



UCD School of Agriculture, Food Science and Veterinary Medicine  
University College Dublin

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# Biennial Report, 2006-07

The Centre for Veterinary Epidemiology and Risk Analysis  
The TB Diagnostics and Immunology Research Centre  
The Badger Vaccine Project



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The Centre for Veterinary Epidemiology and Risk Analysis  
The TB Diagnostics and Immunology Research Centre  
The Badger Vaccine Project

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

ISBN: 978-1-905254-31-6

## PREFACE

The Department of Agriculture, Fisheries and Food (DAFF) provides ongoing financial support to three research units within the School of Agriculture, Food Science and Veterinary Medicine at University College Dublin:

- The Centre for Veterinary Epidemiology and Risk Analysis (CVERA);
- The TB Diagnostics and Immunology Research Centre; and
- The Badger Vaccine Project.

These units each work to support DAFF policy, inspectorate and laboratory staff in the area of animal health. The TB Diagnostics and Immunology Research Centre and the Badger Vaccine Project focus on bovine tuberculosis research. CVERA is a national resource centre, providing policy advice and conducting epidemiological research on a wide range of animal health issues. In addition, CVERA provides general support to government, industry and the veterinary profession (pre- and post-graduation) on these and other animal health issues.

This report documents work conducted by, or in association with, these three UCD-based research units during 2006 and 2007.

Simon More  
Eamonn Gormley  
Leigh Corner

Veterinary Sciences Centre  
School of Agriculture, Food Science and Veterinary Medicine  
University College Dublin  
Belfield, Dublin 4, Ireland

# ACKNOWLEDGEMENTS

## THE CENTRE FOR VETERINARY EPIDEMIOLOGY AND RISK ANALYSIS

CVERA works closely with a wide range of organisations, both in Ireland and internationally. The collaborative input of staff from each of these organisations is gratefully acknowledged, including:

- *In Ireland* – DAFF (veterinary policy, inspectorate and laboratory staff – central, regional, local), UCD School of Agriculture, Food Science and Veterinary Medicine, UCD School of Mathematical Sciences, the Irish Cattle Breeders Federation (ICBF), Veterinary Ireland and individual private veterinary practitioners, BirdWatch Ireland, the National Parks and Wildlife Service (within the Department of Environment, Heritage and Local Government), Teagasc, University College Cork, Trinity College Dublin, the Irish Equine Centre, the Marine Institute, a wide range of industry organisations, and individual Irish farmers
- *In Canada* – the University of Guelph
- *In Chile* – Servicio Agrícola y Ganadero (SAG)
- *In Korea* – the National Veterinary Research and Quarantine Service
- *In the Netherlands* – Wageningen University, GD Animal Health Service Deventer, ID Lelystad
- *In New Zealand* – Massey University
- *In Norway* – Norges veterinærhøgskole (Norwegian School of Veterinary Science)
- *In the UK* – the Department of Agriculture and Rural Development of Northern Ireland (DARDNI), veterinary organisations in Northern Ireland (North of Ireland Veterinary Association, Association of Veterinary Surgeons Practising in Northern Ireland), Defra (the UK Department of Environment, Food and Rural Affairs), Office of the Chief Veterinary Officer in the Welsh Assembly government, the Roslin Institute, Royal Veterinary College, Scottish Agricultural College, Veterinary Laboratories Agency
- *In the US* – Colorado State University.

## THE TB DIAGNOSTICS AND IMMUNOLOGY RESEARCH CENTRE

Staff from the Centre acknowledge the help and support of District Veterinary Office (DVO) staff throughout Ireland for their efforts and assistance in providing samples for the IFN- $\gamma$  assay.

## THE BADGER VACCINE PROJECT

Staff from the Badger Vaccine Project acknowledge Frances Quigley and staff at the mycobacteriology laboratory (Central Veterinary Research Laboratory, Backweston Campus, Celbridge, Co. Kildare, Ireland) for their contributions and assistance in the Badger Vaccine Project, and Paddy Sleeman of University College Cork for fieldcraft. Glyn Hewinson, Mark Chambers and staff at Veterinary Laboratories Agency (VLA, UK) are also thanked for developing and carrying out many of the immunoassays used in the badger vaccine studies, and for contributing technical expertise and advice for the research programme.

*Some photographs in the report kindly supplied by An Bord Bia.*

## FURTHER INFORMATION

In this report, projects are either:

- *Complete*, which includes those projects where relevant peer-reviewed papers, or equivalent, have been published, or
- *Current*, which includes the balance covering the spectrum from conceptual through to final write-up. A number of these latter projects are presented in the *Selected reports* section.

Manuscript preparation is conducted in accordance with Uniform Requirements for Manuscripts Submitted to Biomedical Journals of the International Committee of Medical Journal Editors (previously the Vancouver Group). For further information, see [www.icmje.org](http://www.icmje.org). Guidelines for the transparent reporting of specific study types (for example, the CONSORT statement for transparent reporting of trials, [www.consort-statement.org](http://www.consort-statement.org)) are followed.

Information about published papers is available at:

BMC Genomics

Clinical and Experimental Immunology

Irish Veterinary Journal

Journal of Veterinary Medicine Series A

Preventive Veterinary Medicine

Research in Veterinary Science

UK Vet Livestock

Vaccine

Veterinary Anaesthesia and Analgesia

Veterinary Immunology and Immunopathology

Veterinary Microbiology

Veterinary Record

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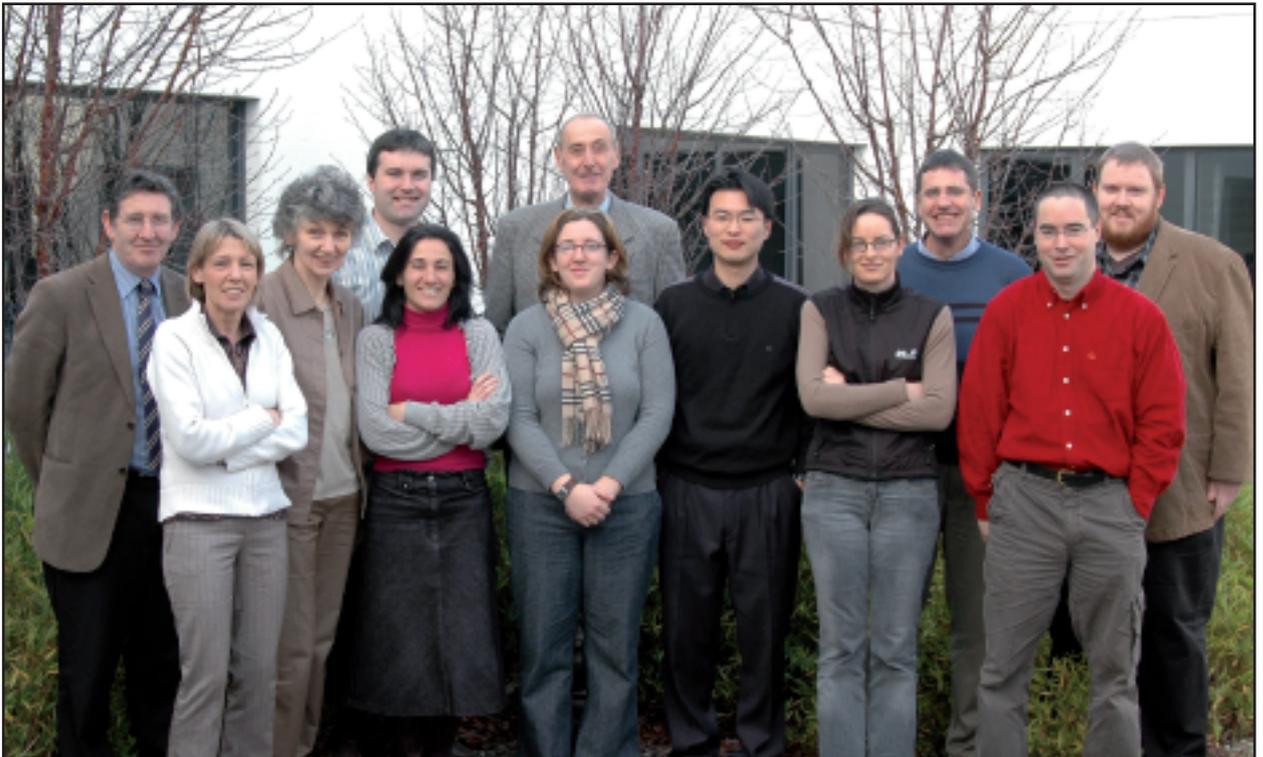
## THE BADGER VACCINE PROJECT

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Damien O'Meara (*to March 2006*)  
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### DR. ROBERT F. HAMMOND

Dr. Robert F. Hammond died tragically in a road traffic accident whilst abroad last February. Bob was an integral member of CVERA (formerly the Tuberculosis Investigation Unit) since its establishment in 1989. He retired in April, 2004. Bob brought a wide range of skills and expertise, and made a major contribution to the development of the Centre and its interdisciplinary approach to research and investigation. His courtesy, enthusiasm and willingness to be of assistance were much appreciated by his colleagues and all who worked with him. He had an abiding interest in new technologies and played a major role in the development and application of Geographical Information Systems technology in the study of the epidemiology of animal diseases, as a result of which the Centre is now recognised internationally as a leader in this field. Bob made a valuable contribution to our research on the nature and control of such major animal diseases as tuberculosis and brucellosis in cattle and the epidemiology of bovine spongiform encephalopathy in Ireland. For these many contributions, and for his enduring support and friendliness, he will always be fondly remembered by his colleagues here at UCD and in the wider agricultural community.

To his wife Adrienne and sons Ian and Alan, we offer our sincere sympathy.



UCD Veterinary Sciences Centre, December 2006

Martin Hayes, Tracy Clegg, Isabella Higgins, Paul White, Inma Aznar, Bob Hammond, Mary Canty, Lee Byeong-yong, Elizabeth Lane, Simon More, Guy McGrath and Daniel Collins

## OVERVIEW

### CENTRE FOR VETERINARY EPIDEMIOLOGY AND RISK ANALYSIS

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

- Epidemiological support for the control and eradication of regulatory animal diseases, which includes national programmes for bovine tuberculosis, bovine brucellosis and bovine spongiform encephalopathy;
- Work towards the establishment of a national herd health initiative, to provide a proactive, coordinated and industry-led approach in Ireland to non-regulatory animal health concerns (such as mastitis, fertility and infectious bovine rhinotracheitis); and
- Epidemiological support for emergency animal disease preparedness and response (for example, avian influenza, bluetongue and equine infectious anaemia).

CVERA staff work closely with national policy-makers, both in government and industry. In collaboration with staff from Herd and Veterinary Public Health within the UCD School of Agriculture, Food Science and Veterinary Medicine, CVERA staff also contribute on a weekly basis to on-farm animal health investigations throughout Ireland. A broad range of expertise is represented within the Centre, including agriculture and animal sciences, database development and management, geographic information systems, statistics, veterinary medicine and epidemiology. The Centre is staffed by employees of University College Dublin and of DAFF.

### TB DIAGNOSTICS AND IMMUNOLOGY RESEARCH CENTRE

The interferon-gamma (IFN- $\gamma$ ) assay is used as a tool to assist in the eradication of bovine tuberculosis from the national cattle herd. All of the testing is carried out in the laboratory based at UCD. During 2006-2007, over 25,000 blood samples were submitted to the laboratory for testing. This represents a 60% increase in submissions compared with the previous two years. The majority of samples originate from reactor re-test herds where the test is used to identify infected animals that were missed by the skin test. Other strategic uses of the test are targeted at inconclusive reactor re-tests. The constraint of carrying out preliminary procedures on the blood within 8-12 hours of sampling remains, and this first stage of the test is now being carried out in a regional laboratory serving the west and north-west of the country. This has facilitated a significant increase in the numbers of samples submitted for testing from that region. It is hoped to extend the introduction of this service to additional regional laboratories.

### THE BADGER VACCINE PROJECT

The Badger Vaccine Project is a comprehensive programme of research that seeks to develop a vaccine to control tuberculosis in badgers and to break the link of infection to cattle. We have recently demonstrated that oral vaccination of badgers with the BCG vaccine generates high levels of protective immunity against challenge with *Mycobacterium bovis*. The key to the success of the vaccine lies in the encapsulation of the vaccine in a specific lipid formulation that protects it from degradation as it passes through the stomach. The encapsulation technology designed for this purpose has been developed by collaborators at the University of Otago, New Zealand. We have also shown that the commercially available BCG-Danish strain is as effective a vaccine as the well-characterised BCG-Pasteur laboratory strain. We are continuing to carry out studies with our captive population of badgers to refine the vaccine and address issues relating to the eventual registration of the vaccine as a veterinary medicine. We are also developing and evaluating diagnostic tests with colleagues at VLA (Weybridge, UK). The results of our studies to date have increased our understanding of the progression of the disease following infection and have improved our ability to accurately diagnose *M. bovis* infection in badgers. The work programme has reached a stage where it is necessary to test the vaccine under conditions of natural transmission of infection. A field trial will commence in 2008 to test the efficacy of the vaccine in a large number of badgers over a wide geographic area. Success in the field trial will lead to implementation of a vaccination strategy as part of the national control programme.

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**BOVINE TUBERCULOSIS**

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# BADGER ECOLOGY

## HOW MANY EURASIAN BADGERS (*MELES MELES*) ARE THERE IN IRELAND?

### a. An ecological approach

*Paddy Sleeman, John Davenport (UCC Zoology), Simon More, Tracy Clegg, Daniel Collins (UCD CVERA), John Griffin, Ian O'Boyle (DAFF)*

An understanding of the total number of badgers in Ireland is important, noting the contribution of this species to the epidemiology of bovine tuberculosis. Using data from the four area project, this study seeks to ascertain the size of Irish badger social groups, and thereby more accurately estimate the size of the badger population of Ireland.

### b. A GIS approach

*Guy McGrath (UCD CVERA)*

The objective of this study is to estimate the current population of badgers in the Republic of Ireland. An up-to-date census of population data are required to assess the impact of badger removal activities conducted by DAFF through the bovine tuberculosis eradication scheme. Geographical Information System modelling techniques will be used to extrapolate a total population from known populations within surveyed sites.

## THE REPRODUCTIVE CYCLE OF THE MALE AND FEMALE EURASIAN BADGER (*MELES MELES*) IN IRELAND

*Lynsey Stuart, Nicola Marples (TCD Zoology), Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), James O'Keefe (DAFF)*

The aims of this project are to describe the annual reproductive cycle of the male and female Eurasian badger, *Meles meles*, in Ireland, to determine the reproductive potential of the badger population and to develop an understanding of the factors that may affect its reproductive success. The results to date suggest the Irish badger population has a high reproductive potential, which is neither affected by reproductive competition between individuals nor by infection with tuberculosis. The high reproductive potential is likely to be related to the low density of the Irish badger population.

## SEASONALITY OF PARTURITION IN THE EURASIAN BADGER (*MELES MELES*)

*Rosario Carroll, Nicola Marples (TCD Zoology), Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), James O'Keefe (DAFF)*

The primary aim of this project is to predict the annual cubbing times in Irish badger populations and to investigate if the cubbing period varies from year to year. This will enable DAFF to limit the culling of lactating females during the months when the dependent cubs are most vulnerable. The study will also investigate the differences in badger group composition between undisturbed groups and newly established groups. This will provide information concerning the diversity in foraging activity and social interactions in both groups.

## BAIT-MARKING AND LIVE TRAPPING STUDIES DURING THE FOUR AREA PROJECT

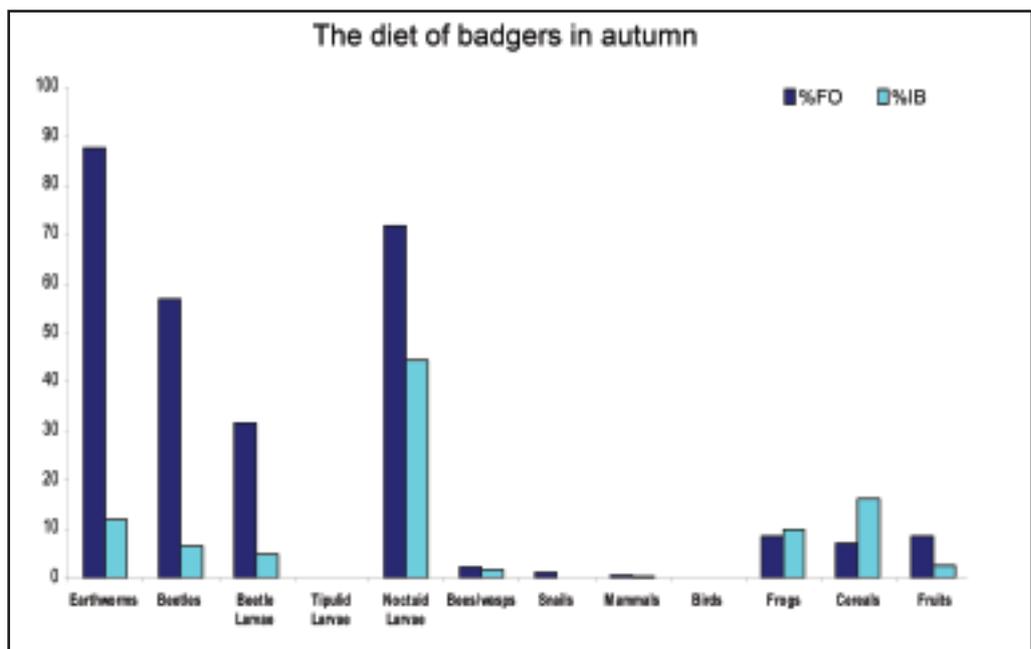
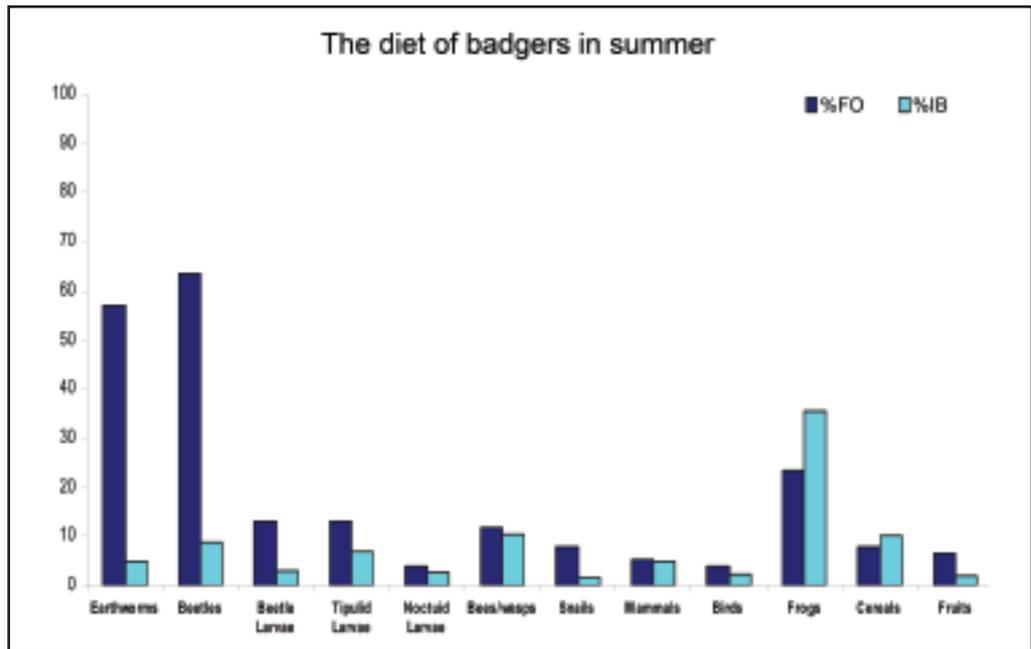
*Chris Smal, Julian Brown (independent consultants), John Griffin, Ian O'Boyle (DAFF), Paddy Sleeman (UCC Zoology)*

During the four area project, badger social groups were identified using bait-marking and live trapping. These results are now being documented.

### THE FEEDING STRATEGIES AND FORAGING BEHAVIOUR OF THE EURASIAN BADGER (*MELES MELES*) IN IRELAND

Gráinne Cleary, Nicola Marples (TCD Zoology), Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), James O’Keeffe (DAFF)

Although the Eurasian badger (*Meles meles*) has been studied in many of its range of habitats across Europe, a detailed examination of its feeding strategies and foraging behaviour has not been conducted in Ireland. The results of this comprehensive investigation into the diet of badgers demonstrate that they opportunistically consume many prey items throughout the year. However, during spring and autumn, badgers display strong preferences for seasonal insect larvae, in particular Tipulids and Noctuids. They are probably best described as generalist foragers displaying seasonal preferences.



Seasonal variation in the diet of badgers  
 (%FO = number of stomachs found to contain a given item expressed as a percentage of the total number of stomachs, %IB = proportions of food categories in the stomach sample in relation to the total stomach contents)

# BADGER-TO-BADGER TRANSMISSION

## GENOTYPING OF *MYCOBACTERIUM BOVIS* ISOLATES FROM BADGERS IN FOUR AREAS OF THE REPUBLIC OF IRELAND BY RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS

Costello, E., Flynn, O., Quigley, F., O'Grady, D., Griffin, J., Clegg, T., McGrath, G.

Veterinary Record 159 (2006), 619-23.

An analysis of the molecular epidemiology of *Mycobacterium bovis* isolated from badgers was made in four selected areas of the Republic of Ireland in which an intensive badger removal programme was being carried out over a period of five years. Tissue samples from 2310 badgers were cultured. Restriction fragment length polymorphism (RFLP) analysis using IS6110, polymorphic GC-rich sequence (PGRS) and direct repeat sequence (DR) probes was applied to the isolates from 398 badgers, and 52 different RFLP types were identified. Most of the isolates belonged to seven predominant types. The other 45 types were represented by few isolates. An analysis suggests that some of these 45 types may have been introduced by the inward migration of badgers and others may have been the result of genetic changes to one of the prevalent types. The badgers were divided into groups on the basis of the sett at which they were captured, and RFLP typing was applied to isolates from two or more badgers from 85 groups. Multiple RFLP types were identified among isolates from 50 of these groups, suggesting that badgers probably moved frequently between group territories.

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**“The results of the RFLP analyses support the hypothesis that there is a considerable level of extraterritorial movement by badgers.”**

## THE PATHOGENESIS OF *MYCOBACTERIUM BOVIS* INFECTION IN WILD BADGERS

Denise Murphy, Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine)

The European badger (*Meles meles*) is recognised as the principal wildlife reservoir of *M. bovis* infection in Ireland. Understanding of the pathogenesis of the disease in naturally infected badgers will help to decipher transmission pathways between badgers and cattle, which will be essential for the successful development and application of a vaccine. In the present study, we have investigated the prevalence and distribution of *M. bovis* infection in a group of naturally infected wild badgers (n=215). The findings of this study confirm that most infected badgers have non-visible lesions and the majority of infected badgers with visible lesions are not severely diseased. The distribution of infection indicates that the lungs and/or pulmonary lymph nodes of infected badgers are the principal tissues involved, confirming that tuberculosis in badgers is primarily a respiratory disease.

## THE 'GREENFIELD' AND 'REDFIELD' STUDIES

Denise Murphy (UCD Agriculture, Food Science and Veterinary Medicine), Guy McGrath, Daniel Collins (UCD CVERA), Leigh Corner, Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine)

The objective of this study is to test the hypothesis that infection prevalence in cattle can be used to identify infection prevalence in associated badger populations. To date, infection prevalence in badgers has been studied in areas of high prevalence of infection in cattle following badger culling associated with herd breakdowns. The 'Greenfield' study focuses on the infection prevalence in badgers in areas of low prevalence of infection in cattle. The 'Redfield' study concerns the infection prevalence in badgers removed in the first trapping event in areas of high prevalence of infection in cattle. While not directly comparable due to different selection criteria, the results of the studies will identify any significant difference in the prevalence of infection in the two badger populations.

## GREENFIELD SITE SELECTION

*Guy McGrath (UCD CVERA), Paul White (DAFF), Daniel Collins (UCD CVERA)*

The relationship between TB infected badgers and TB breakdowns in cattle have been established in the absence of an understanding of the prevalence of TB in the badger population where there are no significant TB problems in the local cattle population both currently and historically (Greenfield sites). Based on existing assumptions of TB transmission pathways, we would expect to find levels of TB in badgers to be significantly lower in areas where there has never been a TB problem in cattle. If, however, TB levels in badgers from Greenfield areas are found to be the same as those found in close proximity to herd breakdowns attributed to badgers, our understanding of the mode of transmission will need to be re-examined. The aim of this study was to identify areas of land with either no or a very low historical prevalence of TB in local cattle populations (Greenfield sites).

Ireland was divided into 112,440 equal sized hexagons with a maximum cross sectional width of 1 km (Figure 1, highlighting an area in west Co. Cork, east Co. Kerry for illustration). The locations of herds in Ireland are held in polygon format on a spatial database through the Land Parcel Identification System (LPIS). Greenfield study sites were identified using Geographical Information Systems (GIS), following the following exclusions:

- Exclusion of all hexagons associated with herds with a historic TB problem. The TB history of all herds in the country is recorded and maintained within the Animal Health Computer System (AHCS). A unique identifier, the herd number, is used to join the spatial data with the herd TB testing history. A herd was permitted a single TB breakdown of no more than 2 reactors in the 5 years period between 2002 and 2006. Any herds failing to meet this criterion were flagged. A spatial query was then performed identifying any hexagons that touched a flagged herd (Figure 2a)
- Exclusion of hexagons not touching farms stocked with a minimum of 17 animals and maximum of 80 animals (2nd and 3rd quartiles of the population) (Figure 2b)
- Exclusion of all hexagons within 1 km of badger setts treated under the Government's reactive cull strategy (Figure 2c)
- Exclusion of hexagons touching any hexagons excluded in criteria 1 – 3 (Figure 2d)
- Exclusion of hexagons overlaying commonage (common grazing land) (Figure 2e)

The internal hexagon boundaries of the remaining hexagons were then dissolved creating Greenfield areas. Very small 'island' Greenfield areas were excluded. An approximate centroid was calculated for all remaining Greenfield areas. Each centroid was then inspected against a backdrop of geo-rectified orthophotography to ensure it was on or close to agricultural land and assigned a unique identification number (Figure 3).

