remove infected individual animals and herds. The last infected cattle herd was detected in 2008, the last infected white-tailed deer in 2009 and the last infected elk in 2014, with no further infected deer, elk or cattle detected over the last 5 years despite ongoing testing and surveillance. Mandatory on-farm cattle testing ceased in 2016, but ongoing abattoir surveillance continues. Traditions restrictions on cattle and bison importation by the USDA were also removed in 2018. A combination of management activities including regulation against baiting and feeding wildlife, fencing of domestic livestock feed, test and removal of infected wildlife, wildlife density reduction and on-farm biosecurity led to success in the control and eventual eradication of this wildlife reservoir. Adaptive management and incorporation of epidemiological and ecological information into management decisions allowed agriculture and wildlife interests to work cooperatively toward eradication. Social science was also critical to understanding barriers and attitudes preventing action at a local level, and establishing trust amongst local beef producers, government agencies, First Nations and non-governmental organizations. Ongoing surveillance in wildlife will likely be necessary for the next five years to determine if eradication has truly been accomplished; current scenario tree model outputs indicate a 90% probability of freedom in this region. The relative simplicity of this ecosystem, with only a single wildlife reservoir host (elk), together with sustained management effort over 20 years allowed for the successful gradual elimination of bTB from this ecosystem. This has contributed to national eradication efforts at a country level, and demonstrates that eradication of bovine TB from a wildlife reservoir is possible.
The devil you know and the devil you don’t: current status and challenges of bovine tuberculosis eradication in the United States

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Having now entered into its second century, the eradication program for bovine tuberculosis (bTB, caused by Mycobacterium bovis) in the United States of America occupies a position once both enviable and daunting. With the exception of four counties in Michigan comprising only 6109 km² (0.06% of US land area) which were classified as Modified Accredited, as of April 2022 the entire country was considered Accredited Free of bTB by the US Department of Agriculture for cattle and bison. Considering where the US bTB eradication program began in 1917, with 5% of US cattle tuberculin reactors, approached 23,000 to 50,000 human deaths per year in cattle tuberculosis, and the estimated US$3–$5 billion annual economic return up to 2003, the progress and benefit of the eradication program is astonishing. On the surface, the now well-described circumstances of endemic bTB in Michigan, where white-tailed deer (Odocoileus virginianus) serve as a free-ranging wildlife maintenance host, may appear to be the principal remaining barrier to national eradication. However, the situation there is unique in the US, and in some respects far-removed from the broader issues of bTB control in the remainder of the country.

In Michigan, extensive surveillance for bTB in deer over the last quarter century, and regulatory measures to maximize the harvest of publicly-owned wildlife (to minimize densities of deer and other putative spillover hosts of M. bovis) have been implemented and sustained. Prevalence of bTB in deer has remained at a low level as a result, although not sufficiently low to eliminate cattle herd infections. Public attitudes about bTB, cattle and deer, and their relative importance, have been more influential in the management of the disease than any limitations of biological science.

However, profound changes in the demographic characteristics and social attitudes of Michigan’s human population are underway, changes which are likely to force a critical reevaluation of the bTB control strategies thus far considered integral.

More broadly, in the rest of the US where bTB is not self-sustaining in wildlife, changes in the scale of cattle production, coupled with both technical (e.g., limitations in diagnostic tests, deficiencies in trace methodologies) and non-technical (e.g., antiquated regulations, shrinking fiscal resources for bTB eradication) issues have created their own substantial challenges.

It is against this diverse backdrop that the evolution of whole genome sequencing of M. bovis has revolutionized understanding of the history and ecology of bTB in Michigan, resolved previously undecipherable epidemiological puzzles associated with cattle herd breakdowns, provided insights into zoonotic transmission and pathogen evolution, and unified eradication efforts across species and agencies. Yet many of the fundamental challenges of eradication remain substantially unresolved. Here, we describe the current status of bTB eradication in the US, how circumstances and management have changed, what has been learned, and what remains more elusive than ever.

Australia’s Colourful Path to Tuberculosis Freedom

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Australia eradicated bovine tuberculosis over a 27-year period from 1970 when the Brucellosis and Tuberculosis Eradication Campaign (BTEC) commenced, through to when TB freedom was declared on 31 December 1997.

The key elements of this AUD$1 billion program have been well documented elsewhere. Hence, the presenter will add significant ‘colour’ by reflecting on personal experiences in the far north-west of Queensland during the very difficult latter phases of the program in the mid 1980s and subsequently as State Chief Veterinary Officer. The Mount Isa Veterinary Division was roughly double the size of Ireland, with around one million cattle and at the start of 1987, 51 holdings remained under TB restrictions out of a total of 400. The aim was to achieve impending freedom by the end of 1989, underpinned within a holistic epidemiological approach. The mechanism to achieve this was an approved property program for each of these large cattle stations, tailored to accommodate individual circumstances.

A key issue was to recognise the limitations of the tuberculin test. Hence, it was used largely to indicate presence or absence of infection exclusively within a single railway boundary, rather than as a control method per se. Coupled with this, the depopulation of infected groups, herds or age cohorts was essential to meet targets. The region also featured some large areas with feral cattle populations that had to be controlled and/or depopulated. Innovative strategies to help deal with these situations included construction of ‘strategic’ fences and the ‘Judas cow’ technique. The last cattle property infected with TB in Queensland was also located within the region, providing an interesting case study.

Is it possible to control bovine tuberculosis without compensation? Reviewing ten years of the Chilean program and its progress

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In 2011, the Chilean bTB program was launched by the Livestock and Agriculture Service (SAG) as a compulsory compulsory control and eradication program under the form of Animal Health Australia, establishing the infrastructure for a modern traceability system and a strict regulatory regime. Progress on individual farms was driven by risk-based movement controls linked to the disease status. However, a range of financial assistance measures were also introduced to reduce the impact on individual enterprises. Effective abattoir surveillance was essential throughout, but attention was required to maintain interest in the TB prevalence became very low. Various difficult challenges had to be faced towards the end of BTEC, including elimination of residual infection, TB in water buffalo and recallant farmers.

BTEC has had an ongoing legacy within Australia’s animal health system, in fact it underpinned the system for many years. It drove the modernising of the northern cattle industry, led to establishment of an ongoing government-industry partnership for Animal Health Australia, established the infrastructure for a modern traceability system and provided the template for the Emergency Animal Disease Response Agreement, which now includes bovine TB as an exotic disease.

The key take-home messages translatable to other jurisdictions are the need for a clear vision and objectives, flexible strategy, collaborative decision making and the need to hold firm.

Bovine tuberculosis control in a disease-free country, France: does the long and winding road really lead to eradication?