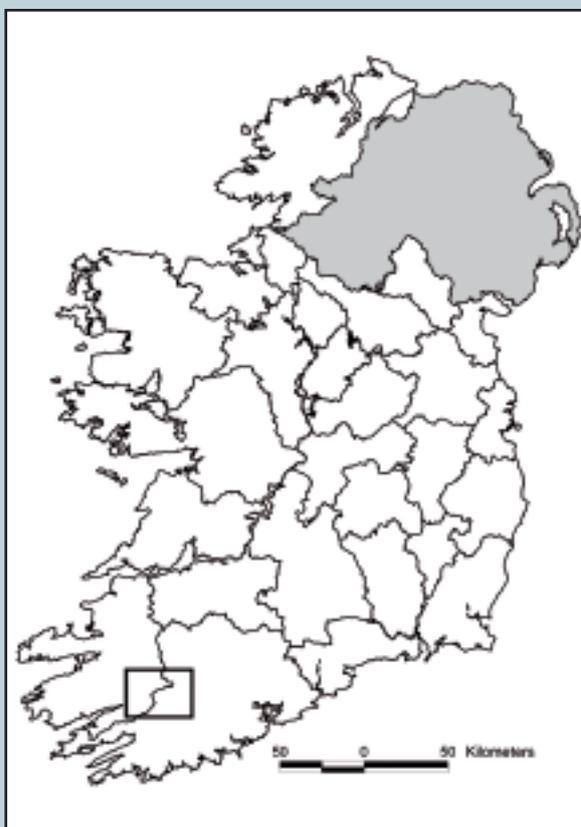


Figure 1. Selected area for illustration

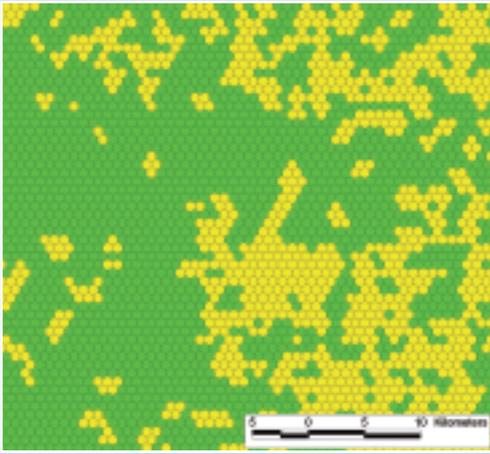


Figure 2a. Greenfield site selection, step 1

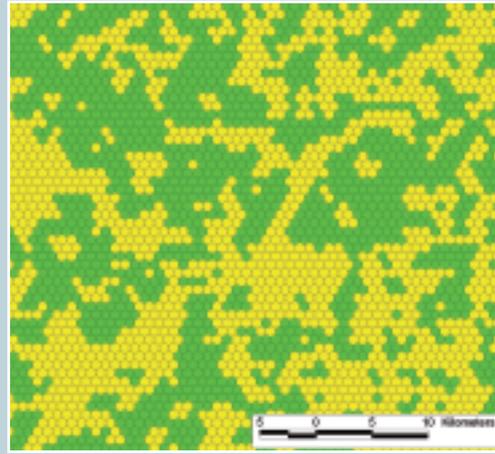


Figure 2b. Greenfield site selection, step 2

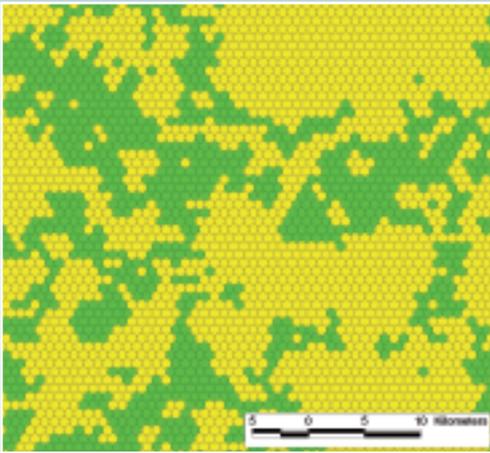


Figure 2c. Greenfield site selection, step 3

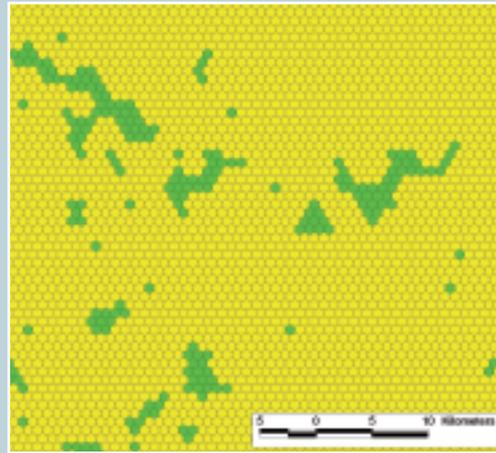


Figure 2d. Greenfield site selection, step 4

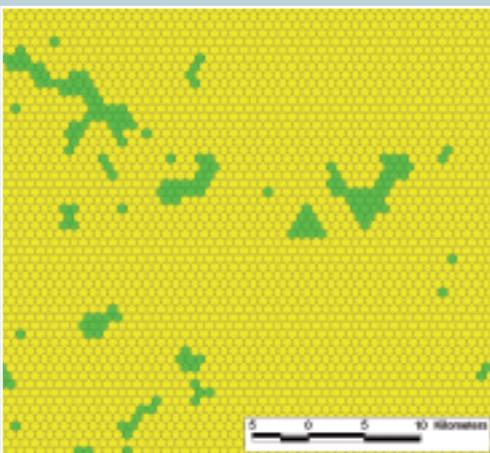


Figure 2e. Greenfield site selection, step 5

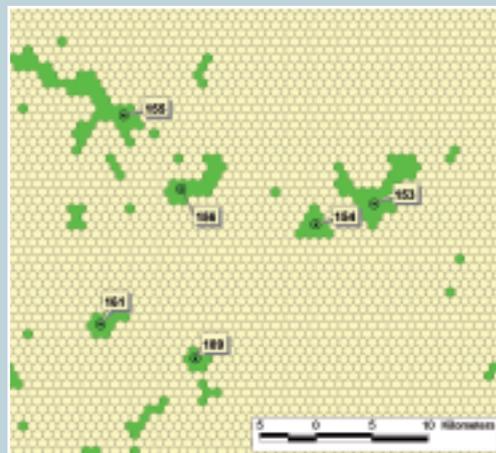


Figure 3. Greenfield areas and identified survey sites

## BADGER-TO-CATTLE TRANSMISSION

### a. Evidence and understanding

#### THE ROLE OF WILD ANIMAL POPULATIONS IN THE EPIDEMIOLOGY OF TUBERCULOSIS IN DOMESTIC ANIMALS: HOW TO ASSESS THE RISK

Corner, L.A.

Veterinary Microbiology 112 (2006), 303-312.

Tuberculosis is present in wild animal populations in North America, Europe, Africa and New Zealand. Some wild animal populations are a source of infection for domestic livestock and humans. An understanding of the potential of each wild animal population as a reservoir of infection for domestic animals is reached by determining the nature of the disease in each wild animal species, the routes of infection for domestic species and the risk of domestic animals encountering an infectious dose. The mere presence of infection in a wild animal population does not of itself provide evidence of a significant wildlife reservoir. Although at times counterintuitive, wildlife populations with high disease prevalence may not necessarily have a role in the epidemiology of disease in domestic livestock. The key concepts used in deciding whether an infected wild animal population is involved in the epidemiology of tuberculosis in domestic livestock is illustrated by reference to six well-researched cases: the feral pig (*Suis scrofa*) and feral Asian water buffalo (*Bubalus bubalis*) in Australia, white tailed deer (*Odocoileus virginianus*) in Michigan, and the brushtail possum (*Trichosurus vulpecula*) and other species, such as the ferret (*Mustela furo*), in New Zealand. A detailed analysis of *Mycobacterium bovis* infection in the Eurasian badger (*Meles meles*) in Ireland and its role as a reservoir of infection for cattle is also presented.

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**“An understanding of the potential of each wild animal population as a reservoir of infection for domestic animals is reached by determining the nature of the disease in each wild animal species, the routes of infection for domestic species and the risk of domestic animals encountering an infectious dose.”**



*Mycobacterium bovis* has been found in a number of wild animal species, including the kudu

## A LONG-TERM OBSERVATIONAL STUDY OF THE IMPACT OF BADGER REMOVAL ON HERD RESTRICTIONS DUE TO BOVINE TUBERCULOSIS IN THE IRISH MIDLANDS DURING 1989–2004

*Gabrielle Kelly (UCD Statistics), Joe Condon (DIT), Simon More (UCD CVERA), Leonard Dolan (DAFF), Isabella Higgins (UCD CVERA), John Eves (DAFF)*

An observational study is being conducted to critically evaluate the long-term effectiveness of proactive badger culling and to gather insights into the long-term effects of reactive culling, on TB prevalence in cattle. The study is based on data from the Irish midlands since 1989, of badger removal and TB incidence in cattle.

## SPATIAL ASSOCIATION OF *MYCOBACTERIUM BOVIS* INFECTION IN BADGERS *MELES MELES* AND CATTLE IN FOUR AREAS IN IRELAND

*Gabrielle Kelly (UCD Statistics), Simon More (UCD CVERA), David Williams (UCD Statistics), Guy McGrath (UCD CVERA)*

An understanding of spatial associations between *M. bovis* in badgers and cattle can contribute to our understanding of disease behaviour and the effectiveness of existing control policies. In this study, we are investigating local spatial associations between *M. bovis* infection in badgers and cattle, using data from the four area project.

## WINTER YARD SURVEY

*Paddy Sleeman, John Davenport, Anthony Fitzgerald (UCC Zoology)*

Visits by infected badgers to yards where cattle are housed in winter may provide opportunities for transmission of tuberculosis to cattle. Using winter survey periods in 2005/06 and 2006/07, this study has sought to quantify the badger activity in cattle yards in Co. Cork.

## QUANTIFYING BADGER EXPOSURE AND THE RISK OF BOVINE TUBERCULOSIS FOR CATTLE HERDS IN COUNTY KILKENNY, IRELAND

*Olea-Popelka, F.J., Phelan, J., White, P.W., McGrath, G., Collins, J.D., O'Keeffe, J., Duggan, M., Collins, D.M., Kelton, D.F., Berke, O., More, S.J., Martin, S.W.*

Preventive Veterinary Medicine 75 (2006), 34-36.

The objectives of the study were to quantify the levels of badger exposure for cattle and to test the hypothesis that increased badger exposure does not increase the risk of bovine tuberculosis in a herd. Information that became available from the targeted removal of badgers over the study period, and from a badger-removal project in County Kilkenny during 1996-1999, was used. The specific location of cattle within each farm, and the length of time that cattle spent in each farm field during the grazing season, and in the barnyard during winter, was used to build an exposure coefficient to quantify the amount of badger exposure that cattle encountered either on pasture or in the barn. The study design was a matched case-control study in which the control herds were selected using incidence density sampling. During the 4-year study period, 543 badgers were removed and of these 96 badgers were classified as tuberculosis positive; 96 TB herd breakdowns occurred. There was a significant association between case herds and having a higher badger sett exposure coefficient during 1996-1998. No significant association between case herds and having a higher exposure coefficient based on the number of badgers, or the number of tuberculous badgers, during September 1997-December 1999 was found.

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**“We report an association between sett numbers and risk of a TB breakdown, (however,) this has not elaborated possible routes of transmission.”**

## b. The implications of badger control activities

### DOES REACTIVE BADGER CULLING LEAD TO AN INCREASE IN TUBERCULOSIS IN CATTLE?

*More, S.J., Clegg, T.A., McGrath, G., Collins, J.D., Corner, L.A.L., Gormley, E.*

*Veterinary Record 161 (2007), 208-209.*

Badgers play an important role in the epidemiology of bovine tuberculosis in Ireland and the UK, and a range of control measures are in place or have been under consideration, including badger culling. In the UK, there is a concern, based principally on results from the random badger culling trial (RBCT), that reactive badger culling may be counterproductive, leading to increased TB incidence in associated cattle and the residual badger population. A cascade of adverse events following badger culling has been proposed, whereby badger culling results in substantial changes to the spatial and social organisation and the territorial behaviour of badger populations (these steps are collectively termed 'perturbation'), which in turn lead to increased contact and transmission of infection between badgers, increased contact between cattle and the disturbed badger population, and increased infection risk in associated cattle. In this article, we question aspects of the interpretation of the RBCT data, in particular the biological plausibility of measured effects, the precision of these effects and the timing of biological processes, and of the accuracy of spatial data. It is important that interested policy-makers and the general public are aware of varying perspectives surrounding this topic.

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**“It is important that policy-makers and the general public are aware of varying perspectives about the impact of reactive badger culling on tuberculosis in cattle.”**

### REACTIVE BADGER REMOVAL AND LEVELS OF BOVINE TUBERCULOSIS IN CATTLE HERDS IN CO. LAOIS

*Francisco Olea-Popelka (University of Guelph), James O’Keeffe, Paul White, Pat Flanagan (DAFF), Simon More (UCD CVERA), Wayne Martin (University of Guelph)*

One of the current constraints to the eradication of bovine tuberculosis in Ireland is the existence of an important wildlife reservoir for *M. bovis*, namely the badger (*Meles meles*). Targeted (or reactive) badger removal has been conducted in Ireland since the early 1990s. The objective of our study is to assess the impact of targeted badger removal on the subsequent levels of TB for herds in one county in Ireland.

### THE IMPACT OF TARGETED BADGER REMOVAL ON TUBERCULOSIS IN CATTLE HERDS IN CO. MONAGHAN

*Paul White (UCD CVERA), Klaas Frankena (Wageningen University), James O’Keeffe (DAFF), Simon More (UCD CVERA), Mart de Jong (Wageningen University), Wayne Martin (University of Guelph)*

Following the establishment of the Wildlife Unit in October 2003, a policy of targeted badger removal in the areas surrounding TB breakdown herds was implemented in the Republic of Ireland. This study will assess the impact of targeted badger removal on the subsequent levels of TB in herds in Co. Monaghan.

## THE EFFECT OF VARYING LEVELS OF POPULATION CONTROL ON THE PREVALENCE OF TUBERCULOSIS IN BADGERS IN IRELAND

*Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), Tracy Clegg, Simon More (UCD CVERA), David Williams (UCD Statistics), Ian O'Boyle, Eamon Costello (DAFF), Paddy Sleeman (UCC Zoology), John Griffin (DAFF)*

In Ireland, the role of badgers in the epidemiology of TB in cattle has become increasingly understood. As yet, however, there is limited understanding of TB epidemiology in badgers. In this study, we are examining the effect of varying levels of population control on the prevalence of *M. bovis* infection in Irish badger populations.

## AN ASSESSMENT OF INJURY TO BADGERS DUE TO CAPTURE IN STOPPED RESTRAINTS

*Denise Murphy (UCD Agriculture, Food Science and Veterinary Medicine), James O'Keeffe (DAFF), Wayne Martin (University of Guelph), Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine).*

In Ireland, stopped restraints have been used routinely by DAFF to capture badgers for removal as part of the interim strategy to control bovine tuberculosis. The aim of this study was to determine the frequency and severity of physical injuries occurring when badgers were captured using stopped restraints. Badgers were examined from removal operations carried out by DAFF from October to December 2005 and from May to June 2006. The results showed that the severity of physical injury to badgers in association with the use of stopped restraints was low.

## TESTING THE EFFECTIVENESS OF BARRIERS DURING THE IRISH FOUR AREA STUDY

*Paddy Sleeman, John Davenport (UCC Zoology), Simon More, Tracy Clegg (UCD CVERA), John Griffin, Ian O'Boyle (DAFF)*

Knowledge of badger movements will contribute to our understanding of the dynamics of bovine tuberculosis in badgers and cattle. Using data from the four area study, we are examining the effectiveness of various barriers to badger movements.

## DESCRIPTION OF A MEDIUM TERM NATIONAL STRATEGY TOWARD ERADICATION OF TUBERCULOSIS IN CATTLE IN IRELAND

*James O'Keeffe (DAFF)*

Proceedings of the 11th Symposium of the International Society for Veterinary Epidemiology and Economics (ISVEE), Cairns, Australia, p502.

A compulsory national bovine tuberculosis eradication programme has been operating in the Republic of Ireland since 1959. Substantial progress was achieved in the early decades, but since the mid '70s there has been no improvement despite the continuing application of a very intensive national tuberculin testing programme. Geographical information systems techniques including kernelling have been used to identify areas of the county where tuberculosis is consistently identified at high incidence levels. Each year, circa 70% of all standard "skin test" reactors are drawn from roughly 30% of the area of agricultural land. These areas and the techniques used to delineate them are described. A strategy based on reducing the local densities of badgers, weighted toward more intensive removals in the areas of the country defined as "chronic" is described. In the short term, this will result in lowering the risk of cattle herds becoming infected with TB from infected badgers in the local environment. The frequency of significant cattle:badger interactions will be reduced as a consequence of the local reduction in the density of both cattle and badgers. Badger interventions are carefully planned and rigorously monitored and only take place as a sequel to an epidemiological investigation carried out by State Veterinarians who must follow a standardised protocol. The medium term strategy targets a 25-30% reduction in the national badger population. This strategy will be re-visited when the results of planned vaccine trials have been evaluated.

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***“The eradication of tuberculosis in cattle is contingent on reducing levels of tuberculosis in the national badger population.”***

# BADGER TUBERCULOSIS VACCINE

## a. Vaccine development (studies with captive badgers)

### BADGER TUBERCULOSIS VACCINE

*Denise Murphy, Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), Eamon Costello (DAFF), Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine)*

The research on BCG vaccination against tuberculosis in badgers, consisting of an integrated series of experiments and associated studies, is continuing. Further, a series of studies have been completed with a view to implementing field vaccination of badgers. The BCG vaccine was initially chosen for use based on its availability, low production cost and much experience of its application in domestic and wild animals, and humans. To carry out these studies in a controlled environment, the Badger Research and Observation Centre (BROC) was designed to hold 6-7 small groups of badgers. In parallel with the captive badger experiments, studies have also been undertaken in wild, naturally infected badgers, using badgers removed during culling operations. As part of these studies, we helped develop and assess a range of *in vitro* diagnostic assays based on the immunological responses to challenge with virulent *M. bovis*.

#### **BROC 1: Experimental infection with *M. bovis***

As a first step in development of a vaccine, an infection model was required to generate disease in captive badgers. The objective of BROC 1 was to identify a dose of *M. bovis* which, when delivered by the endobronchial route to badgers, generated a disease profile that mimicked natural disease. The results showed that over a wide range of doses, the endobronchial procedure produced disease that was characteristic of natural disease. See *publication below*.

#### **BROC 2: Progression of the experimental infection**

Having established the utility of the endobronchial route and an effective challenge dose, this study was designed to use the optimal infective dose (derived from BROC 1) and follow the progression of the disease over time. This was important to determine the optimal time to examine the differences in the progression of disease between vaccinates and controls. Following experimental challenge, infection progressed slowly with a uniform result across the badgers studied. The optimal time to examine disease in vaccinates was found to be 12 to 18 weeks after infection.

#### **BROC 3: Establishing proof that BCG induces protection against tuberculosis in badgers**

With the infection procedure established, we set out to determine if BCG was protective in badgers and to examine possible routes of vaccination including the subcutaneous and mucosal routes. The results showed that vaccination by either route led to significant protection of vaccinated badgers compared with non-vaccinated controls.

#### **BROC 4: Oral BCG vaccination and protection**

To be of practical use in the field delivery of BCG, an oral bait is likely to be the most cost-effective means of delivery. A lipid formulation that protects the live BCG from gastric secretions has been developed by Dr Frank Aldwell (University of Otago, New Zealand). Having demonstrated that BCG generated protection in badgers, and that a mucosal route was highly effective, we wanted to test the efficacy of BCG vaccine delivered by the oral route after challenge by the endobronchial infection procedure. The outcome was that vaccination by the oral route led to significant protection.

#### **BROC 5: Duration of protection following oral BCG vaccination**

Having demonstrated that oral delivered BCG could induce protection, we set out to determine if badgers vaccinated by oral routes with a lipid-encapsulated BCG would induce protection that could be detected for up to 12 months. The study is due for completion.

#### **BROC 6: Comparison of protection of badgers vaccinated with BCG-Pasteur and commercial BCG-Danish vaccine strains**

To date, all of our studies have been conducted using the BCG-Pasteur strain. However, currently the only BCG vaccine strain produced and registered in the EU is the BCG-Danish strain manufactured by Statens Serum Institut (Denmark). There is now an international consensus that the vaccine submitted for registration as veterinary medicine will use this strain. In this study, we compared oral vaccination with the two BCG strains by feeding badgers with the BCG strains encapsulated in a semi-solid lipid matrix that was prepared specifically for this purpose by the collaborating laboratory in New Zealand (Dr Frank Aldwell, University of Otago). The results indicate that both vaccines generated high levels of protective immunity. There are no significant differences between BCG-Danish and BCG-Pasteur strains.

#### **BROC 7: The protective efficacy of BCG-Danish in badgers against a low dose challenge with *M. bovis***

We have established that the BCG vaccine can protect badgers against experimentally induced disease when the challenge protocol used a high dose of *M. bovis* ( $10^4$  cfu). The purpose of the current study is to determine what effect vaccination will have on the experimental disease against a realistic low challenge dose and over a longer timescale. Badgers have been vaccinated with BCG-Danish strain, encapsulated in a semi-solid matrix. A control group remains non-vaccinated. Twelve weeks after vaccination, the badgers were challenged by the endobronchial route with a low dose of *M. bovis* ( $10^2$  cfu). At 52 weeks post-challenge, the badgers will be euthanased and protection assessed by pathology and culture. The data generated will be used to further our knowledge of the pathogenesis of tuberculosis in the badger and how vaccination alters the progression of the disease.

## EXPERIMENTAL TUBERCULOSIS IN THE EUROPEAN BADGER (*MELES MELES*) AFTER ENDOBRONCHIAL INOCULATION OF *MYCOBACTERIUM BOVIS*: I. PATHOLOGY AND BACTERIOLOGY

Corner, L.A., Costello, E., Lesellier, S., O'Meara, D., Sleeman, D.P., Gormley, E.

Research in Veterinary Science 83 (2007), 53-62.

The aim was to develop an endobronchial infection procedure for the study of *Mycobacterium bovis* infection in badgers. The badgers were anaesthetised and a cannula was passed *per os* to the tracheal bifurcation. When in place, 1 ml of *M. bovis* suspension was inoculated. Three concentrations of *M. bovis* suspension were used; <10 colony forming units (cfu), approximately  $10^2$  cfu and approximately  $3 \times 10^3$  cfu. The badgers were examined at three weekly intervals for clinical signs of disease and a tracheal aspirate was collected at each examination. The badgers were euthanased 17 weeks post infection (pi) and at the *post mortem* examination a wide range of tissues were examined for gross and histopathological lesions of tuberculosis and cultured for *M. bovis*. A sample of bronchial alveolar lavage (BAL) fluid was collected at post mortem for culture. At *post mortem* examination 17 weeks after infection, gross and histopathological lesions of tuberculosis were observed in all badgers inoculated with the high and medium dose and in 1 of 3 animals inoculated with the low dose. *M. bovis* was recovered from all inoculated badgers. Infection in the high dose group was more widely disseminated than in the other groups. The number of sites with gross and histopathological lesions increased with an increasing dose of *M. bovis*. All tracheal aspirates were negative on culture and only one BAL, collected from a badger of the high dose group, was positive on culture. No clinical signs due to the experimental infection were observed. The endobronchial route of inoculation is an effective route for establishing experimental infection, and could be used for studies of tuberculosis pathogenesis, immunology of *M. bovis* infection in badgers and for challenging badgers in vaccine protection studies. Badgers appeared to be very susceptible to infection by this procedure even with a dose of < 10 cfu but appear to control and limit the resulting infection.

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**“Badgers appear to be very susceptible to *M. bovis* infection, but appear to control and limit the resulting infection.”**

## b. Vaccine evaluation (field studies)

### THE VACCINE FIELD TRIAL

Denise Murphy, Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), Eamon Costello (DAFF), Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine)

The results from the captive badgers studies suggest that the BCG might be an ideal vaccine for use in wild badger populations. However, such studies cannot show that BCG vaccine will be protective in free-ranging badgers or provide an estimate of vaccine efficacy. This can only be determined in a field trial. Such a trial is planned with a large population of badgers and will be carried out in a defined area over three years. Badgers will receive vaccine or placebo, sequentially establishing a 50% vaccine coverage. Throughout the trial, estimates of changing incidence will be made from the measurements of individual immune responses. At the end of the study, the area will be depopulated and all badgers examined for tuberculosis by culture. The vaccine efficacy will be estimated from a comparison of the number of infected badgers in the vaccine group with the non-vaccinated control group. The results and experience gained from the field trial will facilitate the development of strategies for introduction of vaccination into the national programme.

## c. Supporting work

### DEVELOPMENT OF BADGER IMMUNODIAGNOSTICS

*Sandrine Lesellier, Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine)*

With the development of a vaccine for use in badgers, accurate tests will be required for tuberculosis surveillance in badger populations and to monitor the effect of vaccination. As part of the captive badger vaccine studies, we have tested a range of novel immunodiagnostic tests, developed through collaborations with VLA (Weybridge, UK) and shown that highly sensitive diagnostic tests are possible for badgers. In addition, with recognition of high specificity antigens it appears that the development of differential diagnosis is possible; such a test would be invaluable for use in association with a badger vaccine strategy.



Laboratory testing plays an important role in the diagnosis of *Mycobacterium bovis*

## ANTIGEN SPECIFIC IMMUNOLOGICAL RESPONSES OF BADGERS (*MELES MELES*) EXPERIMENTALLY INFECTED WITH *MYCOBACTERIUM BOVIS*

*Sandrine Lesellier, Leigh Corner (UCD Agriculture, Food Science and Veterinary Medicine), Eamon Costello (DAFF), Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine) and others*

European badgers (*Meles meles*) are considered to be an important reservoir of infection for *M. bovis* and are implicated in the transmission of tuberculosis to cattle in Ireland and the United Kingdom. Accurate tests are required for tuberculosis surveillance in badger populations and to provide a basis for the development of strategies, including vaccination, to reduce the incidence of the infection. In this study, we have developed an endobronchial *M. bovis* infection model in badgers in which we measured cell-mediated immune and serological responses for up to 24 weeks post-infection.

## ADVERSE REACTIONS TO BCG VACCINATION AGAINST TUBERCULOSIS

*Denise Murphy, Leigh Corner, Eamonn Gormley (UCD Agriculture, Food Science and Veterinary Medicine)*

The *M. bovis* strain, bacille Calmette-Guérin (BCG) is one of the most widely used human vaccines and remains one of the safest vaccines available. It has been used in human populations for over 80 years and 100 million children receive the vaccine annually. It has also been employed extensively for vaccine studies in laboratory animal hosts and is currently being developed for use in a variety of livestock and wild animals, including badgers. With continued use of the BCG against tuberculosis in different host species, the risk factors associated with adverse reactions may need to be re-evaluated. In this study we are reviewing the development of adverse reactions to BCG vaccination as reported in humans as well as in a variety of laboratory animals, livestock and wildlife.

## INFECTION DYNAMICS AND EFFECTIVE CONTROL STRATEGIES OF TUBERCULOSIS IN BADGERS AND CATTLE OF IRELAND

*Inma Aznar (UCD CVERA), Mart de Jong, Klaas Frankena (Wageningen University), Simon More (UCD CVERA)*

In Ireland, the control of bovine tuberculosis, leading ultimately to eradication, cannot be achieved until badger-to-cattle transmission is effectively addressed. In this study, we seek to develop a mathematical model of *M. bovis* transmission in cattle and badgers. Ultimately, the model will allow us to assess the potential impact of various interventions strategies on the prevalence of infection in both badgers and cattle.

### EVALUATION OF THE ANAESTHETIC EFFECTS OF COMBINATIONS OF KETAMINE, MEDETOMIDINE, ROMIFIDINE AND BUTORPHANOL IN EUROPEAN BADGERS (*MELES MELES*)

Davison, K.E., Hughes, L., Gormley, E., Lesellier, S., Costello, E., Corner, L.A.L.

Veterinary Anaesthesia and Analgesia 34 (2007), 394–402.

The objective of the study was to evaluate the effects of three anaesthetic combinations in adult European badgers (*Meles meles*). The badgers were each anaesthetized by intramuscular injection using the three techniques assigned in random order: romifidine 0.18 mg/kg, ketamine 10 mg/kg and butorphanol 0.1 mg/kg (RKB); medetomidine 0.1 mg/kg, ketamine 9 mg/kg and butorphanol 0.1 mg/kg (MKB); and medetomidine 0.1 mg/kg and ketamine 10 mg/kg (MK). Initial drug doses were calculated based on a body mass of 10 kg. Additional anaesthetic requirements, time to drug effect, duration of action and recovery from anaesthesia were recorded. Heart rate and rhythm, respiratory rate and rhythm, rectal and subcutaneous microchip temperature and oxygen saturation were recorded every 5 minutes. Depth of anaesthesia was assessed using: muscle tone; palpebral and pedal reflexes; and tongue relaxation at these time points. Blood samples and a tracheal aspirate were obtained under anaesthesia. Atipamezole was administered if the badger had not recovered within 60 minutes. Parametric data were analysed using ANOVA for repeated measures, and nonparametric data using Friedman's, and Cochran's Q tests:  $p < 0.05$  was considered significant. The result showed that all combinations produced good or excellent muscle relaxation throughout the anaesthetic period. RKB had the shortest duration of anaesthesia (16.8 minutes compared with MKB 25.9 minutes and MK 25.5 minutes) and antagonism was not required. RKB depressed respiratory rate less than MK and MKB. There was no significant difference between techniques for heart rate and rhythm. All combinations provided anaesthetic conditions suitable for sampling and identification procedures in adult badgers. The RKB protocol provided a significantly shorter period of anaesthesia when compared with the combinations containing medetomidine.

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**“All combinations provided anaesthetic conditions suitable for sampling and identification procedures in adult badgers.”**

### IMMUNOLOGICAL RESPONSES AND PROTECTIVE IMMUNITY AGAINST TUBERCULOSIS CONFERRED BY VACCINATION OF BALB/C MICE WITH THE ATTENUATED *MYCOBACTERIUM TUBERCULOSIS* (PHOP) SO2 STRAIN

Aguilar, D., Infante, E., Martin, C., Gormley, E., Gicquel, B., Hernandez Pando, R.

Clinical and Experimental Immunology 147 (2007), 330-338.

The *Mycobacterium tuberculosis* *phoP* mutant strain SO2 has been shown previously to be more attenuated than *Mycobacterium bovis* bacillus Calmette-Guérin (BCG) and confers protective immunity against tuberculosis in mice and guinea pig models. In this study we have investigated the survival and immunological responses of Balb/c mice infected with the *M. tuberculosis* SO2 strain. All Balb/c mice survived intratracheal infection with *M. tuberculosis* SO2 strain under conditions where all the mice infected with the parental *M. tuberculosis* MT103 had died after 9 weeks. Infection of Balb/c mice with *M. tuberculosis* SO2 was associated with comparatively lower levels of interferon (IFN)-gamma, interleukin (IL)-4 and tumour necrosis factor (TNF)-alpha and higher levels of inducible nitric oxide synthase (iNOS) during the late stage of infection, when compared with *M. tuberculosis* MT103 infection. The delayed-type hypersensitivity (DTH) response against *M. tuberculosis* culture filtrates was similar in mice infected with either the *M. tuberculosis* *phoP* SO2 strain or *M. tuberculosis* MT103. The protective efficacy of *M. tuberculosis* SO2 was compared with *M. bovis* BCG when delivered subcutaneously to groups of Balb/c mice. Following intratracheal challenge with *M. tuberculosis* H37Rv, protection was generated by 60 days post-challenge in mice vaccinated with either vaccine. At day 120 post-challenge the levels of protection were still significantly greater when compared with the non-vaccinated control group. The levels of protection conferred by vaccination with *M. tuberculosis* SO2 or with *M. bovis* BCG were similar, as measured by granuloma coalescence and pneumonia in addition to growth reduction of *M. tuberculosis* H37Rv.

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**“The *Mycobacterium tuberculosis phoP* mutant strain SO2 is more attenuated than *Mycobacterium bovis bacillus Calmette-Guérin* (BCG) and confers protective immunity against tuberculosis in mice and guinea pig models.”**

## THE LIVE *MYCOBACTERIUM TUBERCULOSIS* PHO<sub>P</sub> MUTANT STRAIN IS MORE ATTENUATED THAN BCG AND CONFERS PROTECTIVE IMMUNITY AGAINST TUBERCULOSIS IN MICE AND GUINEA PIGS

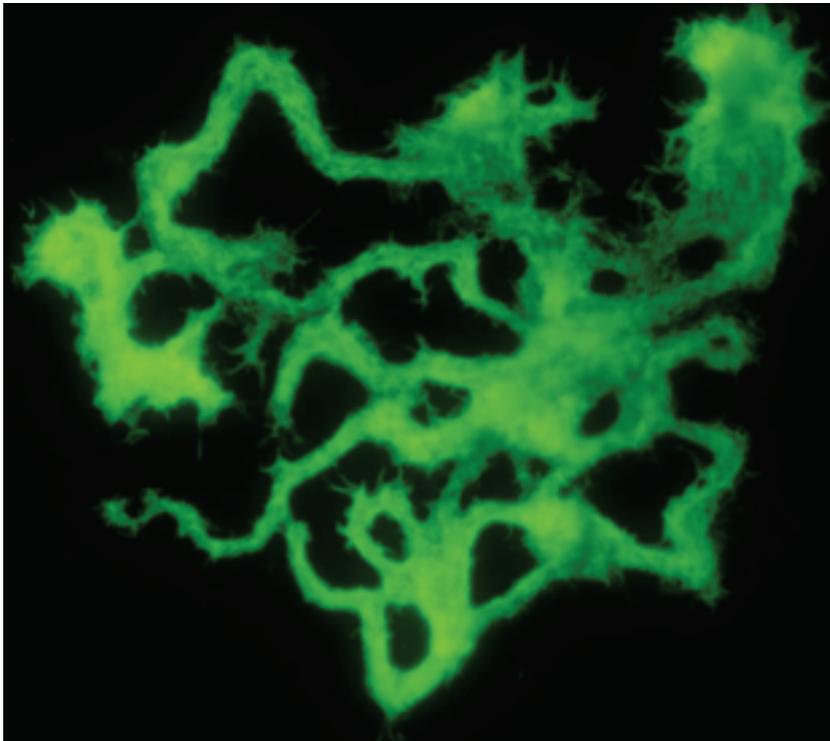
Martin, C., Williams, A., Hernandez-Pando, R., Cardona, P.J., Gormley, E., Bordat, Y., Soto, C.Y., Clark, S.O., Hatch, G.J., Aguilar, D., Ausina, V., Gicquel, B.

Vaccine 24 (2006), 3408-3419.

The *Mycobacterium tuberculosis* phoP mutant strain SO2 has previously been shown to have reduced multiplication in mouse macrophages and *in vivo* using the mouse intravenous-infection model. In this study we demonstrate that the *M. tuberculosis* SO2 is highly attenuated when compared with the parental *M. tuberculosis* MT103 strain and also more attenuated than BCG in severe combined immunodeficiency disease (SCID) mice. Complementation of the *M. tuberculosis* SO2 with the wild-type phoP gene restored the virulence of the strain in the SCID mice, confirming that the attenuated phenotype is due to the phoP mutation. In Balb/c mice subcutaneously vaccinated with either *M. tuberculosis* SO2 or BCG, the proportions of CD4+ and CD8+ populations measured in the spleen were significantly higher in the *M. tuberculosis* SO2 vaccinated group. In addition, the proportion of antigen-stimulated CD4+/CD8+ cells expressing IFN-gamma was significantly higher in the *M. tuberculosis* SO2 vaccinated group when compared with the BCG group. Balb/c mice subcutaneously vaccinated with the *M. tuberculosis* SO2 strain were also protected against intravenous challenge with *M. tuberculosis* H37Rv at levels comparable to mice vaccinated with BCG, as measured by reduced bacterial counts in lung and spleens. Guinea pigs subcutaneously vaccinated with the *M. tuberculosis* SO2 strain were protected against aerosol challenge with *M. tuberculosis* H37Rv delivered at different doses. A high dose aerosol challenge of *M. tuberculosis* SO2 vaccinated guinea pigs resulted in superior levels of protection when compared with BCG vaccination, as measured by guinea pig survival and reduction in disease severity in the lung.

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**“A high dose aerosol challenge of *M. tuberculosis* SO2 vaccinated guinea pigs resulted in superior levels of protection when compared with BCG vaccination.”**



Confocal fluorescence microscopy of auramine stained *M. tuberculosis* bacilli.  
Photo courtesy of Dr Carlos Martin, University of Zaragoza, Spain

## TUBERCULOSIS IN OTHER SPECIES

### BOVINE TUBERCULOSIS IN ALPACA IN IRELAND

Eoin Ryan (UCD Agriculture, Food Science and Veterinary Medicine), Dónal Connolly (Gort, Co. Galway), PJ Dwyer, John Fagan, Eamon Costello, Martin Hayes, Ascinta Kilroy (DAFF), Simon More (UCD CVERA)

Tuberculosis, due to infection with *M. bovis*, was diagnosed in a flock of alpaca in Ireland in 2004. In this study, we describe the case, including an assessment of infection risk for alpaca farmed in areas where TB is endemic, the origin of the infection, the potential for alpaca-to-alpaca transmission, and appropriate control measures, including the efficacy of predictor tests.



An alpaca in low body condition infected with *Mycobacterium bovis*.  
Courtesy of the Irish Veterinary Journal



Tuberculous lesions evident on the lung surface at *post mortem*.  
Courtesy of the Irish Veterinary Journal

## CONTROL OF *MYCOBACTERIUM BOVIS* INFECTION IN TWO SIKA DEER HERDS IN IRELAND

Tom Partridge, John Egan, Dónal Toolan (DAFF), Simon More (UCD CVERA)

In a number of countries, tuberculosis due to *M. bovis* is a significant health problem of captive deer. In this study, we describe outbreaks of bovine tuberculosis in sika deer (*Cervus nippon*) on two farms in Ireland and the methods used to control the disease.

## TUBERCULOSIS TESTING IN DEER

Simon More (UCD CVERA) with other members of the working group (tuberculosis in deer) of the Animal Health and Welfare panel of the European Food Safety Authority (EFSA)

The movement of live deer is linked with the spread of bovine tuberculosis. Ideally, science-based controls are needed to minimise infection risk during intra-community live animal trade, and importation of live animals from third countries. However, such controls are constrained by problems associated with the accuracy of the intradermal skin test in live deer. Given this context, the EFSA working group has sought to address each of the following queries from DG Sanco:

- the suitability of the existing TB tests for deer for the purpose of granting official TB-free status in the framework of Directive 92/65/EEC;
- the modalities for the validation of a TB test for deer; and
- a definition, including options for possible testing regimes giving sufficient guarantees for a animal/holding/region to be qualified/maintained/regained as officially free from TB infection in deer.

## ESTIMATING TB PREVALENCE IN DEER

Francisco Olea-Popelka (University of Guelph), James O'Keeffe (DAFF)

The role of wild deer in the epidemiology of bovine tuberculosis in Ireland remains uncertain. This study was conducted to estimate the sample size required to calculate the prevalence of tuberculosis in deer populations in Ireland.



Deer may play a role in the epidemiology of bovine tuberculosis on farmland adjoining areas of forestry

## IMPROVED UNDERSTANDING OF DISEASE EPIDEMIOLOGY

### a. Why are some herds at higher risk? How can they be managed?

#### RISK FACTORS FOR DISCLOSURE OF ADDITIONAL TUBERCULOUS CATTLE IN ATTESTED-CLEAR HERDS THAT HAD ONE ANIMAL WITH A CONFIRMED LESION OF TUBERCULOSIS AT SLAUGHTER DURING 2003 IN IRELAND

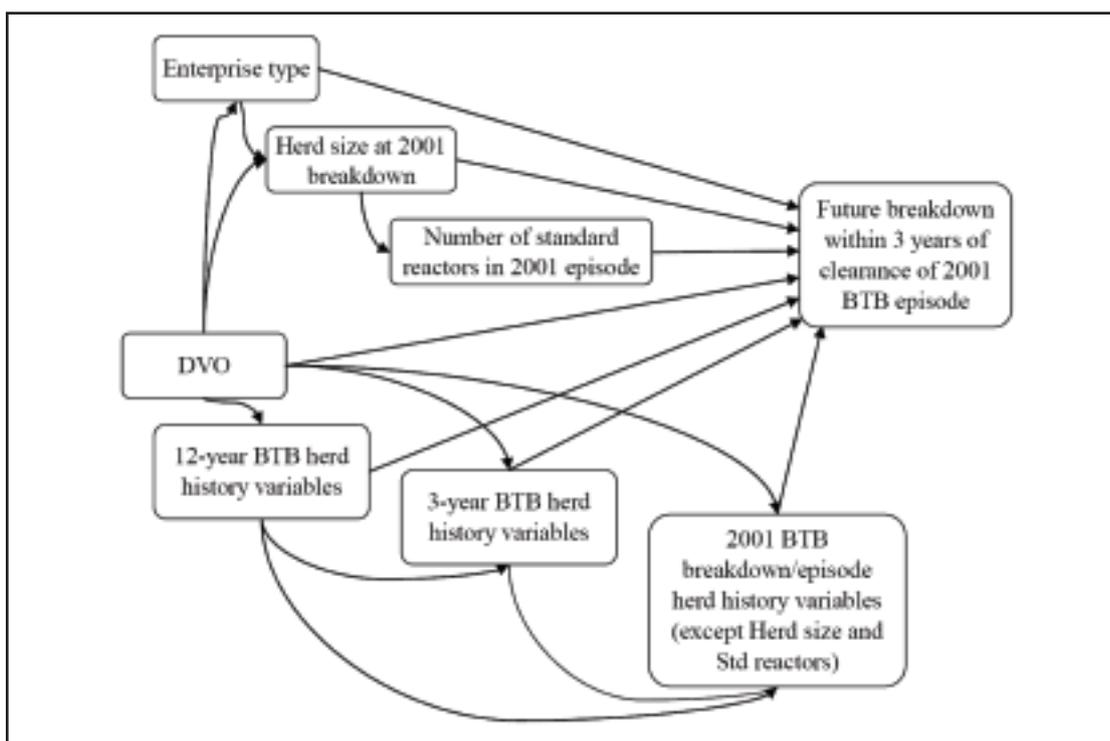
*Francisco Olea-Popelka (University of Guelph), Eamon Costello, Paul White (DAFF), Guy McGrath, Dan Collins (UCD CVERA), James O'Keeffe (DAFF), David Kelton, Olaf Berke (University of Guelph), Simon More (UCD CVERA), Wayne Martin (University of Guelph)*

In Ireland, TB herd breakdowns are first detected using field tuberculin testing (detecting 73.9% of breakdowns during the 12 months from 1 April 2003) and factory surveillance (26.1%). In those breakdowns first detected by factory surveillance, further standard reactor(s) are found during subsequent tuberculin testing in about 20% of herds; the rest test clear or have minimal TB problems. In this study, we will attempt to identify factors that relate to this difference in outcome.

#### DISEASE HISTORY PREDICTORS OF BOVINE TUBERCULOSIS BREAKDOWNS IN IRISH CATTLE HERDS

*Dianna Wolfe, Olaf Berke, David Kelton (University of Guelph), Paul White (DAFF), James O'Keeffe (DAFF), Wayne Martin (University of Guelph)*

In the Republic of Ireland, 20,000 to 50,000 cattle have been slaughtered annually due to bovine tuberculosis over the past 4 decades. Since the inception of the eradication programme, it has been noted that the risk of a TB breakdown is higher in some herds than others. In an effort to focus resources on problem herds, a herd classification scheme has been developed by DAFF based on the number of test-positive animals and the number of slaughtered animals with lesions occurring in a herd over a TB episode. The current study, a retrospective cohort study, was undertaken to investigate risk factors for future TB breakdowns in Irish cattle herds, with a goal of refining this herd risk scoring system.



Causal diagramme of risk factors (relating to the disease history of a herd) associated with a TB recurrence within three years of clearance following a TB episode in Ireland during 2001

## DESCRIPTIVE ANALYSIS OF HERDS DISCLOSING MULTIPLE ANIMALS WITH A BOVINE TUBERCULOSIS LESION AT SLAUGHTER DURING YEAR 2003 IN IRELAND

Francisco Olea-Popelka (University of Guelph), Eamon Costello, Paul White (DAFF), Guy McGrath, Dan Collins (UCD CVERA), James O’Keeffe (DAFF), David Kelton, Olaf Berke (University of Guelph), Simon More (UCD CVERA), Wayne Martin (University of Guelph)

This study involved all Irish cattle herds considered ‘clear’ of bovine tuberculosis but having multiple animals with a tuberculous lesion at slaughter during 2003. In this study, we conducted a descriptive analysis of selected risk factors with the potential to impact upon the result of the herd test immediately after the tuberculous lesion animals were found.

## A CASE CONTROL STUDY OF TEMPORAL AND SPATIAL RISK FACTORS ASSOCIATED WITH BOVINE TUBERCULOSIS BREAKDOWN HERDS IN IRISH CATTLE HERDS IN 2006

Paul White (UCD CVERA), Klaas Frankena (Wageningen University), James O’Keeffe (DAFF) Simon More (UCD CVERA), Mart de Jong (Wageningen University)

The temporal and spatial clustering patterns of tuberculin reactor disclosure are well recognised in Ireland. Using logistic regression techniques, this paper aims to determine the extent to which the presence or absence of a TB episode in year 2006 could have been predicted, based on previous TB history of the index herd over the years 1989-2005 and the TB history contiguous herds over the years 1989-2006.

### b. How important is contiguous spread?

#### A CASE STUDY OF BOVINE TUBERCULOSIS IN AN AREA OF COUNTY DONEGAL, IRELAND

Olea-Popelka, F.J., Butler, D., Lavin, D., McGrath, G., O’Keeffe, J., Kelton, D., Berke, O., More, S., Martin, S.

Irish Veterinary Journal 59 (2006), 683-690.

We performed a descriptive analysis to investigate the potential risk factors that might have contributed to the increased incidence of bovine tuberculosis (TB) herd-breakdowns in the reference area of Co. Donegal during the fifth year of the four-area project (FAP). Seventy two different herds were restricted for TB during the FAP; 10 of these herds were restricted twice, resulting in a total of 82 TB breakdowns. During the first four years of the FAP, the number of TB herd breakdowns in the area varied from a lowest of 9 to a maximum of 18 per year, and were geographically dispersed. In the fifth year of the study a considerable increase in the number of TB breakdowns (n=32) was observed, and there was a spatial ‘cluster’ of infected herds in the eastern part of the study area. The increased number of TB breakdowns during the fifth year most likely occurred because of the recrudescence of infection, herd-to-herd transmission, and to a lesser extent purchase of infected cattle. Infected badgers remain as a possible but less likely source of infection, especially as an explanation for the cluster of infected herds. Our analysis supports the hypothesis that TB in herds is a problem that cannot be addressed successfully by dedicating our efforts to the elimination of single risk factors alone. Neither is it a problem that needs to be investigated only at the herd level, but rather at the area level, including groups of contiguous herds.

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**“TB in herds is a problem that cannot be addressed successfully by dedicating our efforts to the elimination of single risk factors. Neither is it a problem that needs to be investigated only at the herd level, but rather at the area level, including groups of contiguous herds.”**

### ESTIMATION OF THE BETWEEN-HERD REPRODUCTION RATIO FOR CONTIGUOUS SPREAD OF BOVINE TUBERCULOSIS

*Paul White (UCD CVERA), Klaas Frankena (Wageningen University), James O'Keeffe (DAFF), Simon More (UCD CVERA), Mart de Jong (Wageningen University), Wayne Martin (University of Guelph)*

The aim of any eradication programme is to bring the reproductive ratio for the disease below 1. Tuberculin testing data is available from the Animal Health Computer System (AHCS) database for years 1989 to 2007. Together with contiguous data from the Land Parcel Information System, the data will be used for the analysis of possible transmission pathways for bovine tuberculosis between neighbouring herds following initial infection. After back-calculation to determine the sequence of infection between herds, the likelihood of between-herd transmission will be evaluated and an overall reproduction ratio calculated for contiguous spread.

### c. How important is introduced infection?

#### THE RISK OF BOVINE TUBERCULOSIS IN CATTLE PURCHASED FROM HERDS WITH AND WITHOUT A RECENT HISTORY OF BOVINE TUBERCULOSIS IN IRELAND

*Dianna Wolfe (University of Guelph), James O'Keeffe, Paul White (DAFF), David Kelton, Olaf Berke, Wayne Martin (University of Guelph)*

Previous herd-level epidemiological investigation has demonstrated that some 10% of herds that become derestricted from a TB episode will experience a subsequent TB breakdown on the follow-up test 6 months post-derestriction. In part, this may be because these herds were never truly clear of TB on the date of derestriction, and some animals in the herd may still be infected. Subsequently, these herds may unknowingly be selling *M. bovis*-infected animals. The objective of this study was to test the hypothesis that the odds of testing positive for TB were not significantly different for cattle sold from dairy herds with a recent history of TB than for cattle sold from dairy herds without a recent history of TB. Evidence of a significant difference in the odds of TB in these two groups of animals may indicate that a review of policy governing trade restrictions and pre-movement testing should be considered.

#### PREDICTORS FOR HERD-TO-HERD MOVEMENT AMONG CATTLE BORN IN IRELAND DURING 2005

*Paul White (UCD CVERA), Klaas Frankena (Wageningen University), James O'Keeffe (DAFF), Simon More (UCD CVERA), Mart de Jong (Wageningen University), Wayne Martin (University of Guelph)*

The relatively high levels of between-herd movement of cattle within Ireland may pose a risk for transmission of bovine tuberculosis between herds. This study will consist of a survival analysis of a 1% sample of animals born in year 2002. The subsequent between-herd movements, and slaughter events of this population will be monitored over the period from birth up to the end of 2005. Birth data will be derived from the Cattle Movement Monitoring System (CMMS) database, including birth registration and movement/exit data. While animals may move more than once in their lifetime, this study focuses on only the first animal movement during the period from birth up to the end of 2005. The purpose of the study is to identify predictors for this movement based on animal, herd and regional characteristics.

# CONTRIBUTING TO POLICY OPTIONS

## a. Programme management

### TUBERCULOSIS IN CATTLE: STRATEGIC PLANNING FOR THE FUTURE

Collins, J.D.

Veterinary Microbiology 112 (2006), 369-381.

In the later stages of eradication of tuberculosis in cattle, there is a need to take account of the fact that *Mycobacterium bovis* infection in cattle presents, not as cases of clinical disease but most commonly as apparently healthy animals showing an immunological response to tuberculin. This is an entirely different scenario to that seen when national eradication programmes were first devised, at a time when the protection of public health rather than animal health was the prime motivation. In countries with active programmes to eradicate bovine tuberculosis, it is critical for the programme's success that account is taken of this redefinition of tuberculosis, side by side with changes in modern animal production systems and their impact on the transmission of *M. bovis*. This paper highlights factors critical to the success of a national eradication programme, including a clear identification of the goals, of the policies that guide actions, and of the sequences of actions that are required within the programme to accomplish these goals. Experience has illustrated the adverse effects of compromise on outcome when the application of fundamental principles of disease control such as sound animal management, removal of known sources of infection, early diagnosis, quarantine, movement control and environmental hygiene are less than enthusiastically promoted and applied. The reality is that where these principles are applied in a sustained manner, the outcome is more likely to be successful. Therein lies the challenge for the risk manager.

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**“Experience has illustrated the adverse effects when the fundamental principles of disease control are less than enthusiastically promoted and applied.”**

### THE TUBERCULOSIS ERADICATION PROGRAMME IN IRELAND: A REVIEW OF SCIENTIFIC AND POLICY ADVANCES SINCE 1988

More, S.J., Good, M.

Veterinary Microbiology 112 (2006), 239-251.

A national programme to eradicate bovine tuberculosis commenced in Ireland in 1954. During the last 15-20 years, research has been conducted to address gaps in knowledge of disease epidemiology, to objectively evaluate alternative strategy options, and to critically assess the implementation of disease control strategies. This paper provides a review of scientific and policy advances in Ireland since 1988, relevant to the tuberculosis eradication programme in Ireland. There have been substantial advances in knowledge of aspects of disease epidemiology, relating to cattle-to-cattle transmission, the role of wildlife, transmission of infection from wildlife and methods to minimise wildlife-to-cattle transmission. Further, scientific advances have been made both in the detection and management of infected herds. With respect to policy, the paper describes current policy and policy advances in both the detection and management of infected herds, as well as current strategies to prevent herd breakdowns. The Irish programme is a useful example of science-informed policy in a national context.

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**“The Irish programme is a practical example of science-informed policy in a national context.”**

## PROGRESS IN IRELAND TOWARDS THE ERADICATION OF BOVINE TUBERCULOSIS

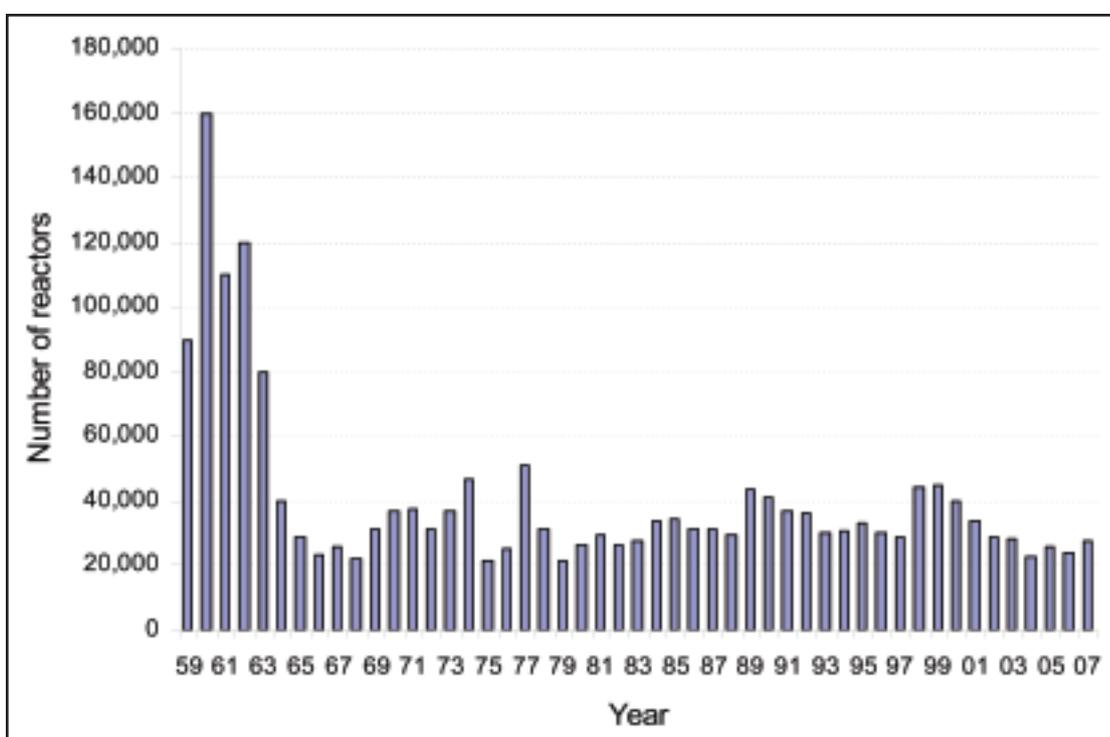
More, S.J.

UK Vet Livestock 12 (2007), 60-63.

There has been a national bovine tuberculosis eradication programme in Ireland since 1954. Initial progress was rapid, but has subsequently stalled despite the implementation of each of the accepted elements of disease control. Based on results from the east Offaly and four area projects, there is now conclusive evidence that wildlife (specifically transmission of infection from badgers to cattle) are a key constraint to disease eradication in Ireland, with cattle-to-cattle transmission of relatively lesser importance. Ireland is currently implementing a comprehensive strategy to address this constraint. In the short-term, a national programme of wildlife control has been implemented in areas of high disease prevalence, in combination with a broad range of other measures. In the longer term, Ireland is committed to the development of an effective badger vaccine and the implementation of a strategic programme of badger vaccination.

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**“The programme is underpinned by a comprehensive research programme to understand and address constraints to eradication.”**



The number of TB reactors detected in Ireland each year between 1959 and 2007

## QUANTIFICATION OF THE CONTRIBUTION OF RISK FACTORS FROM VARIOUS SOURCES, TO CALCULATE AN OVERALL REPRODUCTION RATIO ( $R_0$ ) FOR BOVINE TUBERCULOSIS INFECTION

Paul White (UCD CVERA), Klaas Frankena (Wageningen University), James O’Keeffe (DAFF), Simon More (UCD CVERA), Mart de Jong (Wageningen University), Wayne Martin (University of Guelph)

This project aims to quantify the contribution of several factors to the persistence of bovine tuberculosis under Irish cattle husbandry conditions. Key factors are the effectiveness of the (existing) test and cull programme, the role of animal trade, the contribution of wildlife (badgers) and the role of contiguity. When the relative importance of these factors has been quantified, several alternative eradication scenarios can be evaluated to assess their potential in TB eradication under Irish conditions by means of a between-herd transmission model.

## IMPROVED STATISTICAL MEASURES FOR TB SURVEILLANCE AND CONTROL

*Isabella Higgins, Simon More, Tracy Clegg (UCD CVERA), Paul White (DAFF)*

Proceedings of the 11th Symposium of the International Society for Veterinary Epidemiology and Economics (ISVEE), Cairns, Australia, p814.