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It took France almost fifty years to attain its officially bovine tuberculosis (TB free) status in 2000, securing the country a favourable position as an international live animal trader. The initial TB control program has been adapted at different times in its history in order to suit changing epidemiological contexts. Originally, in the 1950s, it was focused on detection and elimination of infected animals while later on, the herd became the target and protecting TB free herds became a priority. In spite of all the efforts put into the program, final eradication has still not been achieved. Instead, the eradication program has stalled, mostly probably due to changes in rearing practices in the last few decades. Indeed, the beef industry has overtaken the milk industry, which has led to the occurrence of new TB risks. Novel epidemiological situations, mainly in some regions of extensive beef cattle farming, where wildlife species (wild boar, badger) are also involved, have been emerged. More adapted measures have thus been implemented, progressively evaluated and improved in order to reinforce prevention of infection, follow up eradication and strengthen, coordinate and re-motivate field resources. These include, among others, introduction of biosecurity measures in the herd, risk based surveillance and monitoring, herd health management and beef and dairy cattle, improvement of screening in the field and at the abattoir, better diagnosis, but also improvement of communication, awareness, training activities of the main field actors. Very importantly, this new plan has been established through the participation of the majority of stakeholders involved in TB - the farmer industry, hunter associations, vets, scientists and the government, through coordinated specific training courses and international collaborations to feed the program with relevant scientific data enabling the authorities to undertake the most pertinent measures for tackling the disease in the short term.
compensation of infected animals is not allowed in Chile, tools to deal with highly infected herds were required. The Veterinary Service co-led a research to assess the efficacy of the BCG vaccine, which derived into a pilot bTB vaccination plan addressed to highly-infected dairy herds. Additionally, in order to deal with infected herds’ offspring, it has been set up an authorization for fattening farms to receive exposed animals.

Even though bTB condemnation rate has decreased in 82.01%, as well as farm incidence declined, the bTB status classification and surveillance coverage have not surpassed 25%. This means that mainly dairy farms, and middle/large-scale meat systems are covered by active and passive surveillance. Therefore, another challenge is to not overlook surveillance of small and middle bovine holders, because they are relevant in providing and transporting offspring. In order to improve bTB surveillance coverage, the veterinary service has supported the development of bTB strip test as an alternative and massive diagnostic method on field.

The program has shown relevant progress controlling bTB so far, however, to achieve bTB eradication it is essential to improve stakeholders’ commitment, with a frame of legitimate and verifiable regulation, particularly where bTB infection clusters have been found.

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Key results:
We used bovine movement data from the French cattle tracing system and surveillance data from the National reference laboratory to compare time to closure between case farms with a bTB detection and matched control farms between 2004 and 2019. For this purpose, we considered two modes of closure: (i) long-lasting depopulation and (ii) change of farm owner. Using a competing risk analysis, we showed that bTB detection significantly increased the odds of long-lasting depopulation (particularly during the first three months after bTB detection) indicating that farmers renounced restocking after the depopulation, whereas it decreased the odds of a change of owner. Larger farms, characterized by an increased average weekly numbers of cattle, had a lesser risk of long-lasting depopulation. Farms owned by a natural person had an increased risk of closure. We also showed that the possibility to control bTB by test-and-cull protocol decreased the long-lasting depopulation risk.

Significance:
Overall, bTB control measures contribute to reshaping the agricultural landscape by increasing the probability of closure for small vulnerable farms and are favoring large, professionalized and specialized agricultural holdings. Our results also suggest an improvement in control management with the introduction of test-and-cull protocols instead of systematic whole herd depopulation.

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Land Use and bTB: Infected Areas, Farm Fragmentation, Herd Contiguity and Disease Spread in N. Ireland

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Objective
The prevalence of bTB in localised areas, multiple neighbouring herds, exposure to contiguous infected herds and fragmented farm holdings are all recognised risk factors for bTB (Denny & Wilesmith, 1999; Abernethy et al., 2006; Humblet et al., 2009). As part of a wider investigation of why bovine tuberculosis (bTB) has not yet been eliminated in Northern Ireland (NI), this interview-based study explored how land ownership, land use and grazing practices had implications for the spread of bTB both within and between herds.

Key results/findings
Farmers, vets and other industry stakeholders provided their opinions and experiences of land use and farming practices, set within a socioeconomic and historical context. They were very clear that bTB in cattle and badgers was associated with localised districts and even particular parcels of land. Despite the known risks of infection, some farmers continued to use this land to graze cattle, driven by economic pressures to increase milk yield and maximise production efficiency. The common practice of renting land (‘conacre’) separated from the main holding was cited by vets as an important factor explaining the ongoing spread of the disease. Some farmers used grazing strategies to control the risk of infection exposure at their farm boundaries, but they were a minority. Many interviewees believed that the farming landscape was very significant in the epidemiology of the disease.

Significance/Impact of study
It is vitally important to understand the underlying economic and social pressures affecting farmer behaviour in relation to bTB biosecurity. This study reveals how and why farm expansion and intensification, particularly in the dairy sector, is contributing to farm fragmentation, increased within-herd movement, risky grazing practices and the exposure of herds to multiple neighbours. These features and practices create the ideal conditions for infection exposure and increased risk of herd breakdown. To the author’s knowledge, this is the first study of its kind using a social science methodology to focus specifically on the connection between land use and bTB epidemiology.

References

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Farmer Engagement with the TB Advisory Service in England

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The TB Advisory Service (TBAS) provides free, bespoke advice to cattle keepers in the High Risk and Edge Areas of England, to reduce the risk and impact of bovine TB (bTB). The project is funded through the Rural Development Programme for England and managed by Westpoint Farm Vets. TBAS is overseen by a technical board comprising experts in the field of bTB and advice is delivered by vets and consultants from a range of organisations. The project provides on-farm Advice Visits and a Telephone Advice service.

Farmers have been made aware of the TB Advisory Service through a variety of marketing routes, including farmer meetings, stands at livestock markets, trade events and through the farming press. There is also a strong social media presence for the service, both in its own right and through individual advisers and project team members. When farmers contact TBAS, they are asked how they had heard of the service.

A total of 2111 Advice Visits and 3200 one to one Sessions were completed between October 2107 and December 2019. Over half of farmers (55%) had heard about TBAS through their vet, whilst 18% heard at a farmer meeting. This clearly demonstrates that traditional modes of marketing to farmers remain an important route to reach the target audience. Feedback on the service has been very positive, with 96% of farmers rating the Advice Visit as either good (10%) or excellent (90%). Many have felt empowered to take back some control over bTB on their farms. The Telephone Advice sessions have been invaluable for providing factual information and myth-busting. Additionally, we have developed a network of over 100 passionate, knowledgeable TBAS advisers keen to play their part in eradicating bTB.

The TB Advisory Service is providing much needed advice to cattle keepers in the High Risk and Edge Areas of England, and has been highly valued by those farmers that have requested advice. The project has demonstrated the need to use a variety of methodologies to encourage farmers to engage with the service, and that these activities need to be sustained over a long period of time. Further work to promote the service and encourage uptake will continue for the remainder of the contract, which ends in February 2021.

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Citizen science in a controversy: the making and breaking of collaboration in a ‘Badger Found Dead Study’ to investigate M. bovis prevalence

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What is the role of citizen science in developing knowledge and bringing communities together in a controversy? Here, I draw on an ethnography to examine the use, challenges and benefits of citizen science to measure M. bovis prevalence in found dead badgers. The study formed part of a controversy in England around the culling of wild badgers to manage bovine Tuberculosis in livestock. The doing of the study brought people with divergent views (including farmers, vets, wildlife groups, badger cull protestors and badger vaccinators) together with the aim of establishing the wildlife prevalence of bovine Tuberculosis. However, this fragile coalition tended to revert to pre-existing positions when interpreting the data. During the controversy, citizen science unified divergent communities, but was unable to hold them together as findings became part of long-standing contestation. This talk proposes new ways of thinking about and doing scientific methodologies through the approach of citizen science, arguing it can improve the use of bovine Tuberculosis science and somewhat foster cooperation between people with divergent viewpoints.
Quality Control of Purified Protein Derivative Tuberculins: Essential for Effective Bovine Tuberculosis Control and Eradication Programmes

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Objective:
National bovine tuberculosis (Btb) control programmes rely on surveillance using diagnostic tests with tuberculin PPD (Purified Protein Derivative) as the fundamental reagent. Response differences are frequently reported when different PPDs are used in both routine skin-testing and Interferon-γ assays. Little is known about the quality of the different PPDs used. This study set out to:
1) obtain information on relative potency and specificity of a range of commercially available PPDs,
2) compare the impact of different potencies of a single bovine PPD on the field performance of the SICTT and SIT, and
3) determine if potency variation would have an impact on the efficacy of bovine TB eradication programmes.