Objective measures of progress are a critical component of any effective disease eradication programme. As part of a tuberculosis eradication programme, it is important that these measures are based on herd as the unit of interest. Also, they should clearly distinguish the results of surveillance and control activities, and use clearly defined case definitions. In Ireland, new statistical measures were developed to assist with decision-making, both locally and at a national level. Measures relating to surveillance and control activities were used, after creating an 'episode' file which defined periods when each herd was (and was not) restricted due to tuberculosis. During 2005, 94.7% of eligible herds remained disease-free during the year. There was minimal correlation between duration of restriction (days) and herd incidence (Pearson's correlation = 0.297,  $p = 0.111$ ). Based on herds restricted on 31 December 2005, there was an average of 5.7 reactors per restriction, with a single reactor detected in 41.2% of restrictions. These herd-level measures effectively partition activities relating to detection of new cases (surveillance) and the resolution of cases following detection (control). They also support earlier findings about herd-level risk factors for herd TB breakdowns in Ireland. Further work is ongoing.

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## POTENTIAL INFECTION-CONTROL BENEFIT FOR IRELAND FROM PRE-MOVEMENT TESTING OF CATTLE FOR TUBERCULOSIS

*Tracy Clegg, Simon More, Isabella Higgins (UCD CVERA), Margaret Good, Martin Blake (DAFF), David Williams (UCD Statistics)*

There is now only limited cattle-to-cattle transmission of bovine tuberculosis in Ireland, as a direct result of a comprehensive national control programme. Additional strategies may help to limit this further. One such option is the use of pre-movement testing for bovine tuberculosis, a strategy that had previously been discontinued in Ireland in 1996. This study seeks to determine the number of restrictions that could be attributed to the movement of infected animals; describe movement events following de-restriction of a herd; estimate the proportion of animals infected at the time of de-restriction; identify high-risk movements (those most likely to involve infected animals) and determine the potential yield of a pre-movement test.

## BOVINE TUBERCULOSIS REACTOR MOVEMENT DATA, 2005

*Francisco Olea Popelka (University of Guelph)*

The bovine TB reactor movement data for 2005 has been collated. The computer code created for this analysis will allow us to describe, compare and contrast the characteristics of each years TB reactor animals and/or herds. These outputs will be an important addition to the range of measures currently used to describe the progress of the bovine tuberculosis eradication scheme in Ireland.

## AN EVALUATION OF THE IRISH SINGLE REACTOR BREAKDOWN PROTOCOL FOR 2005 AND 2006, AND ITS USE AS A MONITOR OF TUBERCULIN TEST PERFORMANCE

*Margaret Good, Anthony Duignan (DAFF)*

The 'Singleton Protocol' has been developed as part of the TB eradication programme in Ireland. This protocol allows for the early restoration of free trading status to herds where:

- a single positive animal was detected, and
- disease in the herd was not confirmed as infected with *M. bovis* by epidemiological investigation, at *post mortem*, by laboratory examination, or by further test.

The study presents data about the Singleton Protocol from 2005 and 2006, highlighting its potential as a monitor for tuberculin test performance.

## b. Improving field surveillance

### DIAGNOSIS OF *MYCOBACTERIUM BOVIS* INFECTION IN CATTLE BY USE OF THE GAMMA-INTERFERON (BOVIGAM®) ASSAY

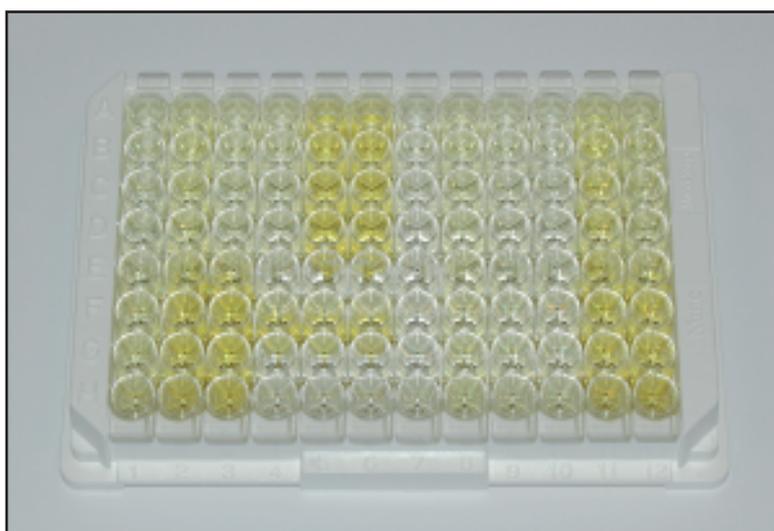
Gormley, E., Doyle, M.B., Fitzsimons, T., McGill, K., Collins, J.D.

Veterinary Microbiology 112 (2006), 171-179.

The strategic use of the gamma-interferon (IFN- $\gamma$ ) assay (Bovigam®) can provide a means for the early identification of *Mycobacterium bovis* infected cattle, thus ensuring their removal from an infected herd. When used in parallel with the tuberculin test, it is capable of identifying infected cattle, which might otherwise not be detected until later, if at all. The early detection and removal of these animals reduces the risk that they will become a source of infection for other cattle. When targeted in herds of high prevalence the benefits to the herd owner directly concerned can be considerable as the assay provides a means of shortening the period of restriction for such herds. This serves to generate confidence among herd owners and other stakeholders that effective schemes, based on sound scientific principles, can be developed to eradicate tuberculosis from infected cattle populations.

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**“The strategic use of the gamma-interferon (IFN- $\gamma$ ) assay (Bovigam®) can provide a means for the early identification of *Mycobacterium bovis* infected cattle, thus ensuring their removal from an infected herd.”**



IFN- $\gamma$  ELISA plate assay

### QUALITY CONTROL IN TUBERCULIN PRODUCTION AND USAGE

Douwe Bakker (Institute for Animal Science & Health, Lelystad), Margaret Good, Eamon Costello, Anthony Duignan (DAFF), Eamonn Gormley (UCD Veterinary Medicine), Tracy Clegg, Simon More (UCD CVERA)

Quality control is a key, and often problematic, issue during tuberculin production and usage. A series of papers are currently being prepared on issues relating to:

- Tuberculin production;
- Tuberculin potency testing;
- A comparison of tuberculins from different sources and of different potencies, as measured through skin testing and interferon-gamma;
- Variability in tuberculin test results; and
- Quality control of tuberculin testing in the field.

## THE COMPARATIVE PERFORMANCE OF THE SINGLE INTRADERMAL COMPARATIVE TUBERCULIN TEST IN IRISH CATTLE, USING TUBERCULIN PPD COMBINATIONS FROM DIFFERENT MANUFACTURERS

*Margaret Good, Finbarr Murphy (DAFF), Tracy Clegg, Simon More (UCD CVERA)*

Featured in the 'Selected reports' section

Ireland currently obtains its avian and bovine tuberculin purified protein derivatives (PPDs) from a single source. Because problems of supply or quality cannot be discounted, it is prudent that Ireland identify alternative supplier(s) as part of a broad risk management strategy. Therefore, the aim of this study was to compare the performance of a number of different tuberculin combinations (that is, pairings of bovine and avian PPD; with different manufacturers) in the single intradermal comparative tuberculin test, as currently performed in Ireland.

## THE TUBERCULIN TEST – A SAFE MEANS TO TEST A CATTLE POPULATION FOR BOVINE TUBERCULOSIS

*Good, M., Higgins, I., Maher, P.*

Irish Veterinary Journal 60 (2007), 680-684.

The bovine tuberculosis eradication programme in Ireland relies almost exclusively on the testing of individual animals using the single intradermal comparative tuberculin test (SICTT) to detect TB infected live cattle. Controls under the eradication programme are then applied at herd level. This paper provides a detailed overview of the use of the tuberculin test in Irish cattle.

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## TUBERCULIN REGISTRATION

*Margaret Good (DAFF)*

Tuberculin registration is now required under EU legislation. A range of papers are being completed in support of the registration process, including:

- The tuberculin test – a safe means to test a cattle population for bovine tuberculosis;
- An evaluation of the Irish Single Reactor Breakdown Protocol for 2005 and 2006, and its use as a monitor of tuberculin test performance; and
- Quality control in tuberculin production and usage, which includes an evaluation of the comparative performance of the SICTT in Irish cattle, using tuberculin PPD combinations from different manufacturers.

## INCONCLUSIVE TEST REACTORS: FUTURE IMPLICATIONS

*Rob Doyle (DAFF)*

There is some uncertainty about the future TB status of animals that are inconclusive to the annual tuberculin test. This study will determine future TB risk for a cohort of these animals as identified by the Sligo DVO over an 8 year period. The study will also seek to examine the risk that these animals posed to their herd of residence in that interim period.

### GENE EXPRESSION PROFILING OF PERIPHERAL BLOOD MONONUCLEAR CELLS (PBMC) FROM *MYCOBACTERIUM BOVIS* INFECTED CATTLE AFTER *IN VITRO* ANTIGENIC STIMULATION WITH PURIFIED PROTEIN DERIVATIVE OF TUBERCULIN (PPD)

Meade K.G., Gormley, E., Park, S.D., Fitzsimons, T., Rosa, G.J., Costello, E., Keane J., Coussens, P.M., MacHugh, D.E.

Veterinary Immunology and Immunopathology 113 (2006), 73-89.

Microarray analysis of messenger RNA (mRNA) abundance was used to investigate the gene expression program of peripheral blood mononuclear cells (PBMC) from cattle infected with *Mycobacterium bovis*, the causative agent of bovine tuberculosis. An immunospecific bovine microarray platform (BOTL-4) with spot features representing 1336 genes was used for transcriptional profiling of PBMC from six *M. bovis*-infected cattle stimulated *in vitro* with bovine purified protein derivative of tuberculin (PPD-bovine). Cells were harvested at four time points (3 h, 6 h, 12 h and 24 h post-stimulation) and a split-plot design with pooled samples was used for the microarray experiment to compare gene expression between PPD-bovine stimulated PBMC and unstimulated controls for each time point. Statistical analyses of these data revealed 224 genes (approximately 17% of transcripts on the array) differentially expressed between stimulated and unstimulated PBMC across the 24 h time course ( $P < 0.05$ ). Of the 224 genes, 87 genes were significantly upregulated and 137 genes were significantly downregulated in *M. bovis*-infected PBMC stimulated with PPD-bovine across the 24 h time course. However, perturbation of the PBMC transcriptome was most apparent at time points 3 h and 12 h post-stimulation, with 81 and 84 genes differentially expressed, respectively. In addition, a more stringent statistical threshold ( $P < 0.01$ ) revealed 35 genes (approximately 3%) that were differentially expressed across the time course. Real-time quantitative reverse transcription PCR (qRT-PCR) of selected genes validated the microarray results and demonstrated a wide range of differentially expressed genes in PPD-bovine-, PPD-avian- and Concanavalin A (ConA) stimulated PBMC, including the interferon-gamma gene (IFNG), which was upregulated in PBMC stimulated with PPD-bovine (40-fold), PPD-avian (10-fold) and ConA (8-fold) after *in vitro* culture for 12 h. The pattern of expression of these genes in PPD-bovine stimulated PBMC provides the first description of an *M. bovis*-specific signature of infection that may provide insights into the molecular basis of the host response to infection. Although the present study was carried out with mixed PBMC cell populations, it will guide future studies to dissect immune cell-specific gene expression patterns in response to *M. bovis* infection.

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**“The pattern of expression of genes in PPD-bovine stimulated PBMC provides the first description of an *M. bovis*-specific signature of infection that may provide insights into the molecular basis of the host response to infection.”**

## c. Improving factory surveillance

### QUANTIFICATION OF THE RELATIVE EFFICIENCY OF FACTORY SURVEILLANCE IN THE DISCLOSURE OF TUBERCULOSIS LESIONS IN ATTESTED IRISH CATTLE

Frankena, K., White, P.W., O’Keeffe, J., Costello, E., Martin, S.W., van Grevenhof, I., More, S.J.

Veterinary Record 161 (2007), 679-684.

In Ireland, factory surveillance of cattle for gross lesions is an important supplementary method for detecting herds infected with bovine tuberculosis (TB), and in recent years between 27 and 46 per cent of all new herd breakdowns in any year have been detected by this method. The aim of this study was to determine the relative efficiency of factories in detecting lesions among attested cattle slaughtered during 2003 and 2004. National databases were available on animal slaughter, programmes of tuberculin testing for bovine TB and laboratory confirmation of suspected lesions. Factories were ranked according to their submission risk (number of animals submitted with lesions/number of attested animals killed) and confirmation risk (number of animals with laboratory-confirmed lesions/number of animals submitted with lesions), adjusting for the risk profile of the animals slaughtered, including potential confounding factors such as their age and sex, whether they were purchased or homebred, the test history of their herd, the prevalence of bovine tb in the area and the season of slaughter. Approximately 3.7 million cattle were slaughtered in 42 Irish export-licensed factories during the two years. Complete data were available for 2,374,987 animals from 84,510 attested herds in 2,845 District Electoral Divisions. Samples from 7,398 animals with suspected tb lesions were submitted for laboratory examination; 4,767 (64.4 per cent)

were positive, 2,011 were negative and 620 were inconclusive. The average unadjusted submission risk for all the factories was 22 per 10,000, ranging from 0 to 58 per 10,000. The unadjusted factory confirmation risk (excluding factories that had sent in fewer than 10 lesions) varied between 34.3 and 86.3%. The unadjusted and adjusted submission and confirmation risks were highly correlated, and animal-related factors (including their characteristics and origin) therefore did not contribute to the variations in factory-level submission and confirmation risks.

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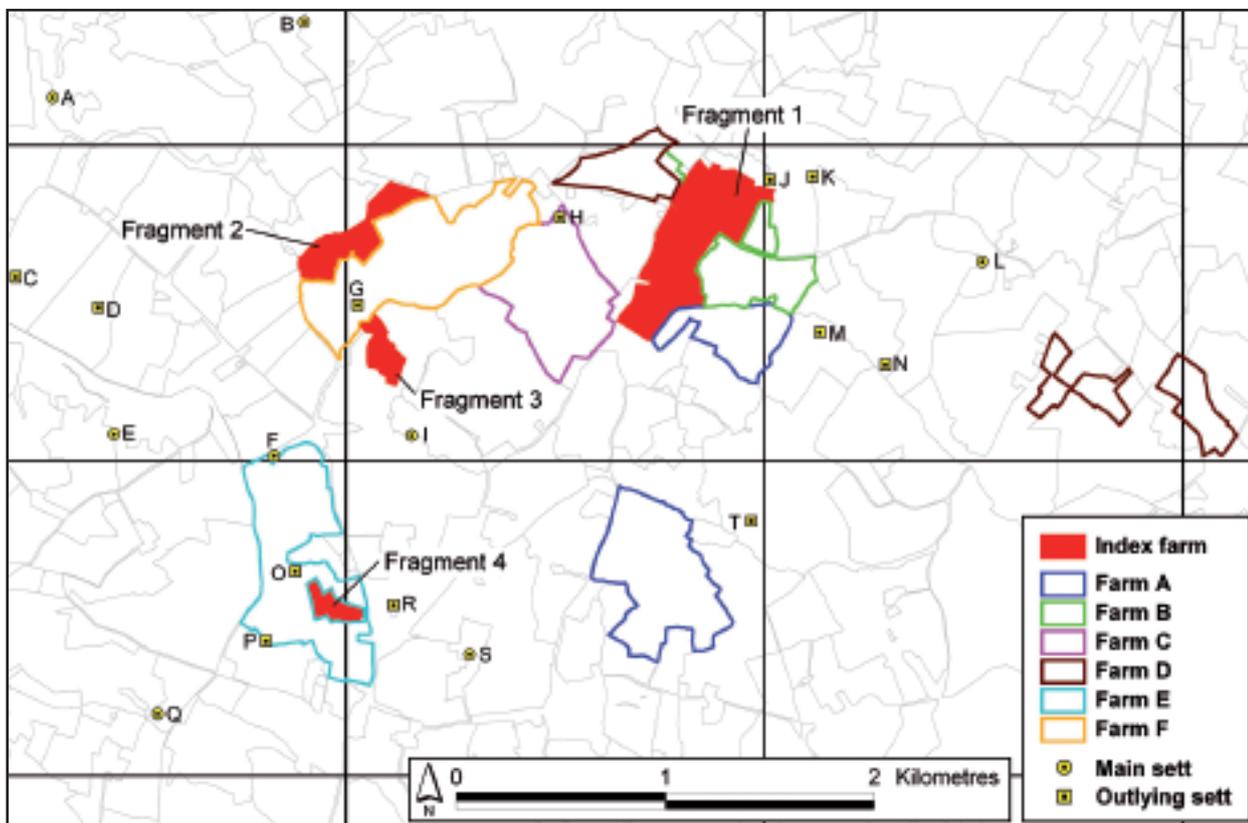
**“Although factory surveillance is not the primary method for detecting *M. bovis*-infected animals in Irish herds, it plays an important role in the early detection of infected herds and in the detection of animals that are not reactive to the tuberculin test.”**

**AN OUTBREAK OF TUBERCULOSIS AFFECTING CATTLE AND PEOPLE ON AN IRISH DAIRY FARM IN 2005, FOLLOWING THE CONSUMPTION OF RAW MILK FROM A COW WITH TUBERCULOUS MASTITIS**

Paul Doran (DAFF), Simon More (UCD CVERA), John Carson (Wexford General Hospital), Eamon Costello (DAFF)

Featured in the 'Selected reports' section

In Ireland, human infection with *M. bovis* is rare. Nonetheless, spillover of infection from cattle to people remains an ever-present possibility, given the current pool of infection in the Irish cattle population. This paper describes an outbreak of tuberculosis affecting cattle and people on a dairy farm in 2005, following the consumption of raw milk from a cow with tuberculous mastitis.



A map of the index farm, including fragments 1 (the home farm), 2 (yearling summer grazing), 3 (tillage only) and 4 (silage production, autumn grazing for calves). The location of six neighbouring farms (A to F) and local badger setts (differentiate by sett type) are also indicated

## ADDITIONAL WORK

### a. Genetics

#### GENETICS OF PREDISPOSITION TO TUBERCULOSIS IN IRISH DAIRY AND BEEF CATTLE

*Máiréad Bermingham, Donagh Berry (Teagasc Moorepark), Margaret Good (DAFF), Simon More (UCD CVERA)*

Little is known about the genetics of tuberculosis in cattle. There are several large animal- and herd-level datasets (animal breeding, disease control) in Ireland which represent an opportunity, unique internationally, to address some of these gaps in knowledge. Using these datasets, we aim to quantify the heritability (both direct and maternal heritability) for susceptibility to tuberculosis, as well as possible genetic associations with other economically important traits. The interaction between gene expression and environment will also be evaluated.

#### INNATE GENE REPRESSION ASSOCIATED WITH *MYCOBACTERIUM BOVIS* INFECTION IN CATTLE: TOWARD A GENE SIGNATURE OF DISEASE

*Meade K.G, Gormley, E., Doyle, M.B., Fitzsimons, T., O'Farrelly, C., Costello, E., Keane, J., Zhao, Y., MacHugh, D.E.*

BMC Genomics 8 (2006), 400.

The advent of high-throughput functional genomics technologies has facilitated large-scale analyses of the immune response to this disease that may ultimately lead to novel diagnostics and therapeutic targets. Analysis of mRNA abundance in peripheral blood mononuclear cells (PBMC) from six *Mycobacterium bovis* infected cattle and six non-infected controls was performed. A targeted immunospecific bovine cDNA microarray with duplicated spot features representing 1,391 genes was used to test the hypothesis that a distinct gene expression profile may exist in *M. bovis* infected animals *in vivo*. These results suggest that large-scale expression profiling can identify gene signatures of disease in peripheral blood that can be used to classify animals on the basis of *in vivo* infection, in the absence of exogenous antigenic stimulation.

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**“Gene signatures of disease can be used to classify animals on the basis of *M. bovis* infection, in the absence of exogenous antigenic stimulation.”**

### b. On-farm production

#### MODELLING THE EFFECT OF BOVINE TUBERCULOSIS ON MILK PRODUCTION

*Fiona Boland, Gabrielle Kelly (UCD Statistics), Margaret Good (DAFF), Simon More (UCD CVERA)*

There is little information on the effect of TB on milk production in dairy cattle. The purpose of this study was to develop statistical models to describe the relationship between TB infection and milk production in dairy cows.

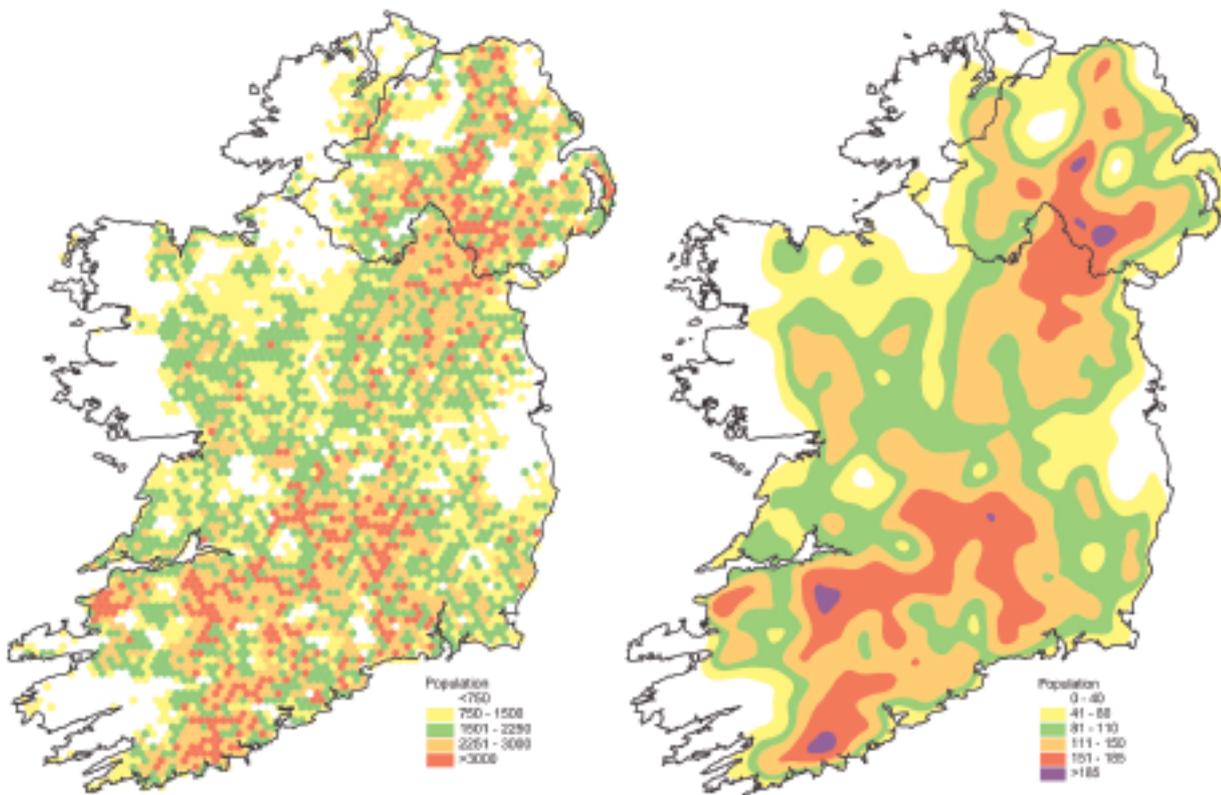
## c. Contributing to North-South collaboration

### AN ALL-ISLAND APPROACH TO MAPPING BOVINE TUBERCULOSIS IN IRELAND

Guy McGrath (UCD CVERA), Darrell Abernethy, Lesley Stringer (DARDNI, Belfast), Simon More (UCD CVERA)

Featured in the 'Selected reports' section

Bovine tuberculosis remains an important animal health issue throughout the island of Ireland. There have been similarities, but also differences, in eradication measures for this disease in Northern Ireland and the Republic of Ireland, which share a lengthy common border. The aim of this project is to use GIS to explore the spatial patterns of TB in the whole island over an 11-year period.



Representation of the TB-tested cattle population on the island of Ireland

### THE DEFINITION OF AN EPIDEMIOLOGICAL UNIT IN THE CONTEXT OF DISEASE SURVEILLANCE AND CONTROL

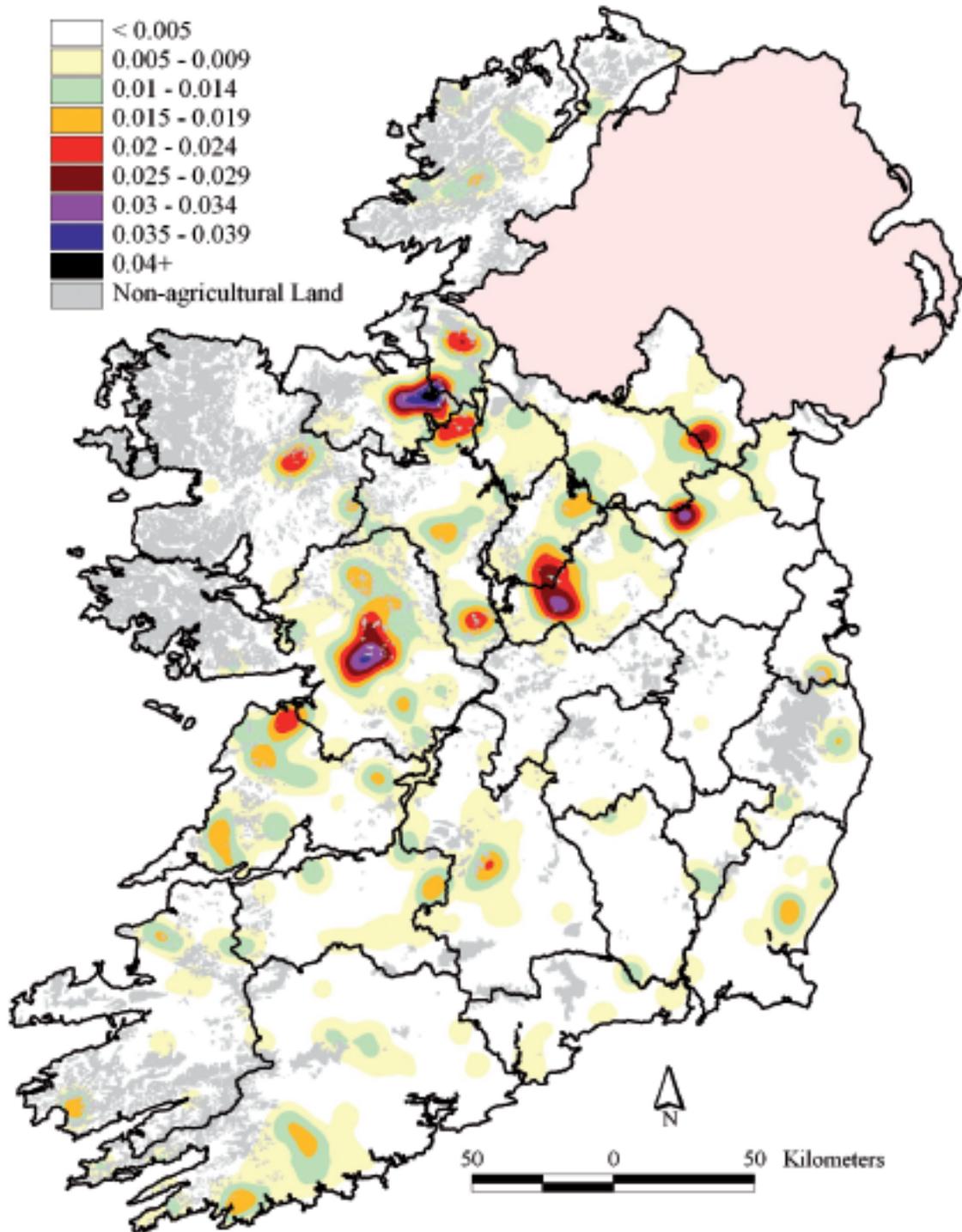
Darrell Abernethy, Fraser Menzies, Nigel Clark (DARDNI, Belfast), Simon More (UCD CVERA), Margaret Good (DAFF)

A North-South working group is seeking to address each of the following questions:

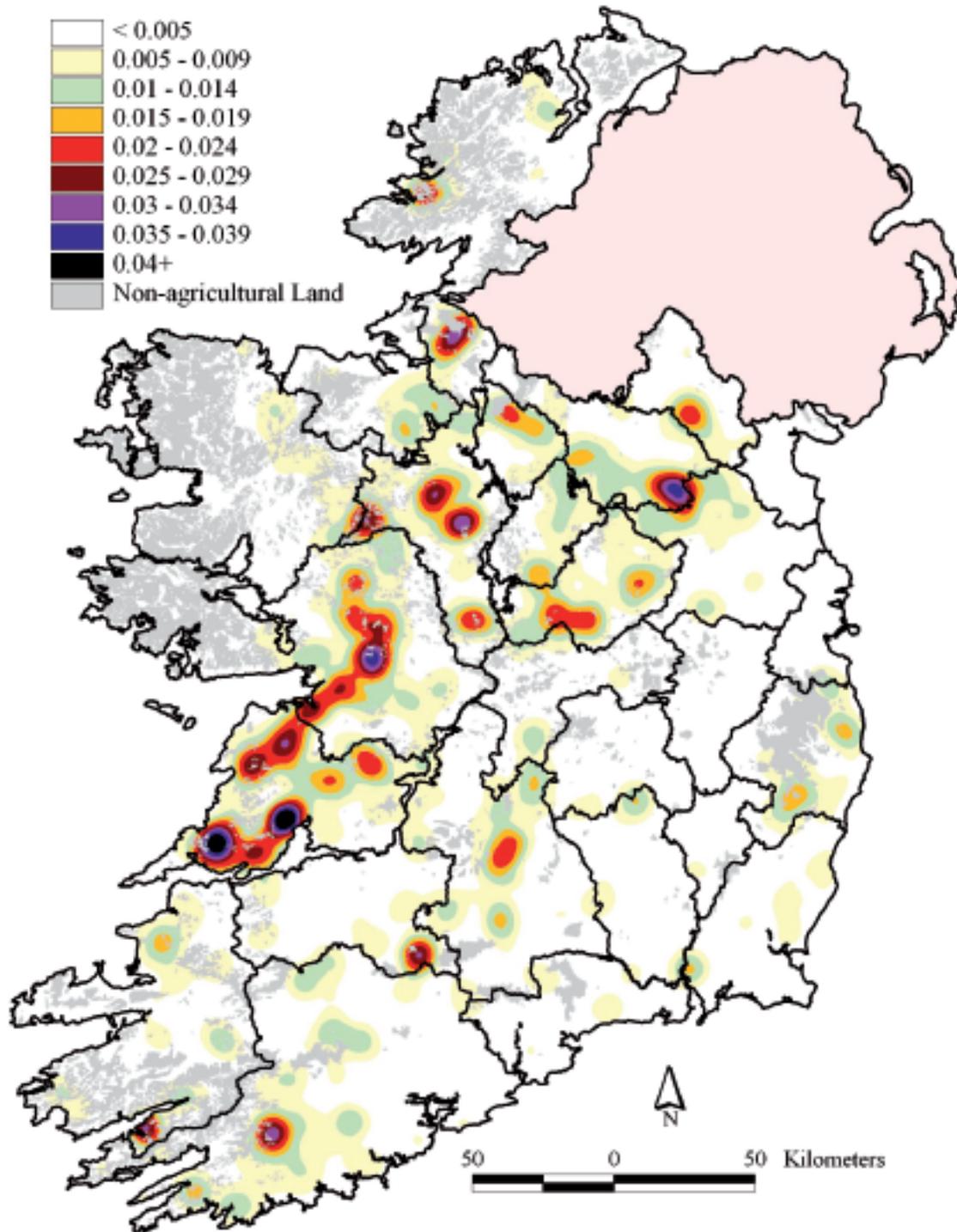
- Are 'herd' and 'epidemiological unit' synonymous?
- Do we agree with the interpretation of the EU concerning epidemiological units?
- Are Northern Ireland and the Republic of Ireland appropriately considering the concept of epidemiological units within the respective TB eradication programmes?