Key results/findings:
Bioassays results showed significant disparity in potency uniformity of avian and bovine PPDs. Guinea pig assays on PPDs revealed that the potency of the bovine PPDs in particular, was highly variable and the majority of the PPDs assayed did not meet the required minimum dose of 2,000 IU. Also, less than 50% of avian PPDs achieved the minimum requirement of 2,000 IU dose.

Conclusions:
For these reasons, we conclude that the quality of PPDs used is a major factor affecting the effectiveness of Btb control programmes. The findings have great potential importance to the standardization and comparisons of tuberculosis control/eradication programmes between countries and for import regulation.

Significance/Impact of study:
There is an urgent need for standardization of PPD quality, and for further research on the impact of potency and specificity on the sensitivity and specificity of Btb tests. The results of this study provide a valuable tool for the development of optimal Btb control programmes.
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Key findings:

Individual serum and milk samples from low and high prevalence TB-infected caprine herds were assayed using an indirect ELISA that detects Ab against a protein complex purified from bovine Purified Protein Derivative (CZV, Spain) named P22 (P22 ELISA) and results were compared with those obtained using cell-based diagnostic tests. A similar sensitivity using serum and milk samples was detected, suggesting the usefulness of milk samples as an alternative for TB diagnosis in dairy herds. Moreover, bulk milk samples from both herds were analyzed using P22 ELISA to evaluate its usefulness as herd screening, suggesting that reactivity is highly correlated to the herd prevalence. In order to evaluate the Ab levels in milk during the lactation period and determine whether time of sampling may affect the results, goat milk samples (n=44) from a high TB prevalence dairy herd were collected every 4 weeks during 6 months and assayed using P22 ELISA, showing no significant variations (p=0.079) throughout the study in terms of Ab levels in milk samples between consecutive analyses. Nevertheless, reactivity to P22 ELISA decreased when samples were collected the last two months (fifth and sixth) of the lactation period compared to initial stages.

Impact of study:

The present study suggests that milk samples are valuable for Ab-based diagnosis of TB in caprine dairy herds and that the reactivity to P22 ELISA can decrease when samples are collected at the final stages of the lactation period. Moreover, bulk milk samples could be valuable to define the herd status.

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Culture-independent PCR detection and differentiation of Mycobacteria spp. from antemortem paediatrical respiratory from African elephants and rhinoceros in South Africa.

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Mycobacterium tuberculosis complex (MTBC) members and environmental non-tuberculous mycobacteria (NTM), frequently infect various wildlife species like African elephants and rhinoceros. In some cases, infections can lead to disease, but even if they do not, NTM infections can prime the host’s immune system to react to shared proteins between NTM and MTBC like M. bovis and M. tuberculosis. Consequently, this sensitization can then interfere with tests used to screen for bovine tuberculosis, producing false-positive test results in M. bovis-uninfected animals. This result can lead to issues with moving animals due to rejected permits and possibly even unnecessary euthanasia. Unfortunately, the only definitive way to distinguish MTBC from NTM is by culture, a technique that takes 6-8 weeks. Therefore, in this study, we aimed to evaluate the culture-independent surveillance for MTBC and NTM by improving the antemortem rapid detection and differentiation of Mycobacteria spp. by PCRs and subsequent amplicon sequencing directly from respiratory samples. Used in combination, veterinarians and managers will be able to thoroughly identify infecting Mycobacterium species and confirm the absence or presence of possible cross-reactive NTM species that may impede M. bovis diagnostics and/or cause disease.

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STREAM 9 ABSTRACTS – EPIEMIOLOGY 1 – THURSDAY, 9TH JUNE 2022

Estimating the rate of cattle-to-cattle transmission of bovine Tuberculosis in endemic settings and the potential for control by vaccination

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Objective:

The design of programs for the control of infectious diseases depends on basal information on the routes and rates of transmission within the target population. The basic reproduction ratio (R0), defined as the expected number of new infections in a completely susceptible population, captures both the potential for an infectious disease to spread and the effort necessary for control. Published estimates of R0 for bovine Tuberculosis have come from countries with established control programs and have been derived from relatively complex and data-hungry within-herd and between-herd transmission models. In endemic settings where control has not yet been introduced, we can only apply relatively simple techniques based on the age distribution of cases to estimate the force of infection within herds. We use age-stratified prevalence data from Ethiopia to develop a framework for inference of transmission rates in endemic infected countries and compare to estimates based on the point prevalence alone.

Key results/findings:

We estimate transmission rates from herds within 13 different sites in Ethiopia from four separate data sets collected over a ten-year period between 2009 and 2018. Within-herd prevalence varies considerably between sites, as does the strength of evidence for a lower than expected rate of reactor animals within older cattle. These “missing” reactors could be the result of anergy – false negative test results due to an advanced stage of infection. However, our models suggest that excess removal (or mortality) of reactor animals from herds is the more parsimonious explanation. We find evidence for large variation between herds which cannot be satisfactorily explained by systematic factors such as herd size, region or time-period. As a consequence, the potential effectiveness of vaccination – or any other control strategy - is also likely to vary considerably between herds.

Significance/Impact of study:

We present a statistical framework to estimate the basic reproduction ratio (R0) of bovine tuberculosis within endemic, unmanaged, cattle populations; demonstrate the key importance of stratifying testing data by age to allow inference of this key epidemiological quantity and present first estimates of the within-herd R0 of bovine tuberculosis in an emerging dairy industry. These results have important implications for the potential use – and effectiveness – of control strategies in Ethiopia.

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Compute Bounds of Transmission Parameters of M. bovis in the Badger-Cattle System from Endemic Prevalences

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Objective:

In the process of eradication of M. bovis in an area, quantification of the reproduction ratio parameter (R) is important to assess the current situation and to guide improvement of the eradication effort. For eradication we strive to have R<1 and thus we want to know during the process how close R is to 1. However, for an infection that is transmitted within and between two hosts (e.g. badgers and cattle) there are in fact 4 partial reproduction ratio parameters, representing the transmission within and between the species. The transmission is now summarized in one 2 by 2 matrix and the R is its largest eigenvalue. Here we want to quantify the bounds on the overall R for the badger-cattle system in Ireland and how the two different host species contribute to that.
Results: We found that the R for whole system is bounded as: 1.07 ≤ R ≤ 1.17, and that the most likely scenario is that both badgers and cattle are needed to maintain this R > 1. Cattle alone with the current test and removal probably has R < 1 as also is the case for badgers alone, i.e. in the absence of cattle in Ireland.

Implications: The implication is thus that for eradication of M.bovis additional control measures are needed whilst current control measures have to be kept up. A possible approach is that vaccination in badgers is undertaken while test-and-removal of cattle is continued with the same intensity and quality. The effect of vaccination estimated in the vaccine trial would be sufficient then to eradicate M.bovis, i.e. R < 1. It needs now to be shown that sufficient vaccination coverage can be achieved and that the vaccine effect is indeed everywhere the same as in the trial areas.

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A badger intervention field trial: the impact of local factors on Mycobacterium bovis BCG vaccination in Irish badgers

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In the Republic of Ireland (RoI), the European badger (Meles meles) is a reservoir for Mycobacterium bovis infection, impeding progress towards the eradication of bovine tuberculosis in cattle. Replacing the badger culling strategy as a means of control, the intra-muscular Bacille Calmette-Guérin (BCG) vaccination of badgers is now being rolled out on a phased basis across the RoI. In a large field trial conducted during 2009-13, vaccination was associated with a reduction in transmission in the badger-cattle system. However, it remains unclear whether vaccination will sufficiently reduce transmission across the badger-cattle system everywhere in the RoI. Spatial heterogeneity plays an important role in pathogen transmission (both between and within host species), and thus for the extinction and the persistence of M. bovis. Moreover, this local variation may influence the impact of badger vaccination. Therefore, the objectives of this study are; 1) to improve our understanding of the infection dynamics of the badger-cattle system at a local level and 2) to assess the efficacy of badger vaccination on the badger-cattle system at a local level. To address these objectives, an ongoing 3-year field trial has been designed. The trial is taking place in 9 established vaccine areas and consists of 8 sweeps. During each sweep, veterinary staff test badgers via a lateral flow antibody test. Both vaccinated and unvaccinated badgers are tested, test-positive badgers are culled, and test-negative badgers are released (unvaccinated badgers are vaccinated prior to release). The trial provides information on local factors including; badger prevalence, badger density, and vaccination coverage. Using the field trial data, in conjunction with cattle surveillance data, we aim to assess the infection dynamics in the badger-cattle system, locally. Furthermore, by retesting vaccinated badgers, thereby monitoring any changes in potential infection status of susceptible vaccinated badgers, insights on vaccine efficacy will be obtained.

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The role of cattle movement networks in bovine tuberculosis incidents in Great Britain

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Objectives

Incidents of bovine tuberculosis continue to spread among and recur on farms in England and Wales. The trading of animals between farms and via markets can provide a conduit for the spread of infections and so by studying trading networks we might better understand the epidemiology of Mycobacterium bovis. We constructed networks of cattle movements and contact chains of cattle farms, to elucidate potential pathways for the transmission of infection and to evaluate their possible effect on the risk of a farm experiencing a bovine tuberculosis (bTB) incident.

Key findings:
We found that some farms are quickly connected to thousands of other farms, some acting as hubs in the network. Multivariable regression results were consistent with variation in risk associated with region, herd size, disease risk area and history of previous bTB incidents on the root farm and nearby farms. However, we also identified effects of both direct and indirect trading patterns, such that connections to more farms in the England High Risk Area up to three movements away from the root farm increased the risk of a bTB incident, while connections with more farms in the England Low Risk Area up to eight movements away decreased the risk.

Impact of study:

Relative to many other risk factors for bTB, trading behaviours are arguably more amenable to change, and consideration of risks associated with indirect trading, as well as those of direct trading, might therefore represent an additional approach to bTB management in Great Britain.

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What happens to cattle that test negative to the interferon-gamma assay?

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Objective:

The interferon-gamma (IFN-γ) assay is a diagnostic test that is most commonly used as an ancillary test in parallel with the single intradermal comparative cervical tuberculin (SICCT) test to improve the sensitivity of detection of bovine tuberculosis (bTB) through the identification of additional cases missed by the skin test particularly in high-risk herds. However, the performance of the IFN-γ test can vary for various reasons depending on location and environmental factors, and the potency of tuberculin. To ensure that the test is optimised for diagnosing bTB at a local and national level in Ireland, regularly reviewing the cut-offs is recommended. IFN-γ results are calculated by comparing the optical density ELISA reading from the cells stimulated by bovine tuberculin (B) to those stimulated by avian tuberculin (A), with cut-offs defined as B-A above a certain threshold. In Ireland, up until 2018, B-A ≥ 0 was used as one of the cut-off values but then changed to B-A > 0. Thus, the aim of this study was to follow the animals that would have been removed under the old criteria but were not, due to the change in the cut-off. A secondary aim was to explore the usefulness of a risk prediction tool that takes other factors into consideration (e.g., age) to supplement the dichotomous IFN-γ result. Key results/findings: Our study cohort comprised of cattle (n = 25762) that had a negative IFN-γ result between 1st May and 31st December 2019. This cohort were then followed until 30th April 2021 with animal-time calculated from the date of their initial negative IFN-γ result to the end of follow-up or slaughter. Different risk prediction models were explored using multivariate Cox proportional hazards models. By the end of follow-up, 927 of the cattle (3.4%) were detected as bTB positive. Under the old criteria (B-A ≥ 0), 1689 (5.8%) animals would have been removed and considered positive, of which 113 (6.7%) were subsequently detected with bTB.

Impact of study:

This study provides evidence to support the decision to review the original cut-off used in IFN-γ tests in Ireland; such cut-offs should be kept under regular review and amended as indicated by the data. Discriminating between high and low risk bTB animals that test negative on IFN-γ is a challenging problem, but the approach presented in this study offers a new avenue to investigate the issue further.
Estimating the direct efficacy of BCG vaccination against bovine tuberculosis

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BCG is increasingly recognized for its potential use as a vaccine against bovine tuberculosis (bTB) in regions where the disease remains endemic and traditional test-and-remove intervention strategies appear unfeasible. We recently performed a systematic review and meta-analysis of BCG vaccines based on the results of 1,902 vaccinates and 1,667 controls and estimated a modest direct vaccine efficacy of ~25% (95% CI: 18, 32). Importantly, scenario analyses considering direct (reduction in susceptibility of vaccinated animals) and indirect effects of vaccination showed that, despite the modest direct efficacy, early implementation of BCG vaccination has the potential to avert an astounding 50-95% of cumulative cases over the next five decades. Despite this promise, studies to assess both the (direct efficacy) and the risk of transmission from vaccinated individuals (indirect efficacy) are lacking. Here, we report preliminary findings from an ongoing field trial conducted in a natural transmission setting in Ethiopia based on the recently described trial design by Conlan et al (Elife, 2018, doi: 10.7554/eLife.27694). Trials with two biological replicates were performed and included an equal number of comparative skin test-positive adult infected animals (seeders, n = 36) held in-contact for a period of one year with an equal number of naïve susceptible calves (2-3 months of age), half of which were vaccinated with BCG (sentinels, n = 18), while the other half were controls that received saline (sentinels, n = 18). Calves were skin tested (comparative skin test) to confirm vaccine take prior to seeder introduction at 2 months post-vaccination. Skin tests using peptide-based defined antigen formulations (DST) and tuberculin were performed at 4-, 8-, and 12-months post-contact, and blood samples for interferon-gamma release assays (IGRA) were collected every 2 months post-seeder contact. Whole blood cultures for IGRA were stimulated with tuberculin and DST. Conversion to positivity in DST and DST-antigen IGRA tests were used to estimate infection rates. At 12 months post-exposure, 59% of vaccinates and 81% of controls were identified to be reactors to the DST. A major trouble is the lack of compensations for culled animals and the subsequent reluctance of owners for removal of reactor cattle. To support the program, in 2016 the sanitary authority has allowed the implementation of BCG vaccination in dairy farms with high tuberculosis prevalence, within a prospective, double-blinded, cohort study. The aim of this work is to describe the efficacy of the vaccination in dairy heifers under a natural transmission setting from the Metropolitan Region of Chile.
Insights for the operational interpretation of Mycobacterium bovis sequence data to elucidate the role of wildlife in cattle TB outbreaks

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Objective: Generation of M. bovis sequence data now provides a step change in our understanding of the epidemiology of tuberculosis in cattle and wildlife. Analysis of bacterial sequence data from very different outbreak scenarios across countries and regions, in combination with associated metadata, has already provided quantitative estimates of the importance of wildlife to the maintenance of TB in domesticated cattle. By comparing across these scenarios, we propose general principles that could be applied to operational use of M. bovis sequence data as these arise in new situations.