In other words, is herd fragmentation a constraint that has not been adequately addressed in the programmes?

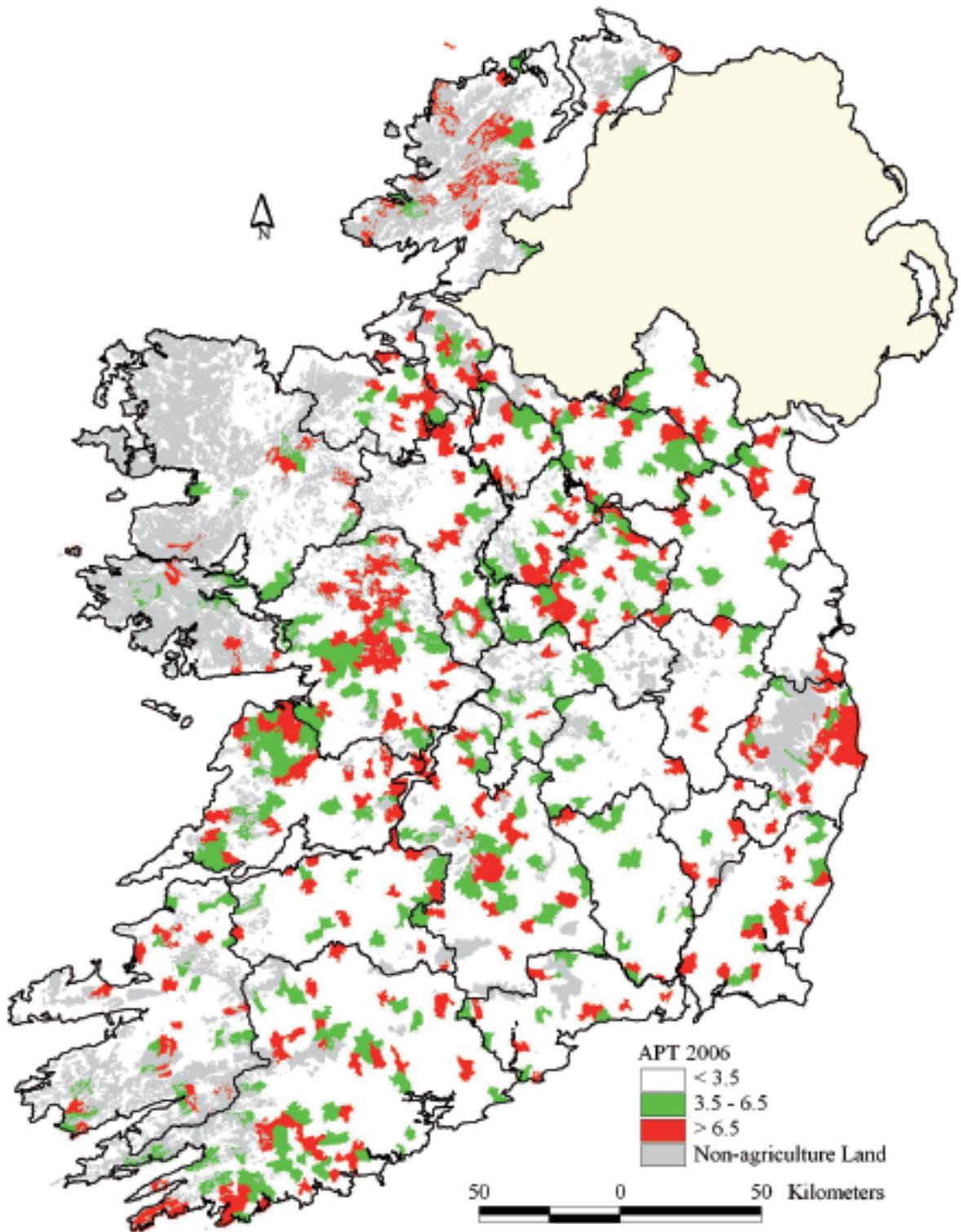
# NATIONAL MAPS



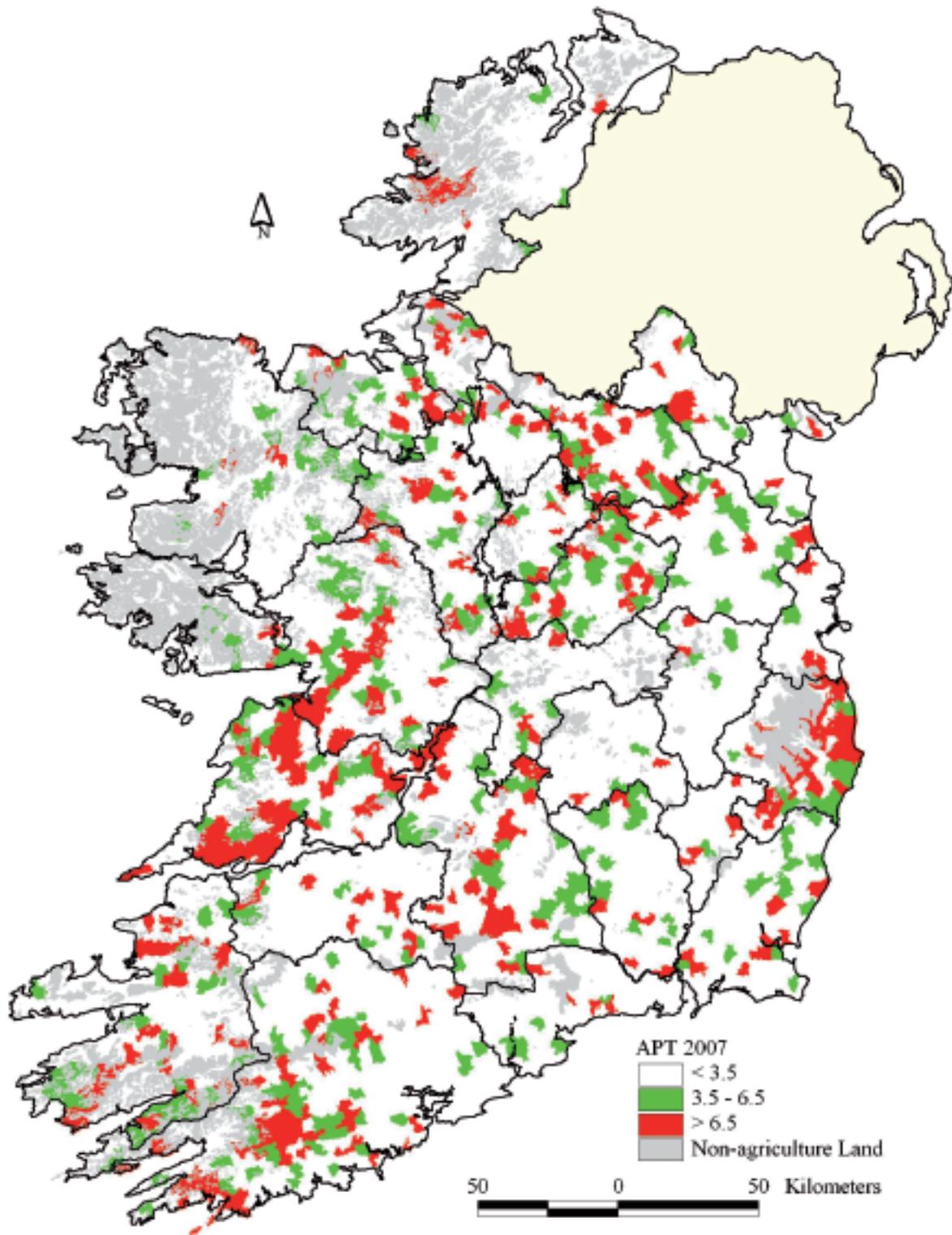
Density of TB incidence per square km during 2006 (kernel density with search radius at 10km)



Density of TB incidence per square km during 2007 (kernel density with search radius at 10km)



APT (reactors per 1000 tests) per district electoral division, 2006



APT (reactors per 1000 tests) per district electoral division, 2007





HERD HEALTH

## CHAPTER CONTENT

### HERD HEALTH

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# THE HERD HEALTH INITIATIVE

## THE HERD HEALTH INITIATIVE

*Simon More, Liz Lane (UCD CVERA), Damien Barrett (DAFF)*

Over the last 4 years, detailed discussions and briefings have been held with a wide range of bodies, including government, industry (organisations representing farmers, processors and international exporters), service providers (including veterinary organisations, Teagasc and the Irish Cattle Breeding Federation [ICBF]) and academia. There is broad acceptance of the need for Ireland to move towards a superior animal health status. There is also acceptance that this can only be achieved if all key players are willing to work cooperatively towards a shared vision.

The Herd Health Initiative (HHI) is a concept modelled on international examples of success in animal health, but adapted to Irish conditions. It aims to focus specifically on non-regulatory animal health issues, complementing existing government-led animal health programmes in Ireland. The HHI approach represents a substantial departure from the classical government-led model to animal health that currently operates in Ireland.

The HHI would focus on two key objectives, as follows:

- *Identifying what needs to be achieved over defined time-periods, in the area of non-regulatory animal health, to maximise the international competitiveness of Irish livestock and livestock products.* This would include an understanding of current practice and future trends in international best-practice, monitoring performance of Irish livestock and livestock products, consulting with all relevant stakeholders, through steering and consultative committees, and assisting in the generation of information (eg cost-benefit analyses) to assist with priority setting.
- *Developing national infrastructure necessary to enable industry, at all levels, to take appropriate and effective action in the area of non-regulatory animal health.* This would include developing and coordinating national disease control programmes (agreed rules, standard diagnostic procedures, computing infrastructure etc), leading national efforts in the delivery of coordinated, high-quality advice for farmers and industry, developing nationally-consistent resources for farmers and their advisors, supporting the development of tools for improved decision-making (benchmarking, detailed herd evaluation etc), identifying and prioritising critical research needs, and influencing relevant national decision-making (legislation, differential product pricing).

A national body is proposed, staffed by a CEO and several technical experts. It would be overseen by a small, competency-based steering committee with responsibility to formulate and monitor HHI's strategic direction and organisational management. The steering committee will report to a forum of founding stakeholders.

There is a clear interface, but no overlap, between HHI and on-farm operations. As indicated previously, the HHI will develop and coordinate the infrastructure that will be needed by industry to take appropriate and effective action. However, action-taking *per se* (that is, making use of this infrastructure with the aim to improve on-farm animal health status) will be the individual choice and direct responsibility of individual farmers, and not the HHI. It is envisaged that on-farm operations would be delivered as a routine commercial arrangement through existing advisory services (for example, Teagasc, veterinarians, etc). Participation in the various HHI programmes is expected to be voluntary. Therefore, farmers will only participate in the HHI if it makes commercial sense for them to do so, either as an individual or as part of a processor supply chain.

Negotiations are continuing.

***“What needs to be done now to maximise the international competitiveness of Irish livestock and livestock products in 5, 10 or 15 years time?”***

## A CASE FOR INCREASED PRIVATE SECTOR INVOLVEMENT IN IRELAND'S NATIONAL ANIMAL HEALTH SERVICES

*Simon More (UCD CVERA)*

Ireland may need to broaden the scope of its national animal health services, given the increasing importance of non-regulatory animal health issues in global markets in animals and animal products. However, there have been concerns about the respective roles and responsibilities (both financial and otherwise) of government and industry in any such moves. This study argues the case for increased private sector involvement in Ireland's national animal health services, based both on theoretical considerations and country case studies (the Netherlands and Australia).

## OPPORTUNITIES FOR IRISH FARMERS TO SHAPE THEIR FUTURE IN A GLOBAL TRADING ENVIRONMENT

*Simon More (UCD CVERA)*

Irish Farmers Journal, 10 March 2007.

Globalisation is driving fundamental change in Irish agriculture. Irish farmers can no longer compete globally on price alone, but must re-focus their efforts towards the quality and safety of their products. Animal health, through its impact on product quality and safety, will play a central role in positioning Ireland as a serious global player. Further, animal health is an important contributor to on-farm profitability, with improvements in health status offering the potential for substantial financial gains. With increasing globalisation, the ability of Irish farmers to shape their own future in the longer-term will largely be determined by decisions they make now.

Globalisation presents Irish agriculture with both opportunities and challenges. On the positive side, Irish agricultural exports are a major contributor to the national economy. In 2004, for example, Ireland was the third largest global exporter of butter and cheese and the seventh largest exporter of beef, by value. On the negative side, declining returns from meat and milk can be directly linked to global trading pressures. In such a competitive international trading environment, exporting countries such as Ireland have the option to differentiate their products on the basis of price on the one hand and/or safety and quality on the other. As a result of the ongoing economic boom in this country, however, it will become increasingly difficult for Ireland to compete on price alone. Therefore, Irish agriculture has no choice but to focus on the issues of safety and quality, and to differentiate with competing countries on that basis.

Animal health is an important contributor to product safety and quality. In addition, animal health is afforded special (indeed, unique) consideration in global agricultural trade. Under the SPS (Sanitary and Phytosanitary) Agreement of the World Trade Organization, countries are fully-entitled (with reasonable checks and balances) to protect the superior health status of their own livestock. The recent outbreak of foot and mouth disease in the UK illustrates the damage that can be done following the introduction of an exotic disease, through legal trade or otherwise. For these reasons, Irish agriculture has much to gain from efforts towards a superior health status for the national herd. These efforts, in the longer term, would benefit on-farm profitability as well as contributing to the international competitiveness of Irish product.

To this point, animal health programmes have mainly been managed by the national Department of Agriculture, Fisheries and Food. As a result of these efforts, there has been substantial progress towards eradication of brucellosis and the resolution of the BSE issue. While there has been only limited progress towards eradication of bovine tuberculosis, Ireland is leading international efforts towards a practical solution to problems caused by an infected wildlife reservoir.

At this time, it is appropriate to re-evaluate the role of government in animal disease control programmes. BSE, tuberculosis and brucellosis are each diseases of public health significance, and a role for government has been appropriate. However, further efforts towards superior health status would likely focus on health conditions that are related to trade, production and welfare, including Johnes' disease, IBR, BVD, mastitis, lameness and fertility. Efforts to control these conditions will lead to substantial benefit to industry, but generally very limited benefit to the broader public. For this reason, new approaches to the national management of animal health should be considered, based on a genuine partnership between industry and government, but with industry providing the lead. Industry and government each bring their own strengths and perspectives, with industry contributing pragmatism, on-the-ground commitment and immediacy towards the problem-at-hand. Further, the separate financial contributions of industry and government ('cost-sharing') to animal disease control should genuinely reflect the relative benefits that separately flow to industry and the broader public. For animal diseases where there is a significant threat to the health of the general public, such as brucellosis, it is reasonable for government to contribute, say, 50% of the costs of disease control. For diseases such as IBR, however, where improved control would primarily benefit industry, this level of government financial support to control costs may not be justified. This approach has been widely adopted by key agricultural competitors, including the Netherlands and Australia. In these countries, industry is now the driving force in long-term planning, coordinated action and continuous improvement of animal health issues. The experience of these, and other, countries offers valuable lessons (both technical and non-technical) that may also be relevant to Ireland. In order for such partnerships to be effective, roles and responsibilities (both financial and otherwise) must be clear. In my view, it is the role of industry to lead, to transform and to innovate, and of government to create the environment to enable this to happen.

The international trading environment will create ongoing 'turbulence' and uncertainty for some time. Regardless, opportunities are certainly available to enable the Irish industry to shape its own future in terms of animal health. The current period offers a window of opportunity, and it is very important that industry and government each take the hard decisions to enable industry to transform into a confident and effective global player.

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## SHAPING OUR FUTURE: ANIMAL HEALTH IN A GLOBAL TRADING ENVIRONMENT

More, S.J.

Irish Veterinary Journal 60 (2007), 541-549.

Irish farming is facing a period of unprecedented change, in large part due to the increasing globalisation of agriculture. The long-term viability of Irish agriculture is dependent on the ability of industry to maximise on-farm profitability, and to effectively compete in a global trading environment. With increasing competition, particularly from low-cost countries, the quality and safety of Irish product will become increasingly important. Animal health is an important contributor to this, as a result of the impact (perceived or otherwise) of animal disease on product quality, and because of the special importance of animal health in international trade. This paper, based on a presentation to the Animal and Plant Health Annual Conference in Killenard on 12 September 2006, examines three related questions relevant to these issues, including:

- Whether Ireland is achieving international best-practice in key areas of animal health?
- If not, whether it matters?
- What can we learn from experiences elsewhere?

The paper highlights a range of issues associated with international best-practice in animal health. A national Herd Health Initiative (HHI) is proposed, to provide focus, leadership and coordination of all non-regulatory animal health issues in Ireland, through a cooperative partnership between all relevant stakeholders.

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***“The long-term viability of Irish agriculture is dependent on the ability of industry to maximise on-farm profitability, and to effectively compete in a global trading environment.”***



Ewes with lambs for the Spring market

## FERTILITY

### MAKING FERTILITY RECORDS TALK

*Liz Lane (UCD CVERA)*

Featured in the 'Selected reports' section

The analysis of herd management records allows for accurate assessment of the current status of the herd, a crucial decision making tool to implement effective change. Monitoring of such changes to ensure their effectiveness is essential to the success of any programme, while participation in discussion groups allows for peer comparisons, a key factor in motivating herd management change. The aim of this review is to evaluate the effectiveness of fertility reports to improve dairy herd performance.

### KEY FACTORS AFFECTING DAIRY COW FERTILITY IN IRELAND

*Liz Lane (UCD CVERA), Mark Crowe (UCD Agriculture, Food Science and Veterinary Medicine), Brian Wickham (ICBF), Simon More (UCD CVERA)*

Intensively managed dairy herds must achieve fertility targets to ensure long-term economic viability. The costs associated with poor fertility have been highlighted in many studies. Integrated computerised programmes for fertility, health and production facilitate herd management. The analysis of herd management records is critical to efforts by farmers and their advisers to assess current herd status, to identify opportunities for improvement and to monitor change. This programme of work aims:

- to optimise the fertility reports of the Irish Cattle Breeder Federation's (ICBF) database to ensure their usefulness to farmers as a herd management decision making tool,
- to evaluate the reproductive efficiency of the national dairy herd utilizing this database and to determine the key drivers of lowered fertility in the national herd,
- to correlate production and management strategies with reproductive performance, and
- to monitor the impact of changes in herd management on the reproductive performance of Irish dairy herds.

## MASTITIS

### A STUDY OF DRY COW THERAPY AND EFFECTS ON SCC IN 10 IRISH DAIRY HERDS

*Barrett, D.J., Clegg, T.A., Healy, A.M., Doherty, M.L.*

Journal of Veterinary Medicine Series A 53 (2006), 140-144.

Somatic cell count (SCC) data for 480 cows in 10 Irish dairy herds from January 2001 to June 2002 were analysed. Herds were selected on the basis of a recent or ongoing history of clinical or subclinical mastitis. An individual cow SCC of 200,000 cells per ml was used as the threshold for elevation of SCC. The duration of elevated SCC prior to drying-off and the magnitude of the elevation in SCC were found to have an impact on the response to dry cow therapy (DCT). A trend also emerged indicating that increasing parity had a negative influence on the response to DCT.

*Printed with permission from Blackwell Publishing.*

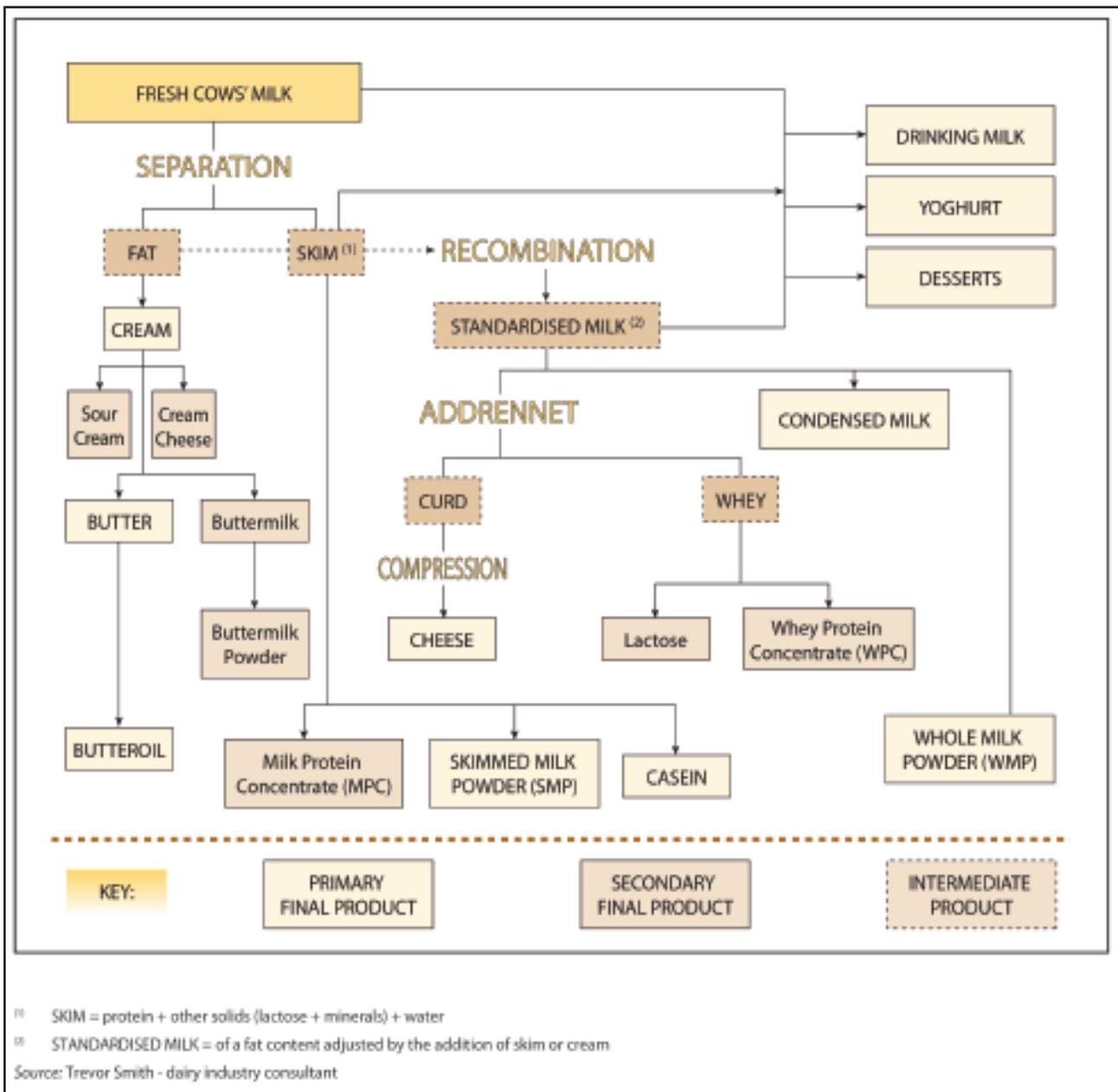
**“Response to dry cow therapy was reduced by both the duration and extent of infection, as measured by SCC.”**

**GLOBAL TRENDS IN MILK QUALITY: IMPLICATIONS FOR THE IRISH DAIRY INDUSTRY**

Simon More (UCD CVERA)

Featured in the 'Selected reports' section

The quality of Irish agricultural products will become increasingly important, with the ongoing liberalisation of international trade. This study presents a review of the global and Irish dairy industries, considers the impact of milk quality on farm profitability, food processing and human health, examines global trends in quality and explores several models that are successfully being used to tackle milk quality concerns.



The conversion of milk, by a range of processes, into a variety of dairy products and food ingredients.  
 From Anon., 2006a

### A STUDY OF FACTORS AFFECTING BULK MILK SOMATIC CELL COUNT ON IRISH DAIRY FARMS

*Paddy Kelly, Bernadette O'Brien, Donagh Berry (Teagasc Moorepark), Simon More (UCD CVERA)*

Ireland is a major exporter of dairy products, and the quality of this product is very important. Based on recent analysis of bulk tank SCC samples from dairy suppliers, there has been an annual increase of 6,000 cells/mL since 2000. This study will examine the impact of farm management factors on national milk quality and individual Irish dairy farm profitability.

### A CRITICAL EVALUATION OF FARM-LEVEL MILK QUALITY, BASED ON MILK RECORDING DATA

*Tracy Clegg, Simon More (UCD CVERA), Luke O'Grady (UCD Agriculture, Food Science and Veterinary Medicine)*

Milk recording is conducted on approximately 6,000 Irish dairy herds, on a regular basis. This represents approximately 30% of dairy herds but 50% of dairy cows. Using this resource, which is managed by ICBF, this study seeks to quantify milk quality parameters and to identify factors associated with high, and low, milk quality performance.