Our objectives are to:
- Describe key differences across outbreak datasets in different regions across multiple countries including Cumbria and Gloucestershire in England, Northern Ireland, the Republic of Ireland, and Michigan USA.
- Provide an overview of the relationship between transmission scenarios and the interpretation of the bacterial phylogenetic data, and describe some methods for their use.
- Identify general principles when extending these methods to other scenarios, in particular where metadata are more sparse.
- Provide recommendations for its operational use, for the practical control of M. bovis transmission.

Key results/findings:
- Evolutionary analysis of sequence data across different systems reveals substantially different roles for wildlife in the maintenance of TB, with these different roles reflected in the phylogenetic sequences, as revealed by evolutionary analysis methods.
- Using simulation models, we show how these roles depend on a combination of animal-to-animal transmission characteristics, the patterns of contact between species, and the time and location of introduction of M. bovis into the system, relative to the available samples.
- We provide recommendations for interpretation of sequence data based on the available data types and densities and for the collection of further data, in light of the extent approaches in our various countries.

Significance/Impact of study: Whole genome sequencing provides an unprecedented resolution for understanding how patterns of contact are related to the transmission of M. bovis in cattle and wildlife. By comparing the interpretation of such data across countries and regions in the context of the generalisable principles that can be applied across countries and epidemiological scenarios, emphasizing how the data allows for a dramatically improved understanding of the differences in the epidemiology of disease in wildlife and cattle to inform better control policies.

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Use of Whole Genome Sequencing for improving understanding of linkages between livestock and wildlife Mycobacterium bovis infection in New Zealand

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Objective: New Zealand’s latest bovine tuberculosis (BtB) National Pest Management Plan includes the objectives of TB freedom in livestock by 2026, and in possum vectors by 2040. At this stage in the maturing programme, knowing the source of every new infection is vital to ensure that objectives can be achieved and sustained. For over 2 decades molecular strain typing has assisted disease managers in determining the most likely source of new infections and has helped inform the wildlife (possum) control programme. Recent advances in technology have decreased the cost and turnaround time making it feasible to use the greater resolution of whole genome sequencing (WGS) analyses for routine surveillance typing.

Key results/findings: WGS provides a significant increase in the level of discrimination between individual Mycobacterium bovis isolates, which has helped link livestock isolates to wildlife isolates and also helps to corroborate case investigation findings of livestock movement related spread of the infection. Genomes of new isolates are currently compared to 1100+ genomes from livestock and wildlife isolates of representative types, spanning over 25 years in our WGS database. The single nucleotide polymorphism (SNP) lineages that result from our WGS analyses provide greater granularity than the “types” characterised by previously employed typing assays. As there are so many more similarities and differences to consider in WGS lineages, there is less chance for misinterpretation of the relationship between isolates. Through comparison of shared and differing SNP content of M. bovis isolates from livestock and wildlife origins, WGS can suggest possible transmission linkages of new isolates to others within the same herd, between livestock herds and within local and distant wildlife populations. Currently WGS results are being coupled with relevant location, demographic and abundance data collected and collated over the years to determine whether the enhanced granularity of this new tuberculosis epidemiology can be used to better understand the relationship between different wildlife species that could potentially be responsible for reseeding future infections.

Significance/Impact of study: A better understanding of how M. bovis is transmitted in different livestock and wildlife populations will help with the most efficient programme design and minimise errors in source attribution.

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Global distribution and evolution of Mycobacterium bovis lineages

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Objective: The aims of this study were to perform a phylogenomic analysis of globally distributed Mycobacterium bovis genomes and to provide date estimates on the origin of this bacterial species.

Findings: We have screened over 2,600 publicly available M. bovis genomes and newly sequenced two wildlife M. bovis strains, gathering 823 genomes from 21 countries and 21 host-species, including humans, to complete a phylogenomic analysis. We have identified 17 distinct global lineages of M. bovis isolates, which can be grouped into four, Lb2, Lb3 and Lb4, each with distinct genetic disease distribution. These lineages are not fully represented by Clonal Complexes (CCs) and are dispersed based on geographic location rather than host species. Accordingly, Lb1 is composed of 32 M. bovis isolated from North and East Africa (n=15), Europe (n=15), and the USA (n=3), encompassing three representatives of CC A2 and the 29 genomes without CC classification. This lineage is also characterized by 15 unique SNPs. Lb2 is composed of six M. bovis genomes of CC A1, isolated from Ghana, Germany and Switzerland. Lb3 is composed of 70 M. bovis of CC Eu2 from Germany (n=1), Americas (n=62), and South Africa (n=7), in addition to three genomes from Germany without CC classification, being supported by five unique SNPs. Finally, Lb4 is composed of 706 genomes of M. bovis of the CC Eu1, identified in Americas, Oceania, Africa, and Europe, indicating that RDEu1 is a stable marker of this evolutionarily recent lineage. Our data divergence analysis agreed with previous studies reporting independent archeological data of ancient M. bovis ([South Siberian infected skeletons at ~2,000 years BP (before present)]) and indicates that extant M. bovis originated during the Roman period, subsequently dispersing across the world with the discovery and settlement of the New World and Oceania, directly influenced by trades among countries.

Significance: Mycobacterium bovis is a major pathogen of tuberculosis in animals and humans, but its phylogenomic and evolution are poorly explored at the global level. Defining and characterizing the different genetic lineages of M. bovis distributed worldwide will help delineate future studies regarding disease epidemiology and pathogen’s host adaptability and virulence. In this study, we phylogenomically evaluated global representatives of M. bovis strains and defined the existence of four lineages with distinct geographical distribution. Furthermore, evolutionary data suggests that bovine tuberculosis originated during the Ancient Roman period, catalyzed by a rising need in cattle breeding for draft, meat and milk and spreading globally through commercial trades.
Genome epidemiology of Mycobacterium bovis infection in contemporaneous, sympatric badger and cattle populations in Northern Ireland

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Objective:

Bovine tuberculosis is epidemiologically complex, affecting both cattle and wildlife. Although useful, traditional molecular typing schemes lack the resolution to describe transmission dynamics and to inform on the relative importance of inter- and intra-species transmission. Having collected 598 Mycobacterium bovis isolates from historical (pre 2014) and contemporaneous (2014-2017) badgers (n=119) and cattle (n=479) in an endemic, 100km2 area in Northern Ireland, we sought to use pathogen whole-genome sequencing methods to improve the resolution of molecular epidemiological investigations in this system.

Key results / findings:

Eight major lineages of M. bovis were present in the endemic area, defined by 1576 single nucleotide polymorphisms (SNPs). Seven of these lineages were not embedded in the area, having possibly been translocated there by cattle movement. One lineage was endemic and probably embedded in the region since the 1970s. Skyline analysis detected an increase in bacterial effective population size consistent with an historic rise in disease prevalence observed in the study area. We applied Bayesian phylogenetic methods (TransPhylo and Discrete traits Analysis) to investigate host transmission dynamics of this endemic M. bovis lineage.

Transphylo found 37 pairs of sampled isolates (24% of total) exhibited good evidence (greater that 50% posterior probability) of direct transmission. The majority of these (35) were cattle to cattle transmissions, with only 2 observed to involve interspecies transmission. Interestingly, no evidence for badger to badger transmission was observed.

Significance / Impact of Study

Our data are consistent with badgers playing a minor role in the maintenance of M. bovis infection in this region. However comparison to other regions in which these techniques have been applied, suggests that transmission dynamics may be context-specific. Profiling different regions with these techniques, and determining which area-specific factors affect inter-species transmission dynamics could help inform policy on the most appropriate intervention strategies.

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Temporal and spatial Mycobacterium bovis prevalence patterns as evidenced in passive badger surveillance across Wales 2014-21

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An all-Wales dead-badger submission scheme was started in 2014 to determine how the geographical associations between the genotype of bovine tuberculosis in found dead badgers and in cattle herds has developed since the previous survey conducted 2005-2006. The results were reported at the level of the newly introduced Wales TB Regionalisation and compared with those from the 2005-06 Wales (RTA) Badger Survey. Based on past mortem examination and culture, a prevalence estimate was calculated for each TB Area and, where appropriate, individual Spatial Unit. Between 2014 and 2021, 2065 usable badger carcases were submitted and M. bovis was isolated from 165 (8.0%), compared to 12% in the 2005-2006 survey. This change was significant (p<0.01). The highest prevalence was observed for Wales’ High TB Area East (18.8%) which differed significantly (p<0.05) from the prevalence in the High TB Area West (9.8%). The lowest proportion of carcases diagnosed with the disease (0.7%) was in the Low TB Area, followed by the two Intermediate TB Areas (2.5%). In the latter part of the survey, there is evidence of a increasing prevalence of M. bovis infection in badgers in the Intermediate TB Area North of Wales while the proportion of infected badgers in High TB Area East, which shares its border with England, has remained high throughout. The M. bovis isolates from badgers belonged to one of ten genotypes, which tended to be similar to the genotypes of cattle in the same area but the direction of any cross-species transmission and the drivers for this cannot be determined from this study. The spatial variations described in this study support the need for regionally adapted surveillance and control measures for bovine tuberculosis in Wales.
Do we know the burden of bovine tuberculosis? – Introduction and a request from the Global Burden of Animal Diseases programme

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Assessing the burden of diseases has become an important aspect of human health policy and decision making with the adoption of the disability adjusted life year (DALY) as the standard metric. The DALY is now core to how human health burdens are measured and also as an outcome metric in cost-effectiveness analysis for assessing interventions. In animal health there has been an agreement of the importance of looking at the production loss and expenditure aspects of disease burdens which has only recently begun to be implemented more broadly through the Global Burden of Animal Diseases programme (https://animalhealthmetrics.org). In One Health there is an absence of agreement on how to bring together human and animal health impacts albeit there have been proposals on a zDALY and also cost of illness methods.

For a zoonotic disease such as bovine tuberculosis the absence of approaches and metrics is problematic. In addition there are difficulties where the impact of the disease on production is probably being masked by heavily subsidised control programmes.

The paper will describe some of the current limitations of economic assessment of bovine tuberculosis and the issues of how we programmes towards targeting on outcomes that have an impact on guiding bovine tuberculosis control. It will also request support in the provision of data and information on bovine tuberculosis for the GBADs programme.

Social Identities and the Eradication of Bovine Tuberculosis: The Role of ‘Good Farmers’ and ‘Real Vets’

Dr Gareth Enticott
Cardiff University

In this paper I discuss the importance of understanding the role of social identities in shaping the eradication of bovine tuberculosis. Focussing on farmers and vets, I examine how the idea of what constitutes a ‘good farmer’ and a ‘real vet’ influence the decisions that farmers and vets take when managing bovine TB – both positively and negatively. Specifically, I consider the interaction between social identities and different practices of disease control. Drawing on historical examples from New Zealand, I firstly examine how conflicts over appropriate disease control can be understood as a contest between different veterinary identities, imaginations of appropriate veterinary conduct and historical examples from New Zealand, I firstly examine how conflicts over appropriate disease control can be understood as a contest between different veterinary identities, imaginations of appropriate veterinary conduct and relationships with farmers. Secondly, drawing on recent research in New Zealand and the United Kingdom, I show how the idea of what counts as ‘good farming’ and who is a ‘good farmer’ is central to the decisions farmers take when purchasing stock and adopting other biosecurity technologies to help limit the spread of bovine tuberculosis. Finally, in conclusion I consider the importance of these social identities for the future of TB eradication and what kind of TB purchasing stock and adopting other biosecurity technologies to help limit the spread of bovine tuberculosis. Finally, in conclusion I consider the importance of these social identities for the future of TB eradication and what kind of TB eradication they make possible.

In conclusion I consider the importance of these social identities for the future of TB eradication and what kind of TB purchasing stock and adopting other biosecurity technologies to help limit the spread of bovine tuberculosis. Finally, the idea of what counts as ‘good farming’ and who is a ‘good farmer’ is central to the decisions farmers take when managing bovine TB – both positively and negatively. Specifically, I consider the interaction between social identities and different practices of disease control. Drawing on historical examples from New Zealand, I firstly examine how conflicts over appropriate disease control can be understood as a contest between different veterinary identities, imaginations of appropriate veterinary conduct and relationships with farmers. Secondly, drawing on recent research in New Zealand and the United Kingdom, I show how the idea of what counts as ‘good farming’ and who is a ‘good farmer’ is central to the decisions farmers take when purchasing stock and adopting other biosecurity technologies to help limit the spread of bovine tuberculosis. Finally, in conclusion I consider the importance of these social identities for the future of TB eradication and what kind of TB eradication they make possible.
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Molecular characterization of Mycobacterium bovis isolates from dairy herds, fresh cheese, and patients with tuberculosis in Baja California, Mexico

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Raw Milk Cheese Produced from M. bovis infected Herds: What is the Risk?

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The PhoPR difference between M. tb and M. bovis and consequence in lipid biosynthesis

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Whole genome sequencing analysis of Mycobacterium bovis isolated from humans and animals in east and southern Africa

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Reverse Zoonoses In A Complex Mycobacterium tuberculosis Outbreak In A Cambodian Wildlife Rescue Centre

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Surveys among tuberculosis patients and farmers from rural communities bordering bovine TB endemic wildlife parks fail to detect Mycobacterium bovis

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Detection of M. bovis strains with Isoniazid drug-resistance in farm animals

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Understudied and overlooked: characterizing M. orygis

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A proof-of-concept study to investigate the efficacy of heat-inactivated autovaccines against tuberculosis in goats.

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Case-control study for tuberculosis risk assessment in beef cattle in northwestern Spain
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Investigation and Control of an Outbreak of Tuberculosis in an Irish Closed, Farrow-to-finish Pig Herd
Margaret Wilson1, Frank Clerkin, Henriette Cameron, Anthony McAuliffe, Declan Murphy, Alma Shanahan, John Moriarty, Dr Maire McErl
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Feline Tuberculosis in Urban Areas of Buenos Aires, Argentina
Dr Maria Jimena Marfil1, Mg. Pablo Borras2, Vet. Indiana Pira3, Vet. Natalia Ponce3, Dr. Marcela Martinez Vivoti1, Dr. Martín Jose Zumarraga1, Dr. Maria Emilia Eirin1, Dr. Soledad Barandiaran1
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Vitamin D Induced Microbicidal Activity Against Mycobacterium bovis BCG is Dependent on Synergistic Activity of Bovine Peripheral Blood Cell Populations
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Transcriptional profiling of gamma delta (γδ) T cells from Mycobacterium bovis-infected cattle
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Association of immune responses of Zebu and Holstein-Friesian cattle with resistance to mycobacteria in a BCG challenge model.
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Immune response in granuloma from Mycobacterium bovis-infected calves
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Non-specific effects of inactivated *Mycobacterium bovis* vaccination in rabbits

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TB Macroscopic Lesions and Spoligotyping Signature: is there a pattern?