Within-parlour transmission is a common source of infection leading to new cases of mastitis on Irish dairy farms

# JOHNE'S DISEASE

## THE ECONOMIC IMPACT OF JOHNE'S DISEASE IN AN IRISH DAIRY HERD: A CASE STUDY

*Barrett, D.J., Good, M., Hayes, M., More, S.J.*

Irish Veterinary Journal 59 (2006), 282-288.

A case study of the economic impact of Johne's disease in an Irish dairy herd is described. An epidemiological investigation concluded that the purchase of 20 heifers from the Netherlands in 1993 introduced Johne's disease to the herd. The practice of feeding pooled colostrum/milk was considered to have disseminated *Mycobacterium avium* subspecies *paratuberculosis* widely within the herd. Performance between 1993 and 2003 declined substantially, as a result of reduced milk yields, increased culling and reduced cull cow values. This in turn reduced the profit margin per litre of milk sold and per cow. The performance of this herd relative to peers also deteriorated over the study period. Performance had been superior to peers until the late 1990's, but had markedly worsened by 2002.

*Printed with permission from the Irish Veterinary Journal.*

**“Herd performance was adversely affected by the presence of Johne's disease.”**

## POST HOC ASSESSMENT ON EXTERNAL VALIDITY AND PRECISION OF FIELD SAMPLES USED TO SURVEY THE IRISH CATTLE POPULATION FOR JOHNE'S DISEASE

*Esther Richardson (Teagasc Moorepark), Margaret Good (DAFF), Guy McGrath, Simon More (UCD CVERA)*

Featured in the 'Selected reports' section

We generally rely on a sample, rather than a census, to gain an understanding of characteristics of animal populations. The value of the sample as a reflection of the population of interest is measured in terms of external validity and precision. This study is being conducted to assess the external validity and precision of field data, following collection of serum samples from 1,000 herds to investigate the sero-prevalence of Johne's disease in Irish cattle.

## PREVALENCE AND DISTRIBUTION OF PARATUBERCULOSIS (JOHNE'S DISEASE) IN CATTLE HERDS IN IRELAND

*Margaret Good (DAFF), Simon More (UCD CVERA), Damien Barrett, Hazel Sheridan, Peter Mullaney (DAFF)*

Johne's disease has been a scheduled and notifiable disease in the Republic of Ireland since 1955. It was uncommon prior to the mid 1990's, but has since increased with the introduction of the Single European Market, facilitating the free movement of goods and services within the EU. In this study, we are seeking to estimate the prevalence and distribution of paratuberculosis (Johne's disease) in cattle herds in Ireland.

## CATTLE MOVEMENTS INTO AND OUT OF JOHNE'S INFECTED SUCKLER HERDS IN IRELAND

*Peter Mullaney, Damien Barrett, John Egan (DAFF), Richie Fallon (Teagasc Grange), Martin Blake (DAFF), Simon More, Tracy Clegg (UCD CVERA), Margaret Good (DAFF)*

In the period 2002 to 2006, a total of 96 beef suckler herds submitted faecal samples to the Central Veterinary Research Laboratory, which yielded a culture positive result for *Mycobacterium avium* subspecies *paratuberculosis* (MAP). Movements into and out of these herds are being analysed and compared with those from a control group of suckler herds.

### A CASE-CONTROL STUDY OF RISK FACTORS FOR PARATUBERCULOSIS (JOHNE'S DISEASE) IN IRISH DAIRY HERDS

*Damien Barrett (DAFF), John Mee (Teagasc Moorepark), Margaret Good (DAFF), Simon More, Guy McGrath, Tracy Clegg, Daniel Collins (UCD CVERA)*

The increased prevalence of paratuberculosis in Ireland is linked, at least in part, to the introduction of the Single European Market. There is little published work on paratuberculosis in Ireland, and none examining risk factors for paratuberculosis incidence in Irish dairy herds. This work seeks to fill this gap in knowledge, and to contribute to a national response to paratuberculosis in the Irish dairy industry. Therefore, the objectives of this study are to identify risk factors associated with the occurrence of paratuberculosis in Irish dairy herds.

### A STUDY OF CATTLE MOVEMENT PATTERNS IN 200 IRISH DAIRY HERDS

*Damien Barrett (DAFF), Isabella Higgins, Tracy Clegg (UCD CVERA)*

The trade and movement of cattle is one of the main mechanisms of introducing disease into cattle herds. Animal movement has the potential to bring infected animals in contact with non-infected animals, and in so doing facilitates the introduction of disease. At its peak, the bovine population of Ireland consisted of over 7.2 million animals in 121,000 herds. In 2004, there were over 1.5 million mart movements and 800,000 farm to farm movements recorded by the Cattle Movement Monitoring System (CMMS). The mart movements included 103,000 movements where the animal was unsold in the mart. The objective of this study is to characterise the animal demographics in the study herds.

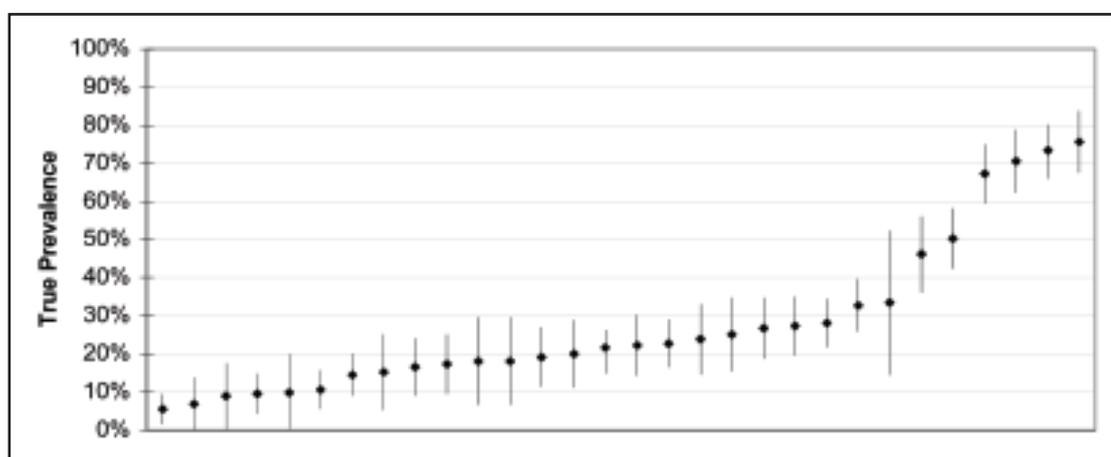
## INFECTIOUS BOVINE RHINOTRACHEITIS (IBR)

### HERD AND WITHIN-HERD IBR PREVALENCE AMONG HERDS THAT SUBMITTED BULLS FOR ENTRY TO A PERFORMANCE TESTING STATION IN IRELAND

*Luke O'Grady (UCD Agriculture, Food Science and Veterinary Medicine), Rónan O'Neill (DAFF), Simon More, Isabella Higgins, Daniel Collins, Tracy Clegg (UCD CVERA)*

Featured in the 'Selected reports' section

Despite its increasing importance in the export of live cattle and semen, there is little information about the epidemiology of IBR in Ireland. In this study, we determine the herd and within-herd IBR prevalence among herds submitting bulls for entry to a performance testing station in Ireland.



The within-herd true IBR prevalence for 30 infected study herds in Ireland during November 2007. The prevalence estimate and 95% confidence limits for each herd are represented by a dot and vertical line, respectively

# A DETAILED FARM INVESTIGATION

## SHORTFALLS IN PRODUCTION ON AN IRISH DAIRY FARM – AN INVESTIGATION DURING WINTER 2006 TO 2007

*Liz Lane, Mary Canty, Guy McGrath, Simon More (UCD CVERA)*

Serious shortfalls in the performance of cattle on a dairy farm (index farm) have been identified. Milk production of dairy cows is between 30 to 50% less than expected when compared with the national average, while growth rates of young cattle on the index farm are much lower than expected, with animals achieving a significantly smaller stature and lower weights than expected for similar production systems. Young growing animals (up to 2 years of age) and cows are predominately affected. Growing cattle are expected to achieve an average growth rate of 0.75 kg per day; however, weight gains on the index farm vary dramatically throughout the growing period. Periods of time have been identified when the majority of young animals on the farm are reported to exhibit very poor or negative growth rates. Visits to a number of farms have indicated that at least two additional farmers, in the immediate area, believe they have experienced similar problems.

The aetiology of the poor performance on the index farm remains uncertain, despite intensive investigation. Disease, both clinical and sub-clinical, management and nutrition have each been suggested as potential causes or contributors to the problem. The aim of this project is to elucidate the underlying mechanisms of poor performance in growing animals on this farm, thereby providing clues about the cause of ongoing problems that are being observed. The project will critically examine the performance of cattle, and of underlying mechanisms of performance, including nutrition, disease, immunocompetence, and endocrinological control of growth and metabolism, during winter 2006 to 2007. These results will be compared, between farms (the index and another farm in the general locality), between cattle (animal raised on the index farm and animals purchased from an unaffected farm) and over time. Temporal relationships between animal performance and environmental conditions (weather, pollution) will be examined. A proportion of the animals from this trial will then be evaluated for growth rate, and blood parameters at intervals following on from the intensive period of the trial.

To broaden the scope of this programme of work, the location and identification of mineral deficiencies and excesses in soil and plants will be correlated with animal samples, as the prediction of herd mineral status using pasture and/or soil analysis without reference to prior animal testing can be unreliable. Soil and herbage sampling surveys will be conducted at two discrete time points, at the start and end of the 2007 grass growing season, using pre-determined sampling points from the national grid with the index farm as the centre of the grid. The aim is to:

- produce point maps of heavy metals, major elements and trace elements;
- determine if these parameters change over time; and
- establish their effects on animal nutrient requirements.

HERD HEALTH





OTHER ANIMAL HEALTH ISSUES

## CHAPTER CONTENT

### OTHER ANIMAL HEALTH ISSUES

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- 60 Miscellaneous

## BRUCELLOSIS

### AN EVALUATION OF IRISH CATTLE HERDS WITH INCONCLUSIVE SEROLOGICAL EVIDENCE OF BOVINE BRUCELLOSIS

*Martin Hayes, Seán Ashe (DAFF), Daniel Collins, Simon More (UCD CVERA), Séamus Power, Kevin Kenny, Michael Sheahan, Garry O'Hagan (DAFF)*

There is concern that the interpretation of serological results may become increasingly problematic, as brucellosis prevalence falls in Ireland. This study seeks to clarify the infection status of Irish herds and animals where serological results are inconclusive.

### AN EVALUATION OF POLICY OPTIONS, INCLUDING CHANGES TO THE PRE-MOVEMENT TEST, WITHIN THE NATIONAL BRUCELLOSIS ERADICATION PROGRAMME

*Seán Ashe, Martin Hayes, Brendan Walsh, Rob Doyle (DAFF), Simon More (UCD CVERA)*

It is prudent to review current eradication strategies, including the use of pre-movement testing (currently, all breeding cattle over 12 months of age), as brucellosis prevalence continues to fall in Ireland. In this study, we are using quantitative risk assessment methodology to evaluate the impact of a range of policy changes on the probability of new disease outbreaks.

### AN OUTBREAK OF BOVINE BRUCELLOSIS IN COUNTY CLARE, DURING 2005

*Martin Hayes, Ascinta Kilroy (DAFF), Simon More (UCD CVERA), Seán Ashe, Séamus Power (DAFF)*

In the latter stages of the national brucellosis eradication programme, information from epidemiological field investigations provides an opportunity to continually evaluate the effectiveness of existing disease control measures. This study describes an investigation of an outbreak of bovine brucellosis in a locality in County Clare, Ireland, during 2005.

## EQUINE INFECTIOUS ANAEMIA

### EQUINE INFECTIOUS ANAEMIA IN IRELAND DURING 2006

*Simon More, Inma Aznar (UCD CVERA), Pat Brangan, John Larkin, Dorothy Bailey, Tom Myers, Pat Lenihan, Brian Flaherty (DAFF), Des Leadon (Irish Equine Centre)*

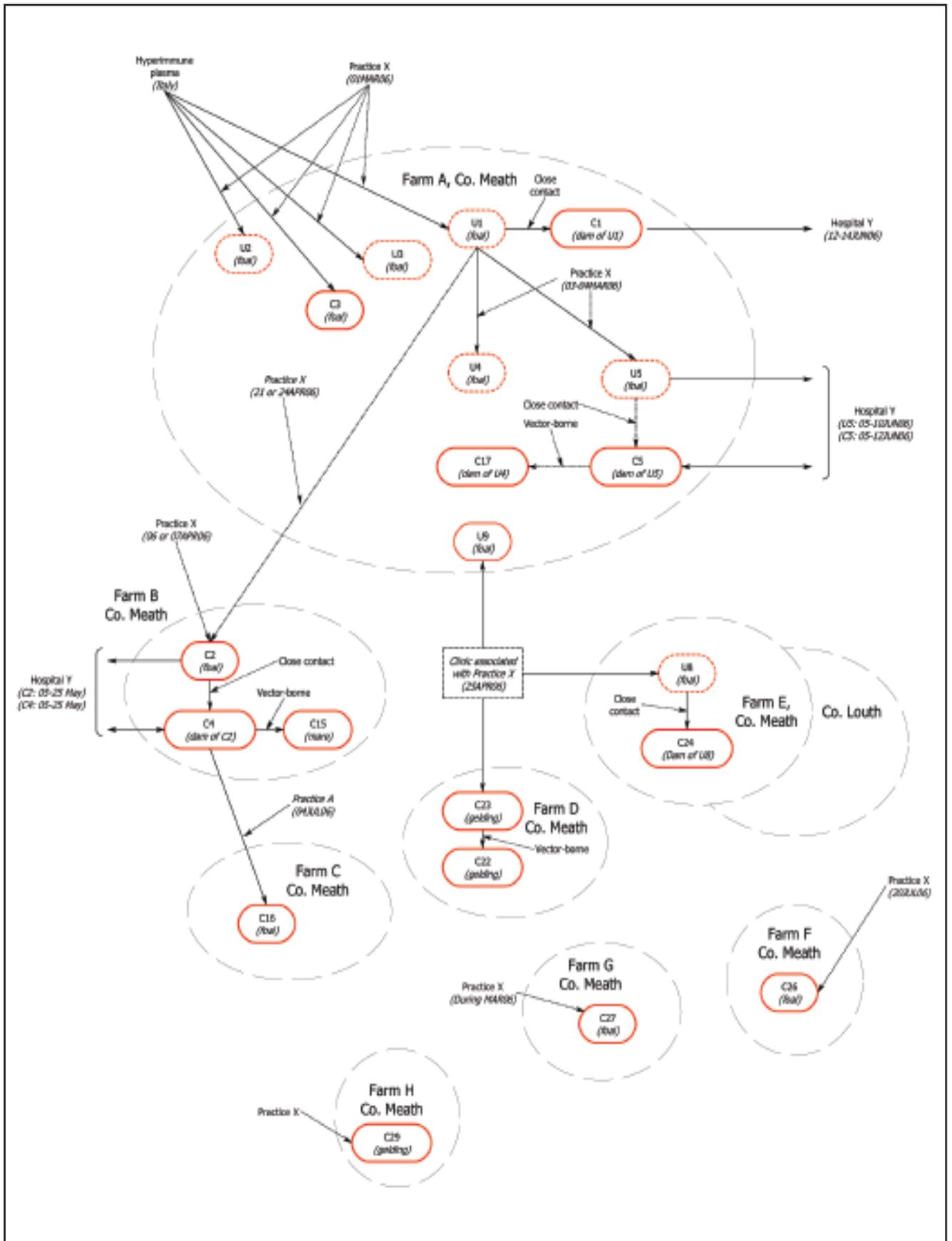
Featured in the 'Selected reports' section

Equine infectious anaemia (EIA) was confirmed in Ireland on 15 June 2006. Over the following six months, until 10 December 2006, a total of 38 EIA cases were identified. This was the first outbreak of this disease in Ireland with evidence of transmission of infection. A detailed epidemiological investigation has been undertaken, with the following objectives:

- To provide an overview of the outbreak, the national response (control and eradication strategies, resource issues, linkages with industry and the international community) and lessons learned;
- To determine the source of infection and modes of transmission;
- To address aspects of the diagnosis and clinical presentation; and
- To report the results of an investigation of nosocomial transmission within an equine veterinary hospital.



A mare (case 17) that was infected during the 2006 EIA outbreak in Ireland



Probable transmission linkages between cases in cluster X during the 2006 EIA outbreak in Ireland

## TSEs

### A QUANTITATIVE ASSESSMENT OF BSE RISK IN STORAGE FACILITIES FOLLOWING MBM REMOVAL AND CLEANING

*Inma Aznar, Simon More (UCD CVERA), John Griffin, John Mullen (DAFF)*

The Irish slaughter sector produces approximately 150,000 tonnes of animal by-product (raw offal and bone) per year. From 2000 until 01 June 2003, DAFF subsidized the rendering of animal by-products into meat and bone meal (MBM), and the subsequent storage of approximately 172,000 tonnes of MBM, awaiting disposal. The objective of the study was to assess the bovine spongiform encephalopathy (BSE) risk posed to cattle from several of these facilities, following MBM removal and cleaning.

#### NATIONAL MAPS

2006



The location of confirmed BSE cases in Ireland during 2006

2007



The location of confirmed BSE cases in Ireland during 2007

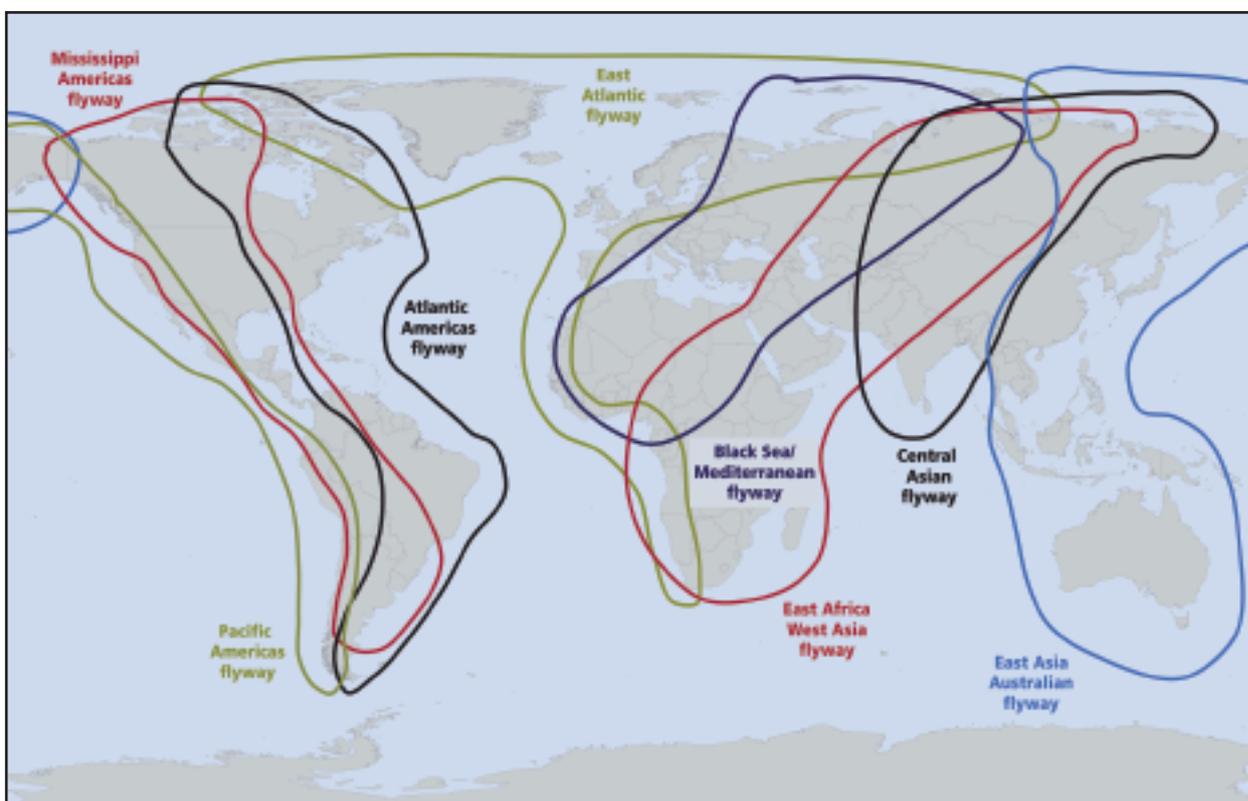
## AVIAN INFLUENZA

### A REVIEW OF IRELAND'S WATERBIRDS, WITH IMPLICATIONS FOR THE INTRODUCTION AND SPREAD OF H5N1 AVIAN INFLUENZA INTO IRELAND

*Olivia Crowe (Birdwatch Ireland), John Wilson (National Parks and Wildlife Service), Inma Aznar, Simon More (UCD CVERA)*

Featured in the 'Selected reports' section

Ireland is characterised by a wide variety and a large abundance of wetlands, making it attractive to waterbirds throughout the year. As such, Ireland has a diverse range of waterbirds, the majority of which are at least partially migratory. This paper presents an overview of Ireland's waterbirds, including ecological factors relevant to the potential introduction, maintenance, transmission and spread of infectious agents, including the H5N1 avian influenza virus, in Ireland. Particular emphasis is placed on five groups of wintering migrants (dabbling and sieving wildfowl, grazing wildfowl, diving wildfowl, waders and gulls), noting that the H5N1 avian influenza virus has mainly been isolated from this subset of waterbirds.



Global flyways. "Flyways: Wetlands International. Compiled by FAO AGAH, EMPRES programme. FAO 2005. All rights reserved"

### ASSESSING THE RISK OF INTRODUCTION AND SUBSEQUENT SPREAD OF H5N1 AVIAN INFLUENZA IN IRELAND BY MIGRATORY WATERBIRDS

*Inma Aznar, Simon More, Guy McGrath, Daniel Collins (UCD CVERA), Olivia Crowe (Birdwatch Ireland), John Wilson (National Parks and Wildlife Service)*

A qualitative risk assessment is being conducted to assess the risk of introduction and subsequent spread of H5N1 avian influenza in Ireland by migratory waterbirds. The work is being conducted in two parts:

- The risk of entry is being examined based on the probability that H5N1-infected migratory waterbirds will enter Ireland; and
- The risk of subsequent spread based on the probability of H5N1 being spread to the Irish commercial poultry industry, following entry of infected waterbirds.

# FOOT AND MOUTH DISEASE

## INTERNATIONAL MODELLING COLLABORATION (THE QUADS GROUP)

*Jarlath O'Connor (DAFF)*

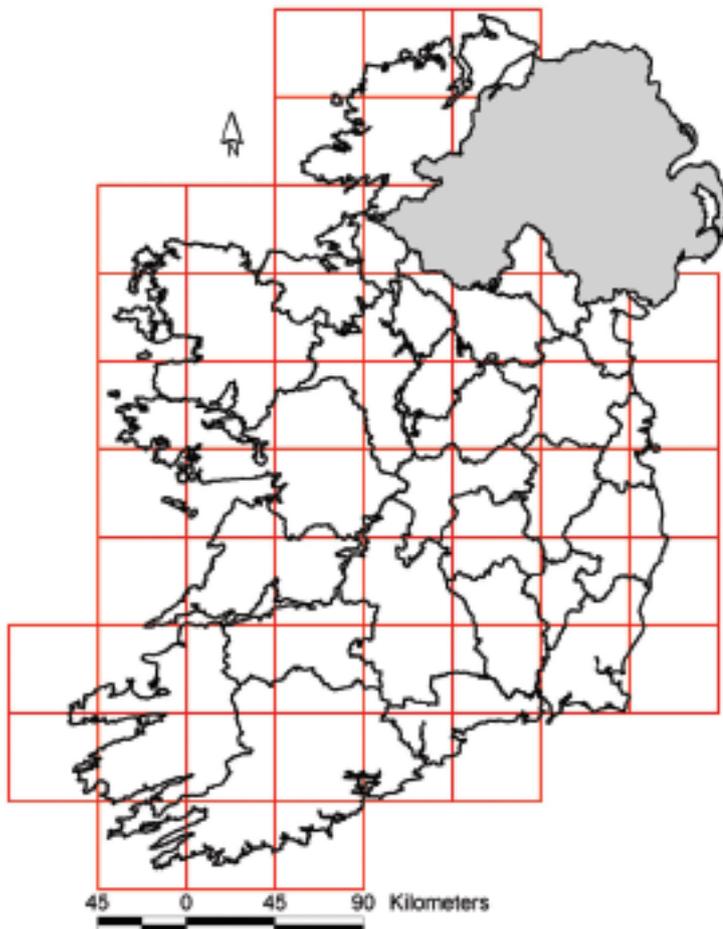
DAFF has become actively involved in disease modelling as a member of the Epitask of the Quadrilateral (QUADS) countries (Australia, Canada, New Zealand, United States), plus Ireland and the United Kingdom. The primary focus of the current work programme is a comparison of the efficacy of a number of FMD models based on common scenarios. The practical implications of DAFF's involvement are to allow for development of expertise in modelling and to assist in international collaboration on disease outbreaks.

# BLUETONGUE

## ACTIVE SURVEILLANCE FOR BLUETONGUE IN IRELAND

*Guy McGrath, Tracy Clegg, Inma Aznar (UCD CVERA), Dónal Sammin (DAFF)*

Based on events in western Europe since August 2006, concern has been raised about the possible spread of bluetongue to Ireland. An active programme of bluetongue surveillance commenced in Ireland in early 2007. In line with European Union recommendations, a sampling grid is being used to guide sample collection.



The 45 x 45km sampling grid that is being used during the active bluetongue surveillance programme

## NATIONAL *CULICOIDES* SURVEY

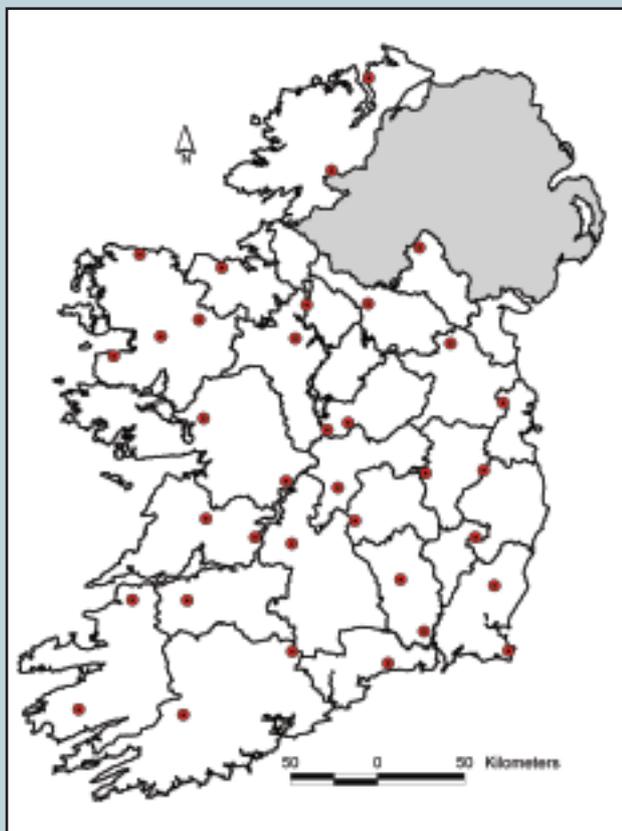
Guy McGrath, Inma Aznar (UCD CVERA)

### Background

In recent years, there have been incursions of the bluetongue virus (BTV) into temperate countries of Europe. This was initially believed to be exclusively as a result of global warming and milder winters, enabling the vector *Culicoides imicola* to extend its viable range from North Africa and the Mediterranean into more temperate areas. However, it has become evident that BTV is being acquired and transmitted in these cooler regions through the *C. obsoletus* complex, a species of *Culicoides* not previously associated with the spread of BTV (Caracappa *et al.*, 2003, Savini *et al.*, 2005). The range of *C. obsoletus* extends over most of central and Northern Europe. The limiting factor for the spread of BTV is therefore no longer the range of the vector but the virus' ability to replicate and disseminate in cold conditions. This has resulted in larger scale outbreaks of greater severity and longevity than those associated with *C. imicola* incursions. In September 2007, the UK reported its first suspected case of BTV, in a Highland cow on a farm for rare cattle breeds near Ipswich, Suffolk. The virus subsequently spread from cattle to sheep. Little is known about the distances *C. obsoletus* can travel, but it is believed that in certain climatic conditions *Culicoides* could passively travel several hundred kilometres (Ducheyne *et al.*, 2007). In light of this, Ireland is at considerable risk of being exposed to BTV and subsequently harbouring an epidemic. Large numbers of *Culicoides* are present in Ireland but very little is known about the true population in terms of its abundance and seasonality. The aim of this study is to establish suitable sampling locations to assist in the modelling of the spatial and temporal patterns of *Culicoides* populations in Ireland.