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Serological Activity of *Mycobacterium bovis* 28 kDa Antigen

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The role of the SigK regulon in the outcome of experimental *Mycobacterium bovis* infection

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Preferential Differential Gene Expression in the WC1.1+ γδ T Cell Compartment in Cattle Naturally Infected with *Mycobacterium bovis*

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Effects of Divergent Vitamin D Concentrations in Vivo on Microbicidal and Immunoregulatory Responses to *Mycobacterium bovis* BCG in Dairy Calves

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Integrative functional genomics of the bovine host response to infection with *Mycobacterium bovis*

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Deciphering the Genomic Architecture of the Bovine Peripheral Blood Transcriptomic Response to *Mycobacterium bovis* Infection

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Diagnostic tools for the detection of *Mycobacterium bovis* infection in leopards (*Panthera pardus*)

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Do European Badgers (*Meles meles*) Cross Major Roads?

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Does BCG vaccination affect badger immuno-diagnostic tests for *M. bovis*? Results from Test, Vaccinate or Remove project in Northern Ireland

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Assessing the role of wild deer in the current bovine tuberculosis (bTB) epidemic in Northern Ireland

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Using whole-genome sequencing to understand the role of wild furbearers in the transmission of Mycobacterium bovis in Michigan, USA

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Monitoring European Badger (Meles meles) Reproduction Under Evolving Bovine Tuberculosis Management in Ireland

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Badger population genetic structure and spatial partitioning of Mycobacterium bovis variation in a wildlife intervention zone in Northern Ireland

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Free Movement across Borders: Extra Territorial Excursions by European badgers in a Medium Density Population

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Disturbance ecology meets bovine tuberculosis epidemiology: the application of an emerging paradigm to wildlife transmission risk

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Hookworm Infection in badgers is useful in predicting their TB Status

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Mycobacterium bovis Infection in a Wild Boar (Sus scrofa) in Campania Region, Italy

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Comparative pathogenicity of a field strain of *Mycobacterium bovis* from wood bison in northern Canada in a mouse model

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Objective quantification of TB lesions volume by MRI applicable to Vaccine Badger Studies

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Assessing the Potential Impact of Alternate BCG Vaccination Strains on MP83-based Badger Field Diagnostics by Utilising a Ferret Vaccination Model

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Use of protein saver cards and modified Idexx ELISA for TB testing in badgers

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Inferring Environmental Transmission of Bovine Tuberculosis Between Cattle and Badgers and Generating Reproduction Ratio Maps

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Control and management of bovine tuberculosis in African buffalo: Cell-mediated immune responses following vaccination and *Mycobacterium bovis* challenge

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* Resolution No. 34, Register of Diagnostic Kits Validated and Certified by the OIE (Registration Number: 20150110)

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Joint control of bovine tuberculosis and paratuberculosis – the case for and against

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Impact on bovine TB from the implementation of six monthly routine testing in Cheshire, England

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Bovine TB control in New Zealand

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An Insight into the bTB Outbreak in East Cumbria- Field Epidemiology, Operational Interventions and Impacts

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Monitoring of bovine tuberculosis in Sweden, an OTF Country

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The rise of interferon gamma testing in Great Britain

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Is there elevated animal-level risk associated with prior inconclusive results under severe interpretation of the comparative tuberculin test?

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Enhanced Management of Persistent breakdowns (EMPB) - summary of factors driving persistence, interventions and estimates of their effectiveness

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Evaluation of Ab-ELISA for Bovine Tuberculosis Monitoring in Belgium

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First Evaluation of a New Enzyme-Linked Immunosorbent Assay (ELISA) for the Diagnosis of Bovine Tuberculosis

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BOVINE TUBERCULOSIS : COMBINATION OF TOOLS TO MAINTAIN FREE STATUS IN BELGIUM

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A science-led integrated TB eradication programme for the Gower Cluster

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Exploring the Impact of Extended Blood Submission Times and Decoupling of the Skin Test on Bovine Interferon Gamma Test Outcomes

Dr Fiona Young¹, Dr Lynne McCallan¹, Ms Claire Barry¹, Ms Cathy Brooks¹, Dr Andrew Byrne¹, Dr Jim McNair¹, Mr Raymond Kirke¹, Dr Georgina Milne¹, Ms Catriona O'Brien¹, Mr Jonathan Cunningham¹, Dr Tom Ford¹
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False Positive Hot Spot Areas: Myth or reality?

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What Happens to Animals and Herds when they Have Inconclusive Comparative Intradermal Tuberculin Test (CITT) Results at Backward Trace Tests?

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Assessment of the frequency of Mycobacterium bovis shedding in the faeces of naturally and experimentally TB infected cattle

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Strategies for Additional Sampling and Whole Genome Sequencing of Persistent TB Incident Herds in England

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Rapid DNA Detection and Enhanced Growth of *Mycobacterium tuberculosis* Complex Organisms from White Rhinoceros (*Ceratotherium simum*) and Elephants (*Loxodonta africana*)

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Evaluation of Three Commercial Interferon-γ Assays in a Bovine Tuberculosis Free Population

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Reinterpretation of SICCT results to assess the performance of Bovine-only test results alongside outcomes analysis of Bovine-only reactors

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USEFUL TOOLS FOR THE ANTE MORTEM DIAGNOSIS OF TUBERCULOSIS IN WATER BUFFALO

Dr. Alessandra Martucciello¹, Dr. Nicoletta Vitale², Dr. Maria Beatrice Boniotti³, Dr Piera Mazzone⁴, Dr Michele Napoletano⁵, Dr Nicola D’Alessio⁵, Dr Anna Cerrone⁵, Dr Maria, Lodovica Pacciarini⁵, Dr Esterina De Carlo⁵

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Evaluation of Mitogens for Use as Lymphocyte Viability Control in Tuberculosis Interferon-gamma (IFN-γ) Testing of Sheep

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An index of tuberculous lesions caused by *Mycobacterium bovis* in European badgers (*Meles meles*) evaluates protection by an oral vaccine

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Nanobodies as a new diagnostic tool for *Mycobacterium bovis*

Optimization of apaca nanobody displaying phage library preparation

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Predicting and preventing faecal shedding of *M.bovis* in anergic infected cows using repeated qPCR, Actiphage and Idexx Elisa

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Rapid phage-based detection of tuberculosis in clinical bovine blood samples

Dr Ben Swift¹, Mr Wade Handley-Hartill², Dr Tania Perehinec³, Dr Helen Jones¹, Dr Catherine Rees²

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Novel Biomarker Identification Through Untargeted Plasma Metabolomics of Cattle Experimentally Infected with *M. bovis*

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Development and Preliminary Characterization of a DIVA Subunit Vaccine Against *Mycobacterium bovis*

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Differentiation of *Mycobacterium bovis* and *Mycobacterium tuberculosis* using a novel catalytic ferromagnetic gold immunoassay

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Tuberculin PPD Potency Assays in Naturally Infected Tuberculous Cattle: a Quality Control Measure in the Irish Bovine Tuberculosis Eradication Programme

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Development of a DIVA skin test for use alongside BCG vaccination of cattle

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Enhanced diagnostic sensitivity of IFN-γ and IP-10 for detection of *Mycobacterium bovis* infected cattle by modulating activity of cytokine IL10

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Comparability study of serum and milk using a Multiplex Serology Test for Bovine Tuberculosis in Cattle

Mr Alastair Hayton¹, Dr Amanda O’Brien¹, Dr John Clarke², Mr Keith Cutler³, Mr Andy Adler³, Dr Darren Shaw³, Dr Clare Whelan³, Dr Eduard Shuralev³, Professor Malik Mukminov³, Dr Neil Watt³, Professor Gordon Harkiss³

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Identification of an IS6110-like insertion sequence in *M. avium* subsp. *hominissuis*: significance and perspectives in the diagnosis of bovine tuberculosis

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High concordance of culture isolation with Real-Time PCR for the detection of *Mycobacterium tuberculosis* complex (MTBC) in tissue samples

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Simultaneous measurement of additional biomarkers complement IFN-γ in detecting early *M. bovis* infection

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Comparison between detailed post-mortem examination and abattoir inspection in the detection of tuberculous lesions in cattle

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Improving the Performance Characteristics of a Multiplex Serology Test for Bovine Tuberculosis in Cattle by Quantitative Analysis of Antibodies

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Co-infection with Mycobacterium bovis and Bovine Immunodeficiency Virus in UK Dairy Herds

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A Novel Multipurpose Rapid Test for the Detection of Tuberculosis Biomarker in Blood, Sputum, Urine, Milk and Culture

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Evaluation of a new P22-based serodiagnostic test for tuberculosis in wild ungulates and pig reared under different management systems

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Impact of Inter and Intra-assay Factors on the Bovine Interferon Gamma ELISA in the Northern Ireland bTB control programme

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Sensitivity of interferon gamma assay for detection of bovine tuberculosis depends on the manufacturer brand of tuberculin PPD-stimulating antigen

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Development of a Fully Quantitative, Standardised Anti-MPB83 ELISA and Comparison with the Dual Path Platform bTB Field Diagnostic Test

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P22 performance for TB serodiagnosis in multiple host species

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Effect of the administration of anti-inflammatory substances on the diagnosis of caprine tuberculosis: dexamethasone and ketoprofen as examples

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IFN-γ Assay for Granting and Maintenance of Officially Tuberculosis-Free Herd Status and Movement of Cattle within the EU

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FLOW CYTOMETRIC DETECTION OF IFN-GAMMA AND ACTIVE CASPASE-3 ON NATURALLY M. BOVIS INFECTED WATER BUFFALO (BUBALUS BUBALIS)

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Metabolomics for Diagnosing Tuberculosis in Badgers: Even After Autoclaving Blood Samples Can Still be Differentiated

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An Indirect Elisa For The Detection Of Anti-M.bovis Porcine Antibodies

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Skin Test Reactions to Different Antigens in Guinea Pigs Sensitized with Non-Tuberculous and Tuberculous Bacteria

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A Tuberculosis Outbreak in an Alpaca Farm in the Republic of Ireland

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The MicroRNAome of Cattle Infected with Mycobacterium bovis: Towards the Characterization of Potential Novel Biomarkers

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Biological Pathways and Gene Regulatory Networks Perturbed during Mycobacterium bovis Infection in a Large Cohort of Cattle

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The detection of IS1561 gene in Mycobacterium bovis using CRISPR-Cas12a system

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Evaluation of diagnostic performance of two M. bovis-specific antibody ELISA tests in rabbits

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Bovine TB Ireland: Reconstructing the Molecular Evolution of Mycobacterium bovis

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The development of an online bTB system for GB – information bovine TB (ibTB)

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Case-control study for evaluating the effects of badger vaccination on bovine tuberculosis incidence in cattle in England and Wales

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TB herd depopulation. An opportunity to investigate diagnostic test performance

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Regression of the tuberculin reactions: results from the Reactor Quality Assurance pilot study in Northern Ireland

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First detection of *Mycobacterium microti* in small mammals and environmental samples in a pre-alpine area of Northern Italy

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Descriptive summary of *Mycobacterium bovis* genotypes in cattle and badgers in a wildlife intervention research area (2014-2018)

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Genomic investigation of two SB0120 genotypes spread in Italy by Whole Genome Sequencing

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Development of a validated, traceable tool to genotype mycobacterial species using Single Nucleotide Polymorphisms (SNPs)

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Inferring transmission between cattle and badgers using the RBCT sampling framework

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Quantifying Farm Fragmentation in Northern Ireland as a Component of Bovine Tuberculosis Risk

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Spatial Associations between *Mycobacterium bovis* MLVA Types Isolated from Badgers Killed in Road Traffic Accidents and Cattle in Northern Ireland

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Cattle movements and potential control strategies for bovine tuberculosis in an endemic setting

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Controlling new bovine tuberculosis infections in a persistently infected dairy herd by focused biosecurity and biocontainment

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Bovine tuberculosis ante-mortem diagnostic test agreement and disagreement in a naturally infected African cattle population

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Comparative Whole Genome Sequence Analyses Suggest Distinctive Virulence Traits among Mycobacterium bovis SNP-Defined Clades from Portugal

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Deciphering the role of host species in two Mycobacterium bovis genotypes circulation within a cattle-badger-wild boar multi-hosts system

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Factors Associated with Increased Duration of Bovine Tuberculosis Breakdowns in Castilla y Leon, Spain (2010-2017)

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Whole genome sequencing to unravel the genetic diversity of a prevalent Mycobacterium bovis spoligotype in a multi-host scenario in Spain

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Characterisation of the helminth parasite community of European badgers in Ireland and exploring the possible ink with M. tb

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A SNP-MLST Method to Decipher the Genetic Diversity of French Mycobacterium bovis Strains of Animal Origin

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Tuberculosis breakdowns investigation based on whole-genome sequencing analysis of Mycobacterium tuberculosis complex strains isolated from livestock and wildlife

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Occurrence of IS6110 copies in genomes of field strains of Mycobacterium bovis revealed high disparity among genetic family

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Application of Whole Genome Sequencing to Assess Within-herd Variation of \textit{M. bovis} SB0121 Isolates in Spain

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Using the results of field epidemiological investigations to estimate source attribution of \textit{Mycobacterium bovis} infection in cattle

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The Application of Whole Genome Sequencing Data within an Operational Epidemiological Investigation of a bTB Cluster

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Bovine Tuberculosis Outbreak Reconstruction in a Multi-host System: Conclusions Drawn from Simulated Data Reflecting the Inherent Sampling Bias

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Various applications of Whole Genome Sequencing for assisting the role of the Irish National Reference Laboratory for Bovine Tuberculosis

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Transmission dynamics for the introduction and spread of bTB in a disease hotspot in the Low TB Area Wales

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A new nomenclature for the livestock-associated \textit{Mycobacterium tuberculosis} complex based on phylogenomics

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New reference genomes of \textit{Mycobacterium bovis} adapted to French genotype diversity

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A new tool to uncover \textit{Mycobacterium bovis} patterns and signature outside the mammal host

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Population genomics and phylodynamics of *M. bovis* at the livestock-wildlife interface, Portugal

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Application of whole genome sequencing for tracing bovine tuberculosis transmission in Canada

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