### Methods

In order to build a robust predictive model for determining how habitat influences the population of *Culicoides*, the selection of sample points should be random. This excludes the introduction of bias by manually selecting sample sites based on observed habitat types. The only rule used in the selection process was that sample points must be on farmed land. This was decided to ensure access to sample site locations and to allow for corresponding BTV serology surveillance on the animals in the associated farms. 50 points were randomly assigned to the area of the Republic of Ireland using ArcGIS 9.1 (ESRI, Redlands, CA, USA). Of these 50 points, 35 were located on farms with livestock and were therefore considered suitable for this study. These 35 points represented a diverse range of habitats. Habitat variables defined in these sample site locations can be used to develop a multivariate predictive model. Sampling sites were established in these locations and count data of *Culicoides* caught in light traps were observed using established methodologies (Goffredo *et al.*, 2004). These data are still being acquired. Additional survey points will be selected manually to validate the preliminary estimates on contribution of different habitat variables to population numbers. These data will be published as a PhD thesis through the NUI, Galway, Ireland in 2009.



Sampling points for the national *Culicoides* survey

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## POPULATION STUDIES

### SURVIVAL AND DISPERSAL OF A DEFINED COHORT OF IRISH CATTLE

*Seán Ashe (DAFF), Simon More (UCD CVERA), James O'Keefe, Paul White (DAFF), Guy McGrath, Inma Aznar (UCD CVERA)*

Proceedings of the 11th Symposium of the International Society for Veterinary Epidemiology and Economics (ISVEE), Cairns, Australia, p808.

An understanding of livestock movements is critical to effective disease prevention, control and prediction. However, livestock movement in the Republic of Ireland has not yet been quantified. This study has sought to define the survival and dispersal of a defined cohort of cattle, born in County Kerry during 2000. The cohort was observed for a maximum of four years, from 01 January 2000 to 31 December 2004. Beef and dairy animals moved on average 1.31 and 0.83 times, respectively. At study end, 18.8% of the beef animals remained alive on Irish farms, including 6.7% at the farm-of-birth, compared with 48.6% and 27.7% for dairy animals, respectively. Beef animals were dispersed to all Irish counties, but mainly to Cork, Limerick, Tipperary and Galway. Dairy animals mainly moved to Cork, Limerick, and Tipperary, with fewer animals going to Galway, Meath and Kilkenny. The 4-year survival probability was 0.07 (male beef animals), 0.25 (male dairy), 0.38 (female beef), and 0.72 (female dairy).

*Printed with permission from Massey University EpiCentre.*

***“An understanding of livestock movements is critical to effective disease prevention, control and prediction.”***

### MODELLING THE DEMOGRAPHICS OF THE IRISH CATTLE POPULATION

*Jarlath O'Connor, John Griffin (DAFF), Simon More (UCD CVERA)*

Featured in the 'Selected reports' section

There is little published information about the demography of cattle populations. Such information would aid in decision making with regard to animal health, animal welfare, resource allocation and planning. This study reports the development of, and outputs from, a demographic model of the Irish cattle population.

### TRENDS IN THE IRISH COW POPULATION AND THE RATE AT WHICH THEY WERE CULLED DURING 2003 TO 2006

*Peter Maher, Margaret Good (DAFF), Simon More (UCD CVERA)*

Featured in the 'Selected reports' section

Cows are the main economic production units of Ireland's cattle industry. Therefore, demographic information, including overall numbers and survival rates, are relevant to the Irish agricultural industry. This study seeks to determine the rate of cow culling from the national herd; to determine the rate of culling by type (dairy, beef), age, method of exit, date of exit and interval between last calving and exit; to calculate the national cow on-farm mortality rate; and to compare the Irish rates with published data from other countries.

## COMPANION ANIMAL EPIDEMIOLOGY

### AN EPIDEMIOLOGICAL STUDY OF THE IRISH PET POPULATION

*Martin Downes, Simon More (UCD CVERA)*

To date, there has been very little work on pet epidemiology in Ireland and no baseline data are available on the number of pet dogs or cats in the country. In this study, we aim to determine baseline data about the demographics of the Irish pet population, and to predict future population trends.

## FISH EPIDEMIOLOGY

### AN INTRODUCTION TO IMPORT RISK ANALYSIS FOR AQUATIC ANIMALS

*Chris Baldock (AusVet Animal Health Services, Australia; deceased), Simon More (UCD CVERA), Ed Peeler (Centre for Environment, Fisheries and Aquaculture Science, Weymouth, UK)*

Featured in the 'Selected reports' section

With increasing international trade, there are increasing risks to countries that unwanted aquatic animal pathogens will enter and spread. Import risk analyses provide an objective, transparent and defensible method of assessing disease risks associated with imports. This paper describes and illustrates the main elements of import risk analyses for aquatic animals and their products, including hazard identification, risk assessment, risk management and risk communication.



Fish farming off the west coast of Ireland

## HORSE WELFARE

### UCD REVIEW OF HORSE WELFARE IN IRELAND 2007-2009

*Joe Collins, Alison Hanlon (UCD Agriculture, Food Science and Veterinary Medicine), Simon More (UCD CVERA), Vivienne Duggan (UCD Agriculture, Food Science and Veterinary Medicine)*

In Ireland, horses are bred and trained for racing, equestrian sports and leisure activities. Each sector of the equine industry has traditionally been represented by entirely independent organisations, leading to a lack of cohesion on policies regarding issues such as the health and welfare of horses. This study aims to describe the welfare standards of horses in Ireland and how these link to industry structures; identify the most significant equine welfare issues as perceived by key stakeholders in the different industry sectors, and determine whether and how these might be addressed; and to document actual welfare issues.

## INTERNATIONAL COLLABORATION

### TUBERCULOSIS CONTROL IN CHILE

*Alejandro Rivera (SAG, Chile), Margaret Good (DAFF), Simon More (UCD CVERA)*

There has been a voluntary control programme for bovine tuberculosis in Chile for some time. With an increasing focus on the production of high-quality product for export, the Chilean government and industry are now developing a national bovine tuberculosis eradication programme. Lessons from Ireland may be helpful as this programme develops. Cooperative links have been developed with the Servicio Agrícola y Ganadero (SAG) within the Chilean Ministerio de Agricultura.



The dairy industry in Chile is mainly located in Regions 8 to 10 (pictured)

## A CRITICAL EVALUATION OF SURVEILLANCE AND CONTROL MEASURES WITHIN THE NATIONAL BRUCELLOSIS ERADICATION PROGRAMME IN THE REPUBLIC OF KOREA DURING 2000 TO 2006

Lee Byeong-yong (National Veterinary Research and Quarantine Service, Korea), Isabella Higgins, Simon More (UCD CVERA), Moon Oun-kyoung (National Veterinary Research and Quarantine Service, Korea), Tracy Clegg, Guy McGrath, Daniel Collins (UCD CVERA), Park Jee-yong, Yoon Hachung, Lee Sang-jin (National Veterinary Research and Quarantine Service, Korea)

Featured in the 'Selected reports' section

Bovine brucellosis has recently emerged as a major animal health problem in the Republic of Korea. This study seeks to critically evaluate the brucellosis control programme in Korea, focusing on the effectiveness of efforts to identify new cases and to control known cases of bovine brucellosis in cattle in Korea, during the period from 2000 to 2006.

## THE FMD OUTBREAK IN KOREA IN 2002

Wee Sung-hwan, Nam Hyang-mi, Yoon Hachung (National Veterinary Research and Quarantine Service, Korea), Simon More (UCD CVERA)

Korea experienced an FMD outbreak in 2002. In total, 16 farms were affected, including 15 farms (all but 'Farm 13') located in clusters surrounding the first two cases. This study reports the results of a detailed epidemiological investigation of the overall outbreak, and of the source of infection on Farm 13, given its relative geographic isolation from other known cases.

## MISCELLANEOUS

### A STUDY OF HELMINTH PARASITES IN CULLED COWS FROM IRELAND

Murphy, T.M., Fahy, K.N., McAuliffe, A., Forbes, A.B., Clegg, T.A., O'Brien, D.J.

Preventive Veterinary Medicine 76 (2006), 1-10.

The objective of this study was to determine the prevalence and intensity of gastrointestinal nematode, lungworm and liver fluke infection in culled cows in Ireland. Abomasa, colorectal contents and livers were collected from 30 to 68 culled beef and dairy cows during autumn 2002 and summer 2003, respectively. *Ostertagia ostertagi* were found in the abomasa of only three (10%) cows sampled in autumn and in 38 (57%) cows examined in summer. The majority of positive animals had low burdens of *O. ostertagi* but a few individuals in the group sampled during the summer had a moderate infection (5000-10,000 adult worms). A proportion of the cows in the summer group were also co-infected with small numbers of *Trichostrongylus axei*. *Cooperia oncophora* predominated in the recoveries from the larval cultures although *O. ostertagi* were also recovered. The overall prevalence of *Dictyocaulus viviparus* was 14%, based on larval identification in faecal samples. Liver fluke, or varying degrees of pathology attributable to *Fasciola hepatica*, were present in 65% of the livers. The results of this study extend those of previous workers, which were largely limited to dairy cows alone and which focussed on gastrointestinal nematodes and did not include simultaneous infections with lungworm and liver fluke. It was concluded, from the level of polyparasitism evident in this study, that adult cattle should be considered in preventive approaches to bovine helminthosis.

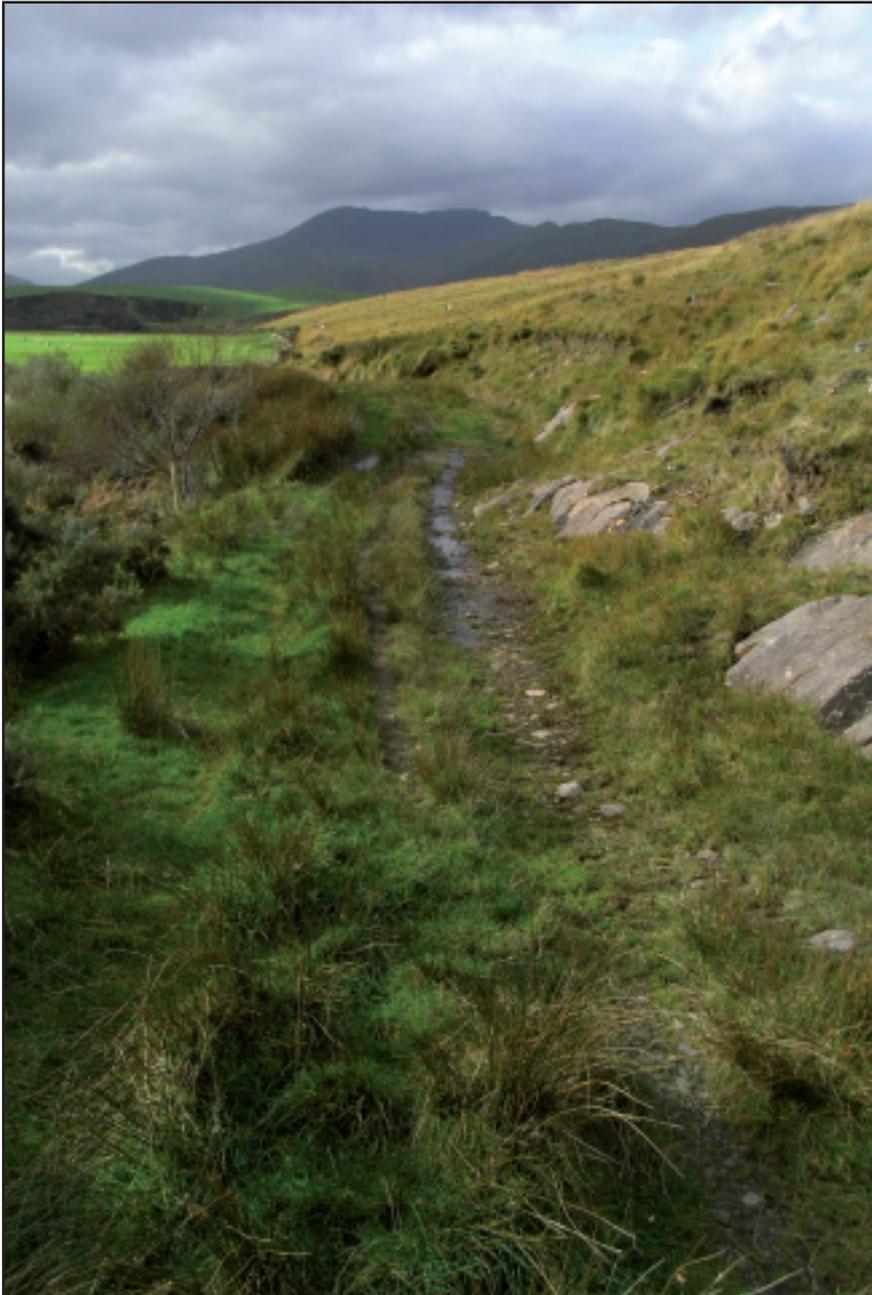
Printed with permission from Elsevier Limited.

**“Adult cattle should be considered in preventive approaches to bovine helminthosis.”**

## DECISION SUPPORT SYSTEM (PREDICTIVE MODEL) FOR FASCIOLOSIS IN IRELAND

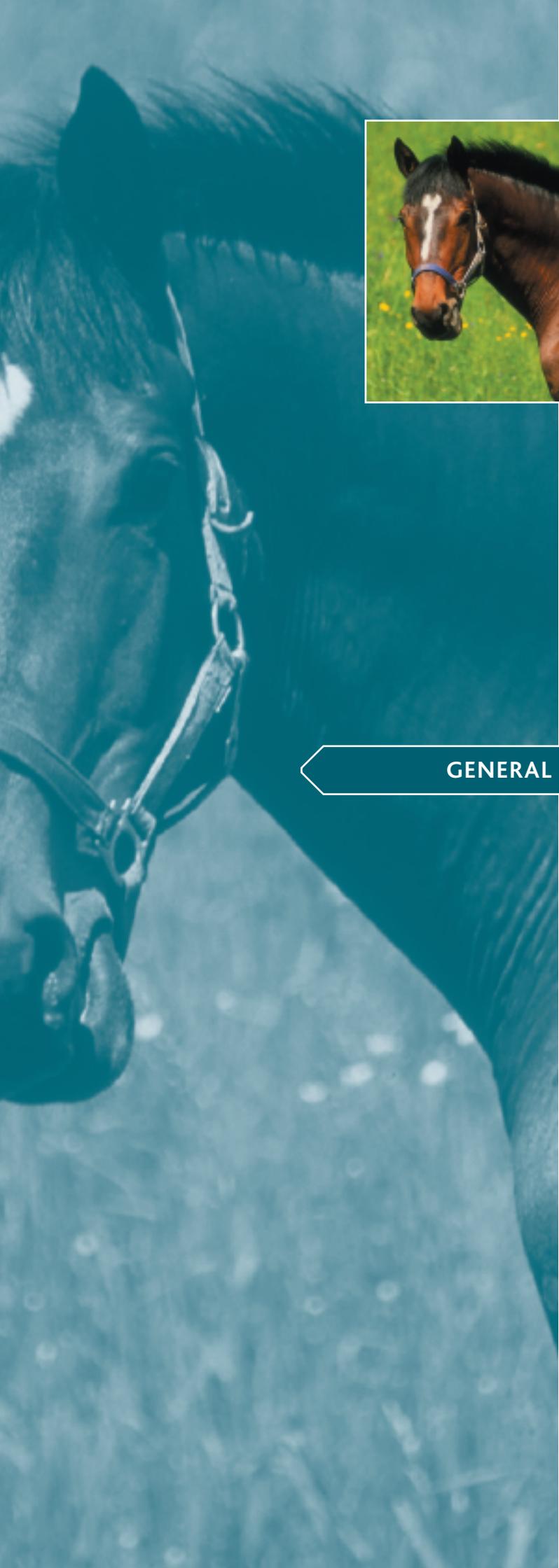
Theo de Waal, Grace Mulcahy, John Kennedy, Valerie Relf (UCD Agriculture, Food Science and Veterinary Medicine), Tom Murphy (DAFF), Guy McGrath, Simon More (UCD CVERA)

Fasciolosis or liver fluke disease caused by *Fasciola hepatica* is one of the major impediments to economic production in ruminants in Ireland. Anecdotal evidence suggests an increase in the incidence of acute fasciolosis amongst sheep in mid-summer. This project aims to develop a more refined model to predict the likely incidence and severity of fasciolosis both regionally and locally. This information will assist with the design and implementation of improved control and intervention strategies.



Ideal habitat for *Lymnaea truncatula*, the intermediate host for liver fluke (*Fasciola hepatica*), in the west of Ireland





**GENERAL SUPPORT**

## CHAPTER CONTENT

### GENERAL SUPPORT

65 Epidemiological support

66 Statistical support

67 GIS support

67 Database support

# EPIDEMIOLOGICAL SUPPORT

Key CVERA contact: *Simon More*

## FARM INVESTIGATIONS

Farm investigations are a critical component of CVERA's work. These investigations offer the opportunity for CVERA staff to support veterinary students in the use of practical epidemiological skills to solve (often complex) on-farm problems. Key epidemiological skills concern the use of simple methodologies to examine patterns of disease presentation in time, in space and among different animal groupings. Farm investigations, which are a key component of the final year curriculum, are conducted in collaboration with local private veterinary practitioners and/or veterinary inspectors. The following investigations were conducted during 2006 and 2007:

- Pneumonia (Co. Meath; January 2006)
- Periparturient problems (Co. Tipperary; February, November 2006, April 2007)
- Multiple health problems in adult cattle (Co. Cork; February 2006, February, May 2007)
- Mastitis (Co. Meath; March 2006)
- Johne's disease (Co. Tipperary; March 2006)
- Tuberculosis (Co. Cork; September 2006)
- Pneumonia (Co. Louth; October 2006)
- Tuberculosis (Co. Wicklow; November 2006)
- Sub-optimal fertility (Co. Tipperary; November 2006)
- Sub-optimal fertility (Co. Offaly; November 2006)
- Mastitis (Co. Waterford; January 2007, March 2007)
- Calf health, infertility, Johne's disease (Co. Kilkenny; February, September, November 2007)
- Pneumonia (Co. Kildare; February 2007)
- Tuberculosis (Co. Waterford; February 2007)
- Sub-optimal fertility (Co. Waterford; March 2007)
- Mastitis (Co. Meath; March 2007)
- Tuberculosis (Co. Wicklow; October 2007)
- Sub-optimal fertility (Co. Wicklow; October 2007)
- Pneumonia (Co. Dublin; November 2007)
- Mastitis (Co. Dublin; November 2007)
- Sub-optimal fertility (Co. Kerry, December 2007)

***“Simple epidemiological methods can be used in the field to examine patterns of disease in time, in space and among different animal groupings. This information then provides clues about the cause of the problem.”***

## GENERAL EPIDEMIOLOGICAL TRAINING

A course in introductory epidemiology was held in Mulraney, Co. Mayo (08-09 November 2007) and Cahir, Co. Tipperary (29-30 November 2007). The following provides a background to this course:

*'Epidemiology is often viewed as a discipline of facts and figures, with only limited application to front-line veterinarians on the ground. The purpose of this one-and-a-half day course is to demystify epidemiology, and provide attendees with a sound understanding of epidemiology in action. The course is problem-based, and will centre on a range of hands-on learning exercises that are relevant to Veterinary Inspectors in the field. Following this course, there will be an opportunity for interested attendees to join a mentored study group that will meet on an ongoing basis.'*

An epidemiological mentoring group has been established, to support veterinary inspectors with an interest in the principles and methods of veterinary epidemiology. The group met in Portlaoise, Co. Laois, in October 2006, May 2007 and November 2007.

Risk analysis has been recognised worldwide as an important tool for decision-making in many fields, including animal and human health. CVERA is working with the DAFF to strengthen capacity in risk analysis among DAFF staff, with workshops in November and December 2006.

## STATISTICAL SUPPORT

*Key CVERA contact: Tracy Clegg*

During 2006-2007, in addition to core projects, CVERA provided statistical support and advice to a range of researchers as follows:

### Department of Agriculture, Fisheries and Food

- Serological surveillance of cattle for Bluetongue in Ireland
- Comparison of the potency of different tuberculins used in the field compared to the Irish standard
- A case-control study of paratuberculosis (Johne's disease) in Irish dairy herds
- Cattle movements into and out of Irish beef herds infected with Johne's disease
- Trends in the number of, and rate at which, cows are culled from the Irish cattle population, 2003 to 2006
- Control of *Mycobacterium bovis* infection in two sika deer herds in Ireland

### UCD School of Agriculture, Food Science & Veterinary Medicine, University College Dublin

- The effect of varying levels of population control on the prevalence of tuberculosis in badgers in Ireland
- Leptospirosis in Irish suckler herds
- A critical evaluation of farm-level milk quality, based on milk recording data
- UCD review of horse welfare in Ireland 2007-2009
- Comparison of the Immulite® and RIA assay methods for measuring peripheral blood P4 levels in Greyhound bitches prior to breeding
- Influence of induction of parturition on the neonatal acute phase response in foals

### UCD Veterinary Hospital, School of Agriculture, Food Science & Veterinary Medicine, University College Dublin

- The influence of sternal vs. lateral recumbency on the L5-L6 mid-laminar distance amongst dogs

### UCC Department of Zoology, Ecology and Plant Science, University College Cork

- How many Eurasian badgers *Meles meles* L. are there in Ireland?

### National Veterinary Research and Quarantine Service, Korea

- A critical evaluation of surveillance and control measures within the national brucellosis eradication programme in the Republic of Korea during 2000 to 2006

### Vet-Aqua International and the Marine Institute, Galway

- Epidemiology of Pancreas Disease amongst Atlantic farmed salmon in Ireland

## GIS SUPPORT

*Key CVERA contacts: Guy McGrath and Daniel Collins*

### THE WILDLIFE UNIT

#### a. An independent monitor

CVERA acts as an independent monitor for the National Parks and Wildlife Services (the Department of the Environment, Heritage and Local Government) to ensure operations of the Wildlife Unit (DAFF) are within pre-agreed criteria. This includes verifying individual badger removal licences and maintaining checks on areas treated by the Wildlife Unit on a county by county basis through time. Ongoing reports with thematic maps are produced for the two government Departments.

#### b. Administration

In addition to monitoring and reporting on Wildlife Unit activities, CVERA maintain the GIS component of the Wildlife Unit administration centre in Johnstown Castle, Co. Wexford. This centre provides all District Veterinary Offices with the relevant maps and ortho-photography to complete badger surveys in areas where tuberculosis breakdowns in cattle have been attributed to wildlife. The badgers setts found through surveying are then digitised and maintained centrally on the GIS.

### GENERAL MAPPING SUPPORT

CVERA provide a broad range of mapping support, including:

- Maps for specific field investigations
- Maps for illustrative purposes in publications and internal reports
- Maps for aiding in the spatial aspects of study design
- Mapping to assist District Veterinary Offices
- Annual production of thematic prevalence maps for tuberculosis, brucellosis and BSE
- Provision of mapping assistance in the event of an emergency disease incursion.

## DATABASE SUPPORT

### THE TB TESTING DATABASE

*Key CVERA contacts: Paul White and Isabella Higgins*

#### *Introduction*

Since the introduction of the Animal Health Computer System (AHCS) and other online computer systems within DAFF, increasing volumes of data in relation to animal disease and movement within the Irish cattle herd are available for research.

#### *Development*

The CVERA national bovine tuberculosis/brucellosis testing database project has been ongoing since 1998. It has continued to play a supportive role in the research programme with the original aim of providing a central database for querying of tuberculosis/brucellosis testing data from the 29 District Veterinary Offices (DVOs).

The database was initiated on Microsoft Access™ which provided user-friendly interface for running queries about the tuberculosis/brucellosis eradication schemes in relation to:

- Tuberculosis test summary data
- Tuberculosis reactor and inconclusive skin results
- Tuberculosis post-mortem results for reactor animals
- Contiguous herds identified by DAF field staff
- Brucellosis test summary data.

Data management within CVERA continues to be a dynamic process with its scale and complexity driven by the ongoing demand for new datasets to be explored within the research programme. Recently, the system has been expanded to deal with laboratory results for TB suspect lesions.

*Management*

The database is updated at monthly intervals by running an AHCS report that outputs data to standardised text files. The text files are uploaded onto the SQL server database using an Access front-end to automate various server stored procedures. The system currently holds in excess of 4 million tuberculosis herd test records along with associated skin test readings and *post mortem* results.

*Interrogation*

The ability to run Structured Query Language (SQL) is a key feature of modern relational database management systems that enables questions to be asked about data stored across various tables. By running queries to combine data derived from disparate sources, the system offers the potential to utilise animal movement data to study animal disease data. As large tables are involved, this process is resource intensive and calls for carefully planned query design.

## GENERAL DATABASE MAINTENANCE AND INTERROGATION

### Key CVERA contact: Isabella Higgins

To assist with a range of research projects, the following national databases are regularly interrogated:

- Animal Health Computer System (AHCS) database;
- Cattle Movement Monitoring System (CMMS) database;
- Factory surveillance database;
- Laboratory Information Management System (LIMS) database;
- Tracing Onward Tracking System (TOTS);
- ER76 database; and
- Badger *post mortem* database (1997-2003).

The following examples illustrate how these data are subsequently used:

- a. The provision of data for ongoing work, PhD theses and various papers, including:
  - A long term study of the impact of proactive badger removal on herd restrictions due to bovine TB in east Offaly 1989-2004;
  - The genetics of predisposition to tuberculosis in Irish dairy and beef cattle;
  - A range of projects relating to tuberculin registration; and
  - APT figures on a DED basis for production of thematic maps.
- b. Data from the east Offaly badger *post mortem* database (1997-2003) was used to reconcile badger licenses from the control area of the east Offaly project during these years.
- c. Data from the calf birth registration database was used to assess the accuracy of individual animal identification. In this study, the DNA profile of the calf was compared with the profile of the registered dam to determine if the dam qualifies as a parent of the calf through DNA testing.
- d. Data relating to tuberculin tests carried out on cattle, and the number of tuberculin reactors disclosed, according to county were compiled to produce the Bovine Tuberculosis Statistics, Annual Summary (2006-2007).
- e. Detailed work was conducted in collaboration with Lee Byeong-yong of the National Veterinary Research and Quarantine Service in Korea to evaluate the effectiveness of surveillance (identifying new cases) and control (clearing known cases) activities within the brucellosis eradication programme in the Republic of Korea during 2000 to 2006. Data from the national animal infectious disease data management system was used to conduct descriptive analyses on a farm basis and then on an episode basis.
- f. National tuberculin testing data were assembled for a project investigating the genetics of predisposition to tuberculosis in Irish cattle. This work is being conducted by Máiréad Bermingham, from Teagasc Moorepark.
- g. Provision of technical support and data for the production of improved statistical measures for TB surveillance and control. Initiated within CVERA, the project is now being led by David Williams and Syed Zeeshan Haider Zaidi from UCD Statistics.
- h. Data of badger removal and TB incidence in cattle, from the Irish midlands since 1989, were assembled for a long-term observational study to evaluate the long-term effectiveness of proactive badger culling, and long-term effects of reactive culling, on TB prevalence in cattle. This work is being led by Gabrielle Kelly (UCD Statistics) and Joe Condon (Dublin Institute of Technology).

**“Database interrogation is central to many national projects.”**



**PUBLICATIONS**

# CHAPTER CONTENT

## PUBLICATIONS

71 During 2006-07

73 Prior to 2006

## DURING 2006-07

### A. PEER-REVIEWED PUBLICATIONS

Aguilar, D., Infante, E., Martin, C., Gormley, E., Gicquel, B., Hernandez Pando, R., 2007. Immunological responses and protective immunity against tuberculosis conferred by vaccination of Balb/c mice with the attenuated *Mycobacterium tuberculosis* (phoP) SO2 strain. *Clinical and Experimental Immunology* 147, 330-338.

Barrett, D.J., Clegg, T.A., Healy, A.M., Doherty, M.L., 2006. A study of dry cow therapy and effects on SCC in 10 Irish dairy herds. *Journal of Veterinary Medicine Series A* 53, 140-144.

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Corner, L.A., 2006. The role of wild animal populations in the epidemiology of tuberculosis in domestic animals: how to assess the risk. *Veterinary Microbiology* 112, 303-312.

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Meade K.G., Gormley, E., Park, S.D., Fitzsimons, T., Rosa, G.J., Costello, E., Keane J., Coussens, P.M., MacHugh, D.E., 2006. Gene expression profiling of peripheral blood mononuclear cells (PBMC) from *Mycobacterium bovis* infected cattle after *in vitro* antigenic stimulation with purified protein derivative of tuberculin (PPD). *Veterinary Immunology and Immunopathology* 113, 73-89.

More, S.J., 2007. Shaping our future: animal health in a global trading environment. *Irish Veterinary Journal* 60, 541-549.

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More, S.J., Good, M., 2006. The tuberculosis eradication programme in Ireland: a review of scientific and policy advances since 1988. *Veterinary Microbiology* 112, 239-51.

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SELECTED REPORTS



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### SELECTED REPORTS

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# THE COMPARATIVE PERFORMANCE OF THE SINGLE INTRADERMAL COMPARATIVE TUBERCULIN TEST IN IRISH CATTLE, USING TUBERCULIN PPD COMBINATIONS FROM DIFFERENT MANUFACTURERS

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## ABSTRACT

Ireland currently obtains its avian and bovine tuberculin purified protein derivatives (PPDs) from a single source. Because problems of supply or quality cannot be discounted, it is prudent that Ireland identify alternative supplier(s) as part of a broad risk management strategy. Therefore, the aim of this study was to compare the performance of a number of different tuberculin combinations (that is, pairings of bovine and avian PPD; with different manufacturers) in the single intradermal comparative tuberculin test (SICTT), as currently performed in Ireland. The study was randomised, controlled and double-blinded. A total of 2,172 cattle were used in the study. Each animal was tested using two SICTTs, the first based on the tuberculin combination in current use, and the second using one of six trial tuberculin combinations. Analyses were conducted to compare both reactor-status and skin increase. For each control/trial tuberculin combination, there was good agreement between the control and trial reactor-status. Differences in skin increases were mainly confined to animals categorised as either negative or severe inconclusive. However, the measured differences were minor, and unlikely to have a significant impact on the actual test outcome, either for individual animals or for herds. In conclusion, there would be minimal disruption of the national programme if alternative tuberculin PPDs were used. In this study, the precision of the guinea pig bio-assay to assess tuberculin potency was low.

## 1. INTRODUCTION

The single intradermal comparative tuberculin test (SICTT) to detect tuberculosis (TB) in cattle is in routine use as part of the bovine TB eradication programme in Ireland (Good et al., 2006). This test is conducted by comparing the separate immunological cell-mediated response in each animal to avian and bovine tuberculin purified protein derivative (PPD) (Monaghan et al., 1994), used in accordance with the protocols laid down in Directive 64/432/EEC (Anon., 2004).

In Ireland, ID-Lelystad BV (Institute for Animal Science & Health, Lelystad, The Netherlands) currently supplies all of the avian and bovine tuberculin PPD used in the programme. Because problems of supply or quality cannot be discounted, it is prudent that Ireland identify alternative supplier(s) as part of a broad risk management strategy. There are a number of national TB eradication programmes in the European Union (Caffrey, 1994; Reviriego Gordejo and Vermeersch, 2006). As yet, however, no work has been reported on the impact of SICTT performance, using tuberculin PPD from different suppliers on these programmes. Therefore, the aim of this study was to compare the performance of a number of different tuberculin combinations (that is, pairings of bovine and avian PPD; with different manufacturers) in the SICTT as currently performed in Ireland. The study was randomised, controlled and double-blinded, and has been reported in accordance with the STARD initiative (Bossuyt et al., 2003).

## 2. MATERIALS AND METHODS

### 2.1 The Single Intradermal Comparative Tuberculin Test

#### a. The test

Detailed information about the SICTT, to diagnose tuberculosis in cattle, is available elsewhere (Monaghan et al., 1994; de la Rue-Domenech et al., 2006). Briefly, the test is conducted by separately injecting avian and bovine tuberculin intradermally into defined sites on the neck of cattle. The test is read 72 hours later, by comparing the relative millimetre increase in skin fold thickness (an *in vivo* cell mediated response to each tuberculin) at each injection site. Tuberculin is a licensed product under EU Regulations, which require it to be manufactured under Good Manufacturing Practice conditions and to comply with the European Pharmacopoeia.

#### b. Test interpretation

In accordance with Directive 64/432/EEC, as amended (Anon., 2004), the reaction at an individual injection site (either bovine or avian) is determined and considered *negative* 'if only limited swelling is observed, with an increase of not more than 2 mm without clinical signs such as diffuse or extensive oedema, exudation, necrosis, pain or inflammation of the lymphatic ducts in that region or of the lymph nodes'; *inconclusive* 'if no clinical signs as mentioned (previously) are observed and if the increase in skin-fold thickness is more than 2 mm and less than 4 mm'; or *positive* 'if clinical signs such as mentioned (previously) are observed or there is an increase of 4 mm or more in the thickness of the fold of skin at the injection site'.

In the current study, each animal was given a 'reactor-status', based on the results of the SICTT:

- A *standard reactor*, if the bovine reaction was both positive and exceeded the avian reaction by more than 4 mm;
- A *standard inconclusive*, if the bovine reaction was either positive or inconclusive, 1 to 4 mm greater than the avian reaction, and the criteria for a standard reactor were not met;
- A *severe inconclusive* if the bovine reaction was either positive or inconclusive, the avian reaction exceeded the bovine reaction by 2 mm or less, and the criteria for a standard reactor or standard inconclusive were each not met; or
- *Negative*, in all other cases.

## 2.2 The trial

The trial was conducted in Ireland over a number of months during 2006. Cattle of mixed age, breed and sex were gathered from a wide range of holdings of origin into a unit, which routinely 'finishes' animals for slaughter as part of a commercial enterprise. A proportion of the animals in this unit, chosen based on convenience, were selected for inclusion in this study. The trial was conducted, with animals being tested in batches shortly before slaughter.

Each study animal was tested using two SICTTs (that is, a control and a trial test), which were administered and read concurrently. Each animal was tested using the tuberculin combination in routine use in Ireland (the control test). In addition, each animal was tested using a trial tuberculin combination (the trial test), selected randomly from a pool of six tuberculin combinations, which included:

- The tuberculin combination currently in use in Ireland;
- Four alternative tuberculin combinations, sourced from three different companies; and
- One further tuberculin combination, equivalent to the control tuberculin combination, apart from the type of dye (Ponceau 4R substituted for Ponceau 2R to comply with EU Regulations on the use of ingredients determined as safe for injection into food producing animals) added to the avian tuberculin.

Each tuberculin in each combination was sourced from a single production batch. The potency of each avian and bovine tuberculin was assessed in TB-sensitised guinea pigs in accordance with annex B to Directive 64/432/EEC, as amended (Anon., 2004), both by each manufacturer during production, and also by ID Lelystad, as blinded samples prior to the start of the study. The potency of the bovine tuberculin was also assessed in naturally infected tuberculous cattle, as described previously (Haagsma et al., 1997), by one of the manufacturers during production, and for each bovine tuberculin at the Central Veterinary Research Laboratory, Ireland, prior to the start of the study (Table 1).

Table 1. The source and potency of the avian and bovine tuberculin purified protein derivative (PPD) in each tuberculin combination

Tuberculin combination	Manufacturer	Potency (mean IU) of the:							
		Avian tuberculin PPD				Bovine tuberculin PPD			
		Guinea pig		Cattle		Guinea Pig		Cattle	
		Prod. <sup>a</sup>	Trial <sup>b</sup>	Prod. <sup>a</sup>	Prod. <sup>a</sup>	Trial <sup>b</sup>	Prod. <sup>a</sup>	Trial <sup>c</sup>	
F(M)	A	25,000	16,500	nd	27,812	13,980	nd	25,900	
G(R) <sup>d,f</sup>	ID Lelystad	nd	27,750	nd	26,070	32,180	nd	45,003	
H(T)	B	38,250	31,500	19,800	19,180	24,500	nd	33,868	
J(N)	C	14,175	10,250	nd	28,350	5,850	nd	11,552	
K(S)	B	19,500	9,250	nd	11,200	22,750	36,550	28,747	
L(P) <sup>e,f</sup>	ID Lelystad	21,780	24,500	nd	26,070	14,950	nd	45,003	

a. As assessed by the manufacturer

b. As assessed by ID Lelystad, using blinded samples prior to the start of the study

c. As assessed by the Central Veterinary Research Laboratory in Ireland, prior to the start of the study

d. Identical to the control tuberculin combination, except Ponceau 4R substituted for Ponceau 2R in the avian tuberculin PPD

e. Identical to the control tuberculin combination

f. The bovine tuberculin PPD in tuberculin combinations G(R) and L(P) was identical. Therefore, only a single potency estimate is available from the manufacturer's guinea pig model. Further potency estimates, using the guinea pig model, were conducted using duplicate samples of the bovine tuberculin PPD; each result was then randomly allocated to one of the two tuberculin combinations. The potency of the bovine tuberculin PPD was only assessed on a single occasion using the bovine model.

nd = not done

A single veterinary practitioner conducted the field aspects of the trial. Prior to the trial, the tuberculin in each combination was decanted into sterile vials of uniform size and shape, then coded using one of two letters (for example, the combination from manufacturer A was coded using either F or M; Table 1). The administering veterinarian was blinded to the identity of the trial tuberculin combinations, and also to the fact that the control and one trial tuberculin combination were identical.

As prescribed in Directive 64/432/EEC (Anon., 2004), the injection sites for each tuberculin combination were located in the middle third of the neck: avian tuberculin was injected about 10 cm from the crest of the neck and bovine tuberculin about 12.5 cm lower on a line roughly parallel with the line of the shoulder. For logistical reasons, the control and trial tuberculin combinations were each administered on the same side of the neck of each animal: the control tuberculin combination at the border of the anterior and middle third of the neck, and the trial tuberculin combination at the border of the middle and posterior third of the neck. The trial tuberculin combination was administered to animals in sequential order, randomised at study start. An individual McClintock 20-dose syringe was supplied for exclusive use for each tuberculin code. The skin-fold thickness at each injection site was measured using sliding calipers (Pan Veterinary, Co. Kildare, Ireland) with broad jaws designed to distribute an even, manually applied pressure. Measurements rounded up to the nearest millimetre were made at 0 hours, and all responses to tuberculin injection were re-measured and assessed at 72 hrs +/- 4 hrs, as required in the Directive. Results were recorded onto a hand-held computer operating software approved by the Department of Agriculture, Fisheries and Food.

### 2.3 Statistical analysis

The results from each trial and control test were compared, using methods suitable for paired data.

Animals were assigned a trial and a control reactor-status, according to the definitions given earlier, and these data were compared using Cohen's kappa (Dohoo et al., 2003). In addition, we used McNemar's test to compare the proportion of animals allocated to each reactor-status, based on trial and control test results. Since, the number of discordant pairs was small (<10), an exact p-value for the McNemar's test was used (Breslow and Day, 1980, page 165). We accounted for multiple comparisons by reactor-status by applying a Bonferroni adjustment to the alpha value.

For each animal, we recorded the skin increases (in mm) at each bovine and avian site (trial bovine, trial avian, control bovine, control avian). We then calculated the difference between the two paired measurements (for each animal, a trial and a control bovine-avian [B-A] differential). A positive B-A differential indicated that the bovine measurement was greater than the avian measurement. For each animal, we also calculated the difference between the trial and control bovine measurements (bovine difference), the trial and control avian measurements (avian difference), and the trial and control BA differentials (B-A differential difference). Each of these results was positive if the trial measurement was larger than the control measurement. Each animal was then allocated to a reactor-status category based on the control test result. For each reactor-status within each trial/control test combination, we identified the minimum, median and maximum bovine difference, avian

difference and BA differential difference. These differences were compared, overall and within each trial/control test combination, using the Kruskal-Wallis and Wilcoxon signed-ranks tests, respectively.

## 3. RESULTS

### 3.1 The study animals

The SICTT was performed on 2,172 cattle of mixed breeds, including 28 tested twice at an inter-test interval exceeding 60 days. The number of animals tested using each tuberculin and the animal type is presented in Table 2.

Table 2. Number of animals tested, by trial test and sex. All animals were tested using both a trial and control test

Trial test	Number of animals			
	Total	Females		Males
		Heifers	Cows	
F	399	85	63	251
G	333	131	42	160
H	407	99	43	265
J	276	89	34	153
K	393	93	-	300
L	392	166	22	204
Total	2,172	663	204	1,305

### 3.2 The SICTT results

#### a. Reactor-status

In some animals there were discrepancies in the classification of reactor-status, based on results from the trial and control test. Generally, a control standard reactor was also considered at least an inconclusive reactor in the trial test. However, one control standard reactor animal was negative in each of three trial tests (F, H and J). Similarly, each of the trial standard reactors were also considered non-negative in the control test, except for 2 standard reactors identified using SICTT F and one using SICTT G. There was moderate, but significant ( $p < 0.001$ ), agreement between the results from the control and each trial test, as measured using Cohen's kappa (Table 3).

Table 3. Comparison of animal reactor-status, based on control and trial test results

Trial test and reactor status, based on these results	Reactor-status, based on results from the control test				Total	Cohen's kappa (95% C.I.)	P- Value <sup>c</sup>
	Negative	Severe inconc. <sup>a</sup>	Standard inconc. <sup>b</sup>	Standard reactor			
F Negative	342	11		1	354	0.48 (0.36 – 0.61)	<0.001
Severe inconc. <sup>a</sup>	17	12			29		
Standard inconc. <sup>b</sup>	1	4	3	2	10		
Standard reactor	2		1	3	6		
Total	362	27	4	6	399		
G Negative	305	5			310	0.59 (0.44 – 0.75)	<0.001
Severe inconc. <sup>a</sup>	5	7			12		
Standard inconc. <sup>b</sup>	1	1		2	4		
Standard reactor	1	1	1	4	7		
Total	312	14	1	6	333		
H Negative	359	14		1	374	0.61 (0.48 – 0.73)	<0.001
Severe inconc. <sup>a</sup>	7	17		1	25		
Standard inconc. <sup>b</sup>		3	2		5		
Standard reactor			1	2	3		
Total	366	34	3	4	407		
J Negative	239	7		1	247	0.56 (0.42 – 0.71)	<0.001
Severe inconc. <sup>a</sup>	6	10			16		
Standard inconc. <sup>b</sup>	3	4	2		9		
Standard reactor		1	1	2	4		
Total	248	22	3	3	276		
K Negative	352	13			365	0.46 (0.31 – 0.61)	<0.001
Severe inconc. <sup>a</sup>	9	9			18		
Standard inconc. <sup>b</sup>	3	2		2	7		
Standard reactor				3	3		
Total	364	24	0	5	393		
L Negative	337	9			346	0.54 (0.42 – 0.66)	<0.001
Severe inconc. <sup>a</sup>	16	13			29		
Standard inconc. <sup>b</sup>	2	5	5	1	13		
Standard reactor		1	1	2	4		
Total	355	28	6	3	392		

a. Standard inconclusive result

b. Severe inconclusive result

c. Significance test of the level of agreement between the control and respective trial SICTT

Table 4. The percentage of animals in each control/trial test combination that were classified to each reactor-status category, based on control and trial test results

Reactor-status <sup>a</sup>		Control/trial test combination					
		Control/F	Control/G	Control/H	Control/J	Control/K	Control/L
All non-negative results <sup>b</sup>	Control % +ve	9.3	6.3	10.1	10.1	7.4	9.4
	Trial % +ve	11.3	6.9	8.1	10.5	7.1	11.7
	P-value <sup>c</sup>	0.215	0.774	0.134	1.000	1.000	0.122
	Kappa	0.57	0.71	0.67	0.67	0.53	0.64
	(95% C.I.)	(0.43, 0.70)	(0.55, 0.86)	(0.55, 0.80)	(0.52, 0.81)	(0.36, 0.69)	(0.51, 0.76)
Standard reactors	Control % +ve	1.5	1.8	1.0	1.1	1.3	0.8
	Trial % +ve	1.5	2.1	0.7	1.5	0.8	1.0
	P-value <sup>c</sup>	1.000	1.000	1.000	1.000	0.500	1.000
	Kappa	0.49	0.61	0.57	0.57	0.75	0.57
	(95% C.I.)	(0.14, 0.84)	(0.29, 0.92)	(0.13, 1.00)	(0.12, 1.00)	(0.41, 1.00)	(0.13, 1.00)
Standard inconclusives	Control % +ve	1.0	0.3	0.7	1.1	0	1.5
	Trial % +ve	2.5	1.2	1.2	3.3	1.8	3.3
	P-value <sup>c</sup>	0.070	0.375	0.625	0.070	0.016	0.039
	Kappa	0.71	0.77	0.71	0.54	0.66	0.68
	(95% C.I.)	(0.51, 0.91)	(0.56, 0.99)	(0.44, 0.98)	(0.27, 0.82)	(0.38, 0.94)	(0.48, 0.89)
Severe inconclusives	Control % +ve	6.8	4.2	8.4	8.0	6.1	7.1
	Trial % +ve	7.3	3.6	6.1	5.8	4.6	7.4
	P-value <sup>c</sup>	0.860	0.774	0.108	0.238	0.307	0.858
	Kappa	0.57	0.71	0.68	0.68	0.53	0.64
	(95% C.I.)	(0.44, 0.71)	(0.55, 0.86)	(0.56, 0.81)	(0.54, 0.83)	(0.36, 0.69)	(0.51, 0.76)

a. The reactor-status is based on the results from the control SICTT

b. Standard reactors, standard and severe inconclusives

c. The significance of the measurement differences was tested using McNemar's test

The percentage of animals in each trial/control test combination that were classified to each reactor-status category, based on trial and control test results, is presented in Table 4. No significant differences were detected (McNemar's test, with a Bonferroni adjusted significance level of 0.0125 to account for the four comparisons made within each control/trial test combination). There was also no significant difference in the level of agreement (measured using Cohen's kappa) between each trial/control test combination, by reactor-status.

#### b. Skin increase

The median (minimum, maximum) bovine difference, avian difference and bovine-avian differential difference, by reactor-status and trial/control test combination, is presented in Table 5. Among all animals positive to the control test, there was no significant difference in either the bovine (Kruskal-Wallis test:  $p = 0.106$ ) or avian ( $p = 0.202$ ) difference, nor in the bovine-avian differential difference ( $p = 0.532$ ).

Among animals with non-negative results, there was a significant difference between the bovine and avian difference in each trial/control combination, except G/control (bovine difference:  $p = 0.536$ ; avian difference:  $p = 0.829$ ). These differences mainly relate to animals classified as severe inconclusives. There was no significant differences in the B-A differential (with a Bonferroni adjusted significance level of 0.01 to account for the five comparisons made within each control/trial test combination). Among animals with negative results, there were significant differences in the bovine difference (L/control combination), the avian difference (all combinations) and the B-A differential difference (all combinations).

Table 5. The median (minimum, maximum) bovine difference, avian difference and bovine-avian differential difference, by reactor-status and trial/control test combination

Reactor-status <sup>a</sup>	Median value (minimum, maximum)					
	F/control combination	G/control combination	H/control combination	J/control combination	K/control combination	L/control combination
<b>All non-negative results<sup>b</sup></b>						
Number of animals	37	21	41	28	29	37
Bovine difference <sup>c</sup>	-1 (-69, 3)** <sup>d</sup>	0 (-8, 84)	-1 (-9, 2)**	0 (-4, 5) <sup>nd</sup>	-1 (-11, 5)**	-1 (-13, 4)**
Avian difference <sup>e</sup>	-1 (-8, 4)**	0 (-4, 6)	-1 (-4, 11)**	-2 (-4, 9)**	-1 (-5, 3)**	-1 (-9, 4)**
B-A differential difference <sup>f</sup>	0 (-72, 4)	0 (-7, 85)	0 (-11, 5)	0 (-9, 8)	0 (-13, 8)	0 (-9, 9)
<b>Standard reactors</b>						
Number of animals	6	6	4	3	5	3
Bovine difference	-3 (-69, 1)	-0.5 (-8, 32)	-1.5 (-3, 1)	0 (-4, 0)	-4 (-11, 5)	-2 (-13, 1)
Avian difference	1 (-4, 3)	0.5 (-1, 6)	2 (-3, 11)	-2 (-2, 9)	-2 (-5, 3)	-2 (-4, 0)
B-A differential difference	-2 (-72, -1)*	-0.5 (-7, 26)	-4 (-11, 2)	-2 (-9, 2)	-3 (-13, 8)	-2 (-9, 3)
<b>Standard inconclusive reactors</b>						
Number of animals	4	1	3	3	0	6
Bovine difference	-0.5 (-4, 2)	5 (5, 5)	0 (-1, 0)	0 (-1, 2)	-	0 (-1, 3)
Avian difference	-2 (-3, -1)	-1 (-1, -1)	1 (-1, 1)	-2 (-2, 0)	-	-0.5 (-2, 3)
B-A differential difference	1.5 (-1, 3)	6 (6, 6)	-1 (-2, 1)	1 (0, 4)	-	0.5 (-2, 4)
<b>Severe inconclusive reactors</b>						
Number of animals	27	14	34	22	24	28
Bovine difference	-1 (-8, 3)**	0 (-3, 84)	-1 (-9, 2)**	0 (-3, 5)	-1 (-4, 1)**	-1 (-4, 4)**
Avian difference	-1 (-8, 4)**	-0.5 (-4, 3)	-1 (-4, 1)**	-1.5 (-4, 1)**	-1 (-4, 2)**	-1 (-9, 4)**
B-A differential difference	0 (-4, 4)	0 (-3, 85)	0 (-6, 5)	0 (-1, 8)	0 (-3, 4)	0 (-4, 9)
<b>All negative results</b>						
Number of animals	362	312	366	248	364	355
Bovine difference	0 (-6, 8)	0 (-3, 6)	0 (-3, 4)	0 (-4, 8)	0 (-3, 6)	0 (-5, 6)**
Avian difference	0 (-13, 6)**	0 (-10, 33)**	0 (-9, 6)**	0 (-6, 8)**	0 (-8, 11)**	0 (-23, 5)**
B-A differential difference	0 (-6, 16)**	0 (-33, 8)**	0 (-6, 8)**	0 (-8, 6)**	0 (-11, 8)**	0 (-5, 23)**

a. The reactor-status is based on the results from the control SICTT

b. Standard reactors, standard and severe inconclusive reactors

c. The difference in skin measurement (in mm; if positive, trial is larger) at the trial and control bovine sites

d. The significance of the measurement differences was tested using a Wilcoxon signed-rank test. (\*  $p \leq 0.05$ ; \*\*  $p \leq 0.01$ )

e. The difference in skin measurement (in mm; if positive, trial is larger) at the trial and control avian sites

f. The difference (in mm; if positive, trial is larger) between the trial and control bovine-avian differential

## 4. DISCUSSION

As part of the Irish programme, all cattle are assigned a reactor-status (of standard reactor, standard inconclusive, severe inconclusive or negative) on the basis of results from each SICTT result. Therefore, the effect of different tuberculin PPD combinations on reactor-status is of particular importance. For each control/trial tuberculin combination, we found good agreement between the control and trial reactor-status in this study (Table 3). Further, the level and pattern of agreement between the control and trial combinations G and L (each using the tuberculin PPD combination currently in use in Ireland) was similar to that observed with each other control/trial combinations. The level of agreement was also similar ( $\kappa$ : 0.49 to 0.77), and differences almost invariably non-significant, when each category

of reactor-status was considered separately (Table 4). Note, however, that the number of animals in some categories may have been too small to detect any difference, if present. Only a limited number of reactors were identified in the study, which reflects the very low animal-level incidence of tuberculosis in Ireland (More and Good, 2006; -0.4% annually). We could have identified a greater number of reactor animals, but at considerable cost in time and materials.

The study also provided insights into the effect of different tuberculin combinations on skin reactivity to the avian and bovine tuberculin PPD. Among all non-negative animals (standard reactors, standard inconclusives, severe inconclusives), there were no

significant differences between the control and each trial combination in the B-A differential difference (Table 5). The B-A differential (that is, the bovine skin increase minus the avian skin increase) is used to categorise animals into a reactor-status. Therefore, we are confident that similar field results will have been achieved, with each of the tuberculin combinations under investigation. Based on the detailed information presented in Table 5, we can identify some subtle differences in the performance of the different tuberculin combinations. With each of the control/trial combinations, there were significant differences in both the bovine and avian difference (that is, the difference between the trial and control skin increases at the bovine and avian sites, respectively). In most cases, the control (as compared to trial) skin increase was greater, at both the avian and bovine sites. We believe that these differences are the result of site effects, noting that the control and trial tests were conducted at sites on the anterior and posterior neck, respectively. Although it would have been preferable to use equivalent sites on each side of the neck, this was not possible due to concerns relating to access and operator health and safety. Latin square designs are used in the cattle bioassays specifically because sensitivity is known to be greater at the anterior compared with the posterior cervical area (E. Costello, pers. comm.). In a practical sense, this study has shown that it is the relative – rather than the absolute – location of the avian and bovine sites that is of greatest importance. Although a location at the border of the middle and anterior third of the neck is recommended (Anon., 2004), the B-A difference will not significantly alter if sites anterior or posterior to this are chosen. However, to ensure equivalent skin sensitivity at both the avian and bovine sites, it is important that these sites are both located on a line that is parallel to the angle of the shoulder.

The observed differences in skin reactivity to the avian and bovine tuberculin PPD at the control and trial sites were mainly confined to animals categorised as either negative or severe inconclusive (Table 5). However, the measured differences were minor, and unlikely to have a significant impact on the actual test outcome, either for individual animals or for herds. In Ireland, herd control would only be initiated following the detection of at least one standard reactor or an animal that had tested standard inconclusive on two consecutive occasions. Some of these discrepancies may have occurred following the rounding-up of skin measurements, as required in the Directive (Anon., 2004).

An outlier was identified in the control/G tuberculin combination, with one animal achieving a bovine difference of 84 mm. Based on the control test, the animal was negative, and on the trial test, very strongly a standard reactor. Note that the bovine tuberculin PPD was identical in the control and G tuberculin combinations. This difference is unexplainable beyond postulating that it may have been an inaccurate intradermal injection of bovine tuberculin PPD at the anterior site which serves only to highlight the issue of test repeatability and the necessity for two consecutive tuberculin tests clear before restoring disease-free status to a herd as is required under the Directive.

A number of steps were taken during this study to minimise a range of potential biases. The study was conducted in a commercial fattening unit where cattle of mixed age, breed and sex from throughout Ireland are assembled. These animals will each have been tested using the SICTT at some point during the 12 months preceding their entry into the unit, and it was anticipated that at least some would have been exposed under natural field conditions to *M. bovis* infection prior to acquisition by the enterprise. For logistic reasons, the study animals were selected using convenience sampling; essentially whole batches of cattle shortly before slaughter. We have no reason to believe that the study animals are not representative of the general Irish cattle population. A number of steps were taken to minimise measurement bias. The tuberculin

test is a subjective diagnostic test, which can be affected by a range of operator-related factors, including care and accuracy associated with the intradermal injection of tuberculin and the measurement of the skin response. Significant inter-operator variability has been observed previously. Further, Wahlström (2004) reported that the measured thickness of a 'standard' skin fold was a subjective measurement personally set by each veterinarian. As long as the veterinarian is consistent, such differences should not affect test accuracy. A single veterinary practitioner conducted all field aspects of this study specifically to minimise the potential for measurement bias. In compliance with international norms (Bossuyt et al., 2003), the study was randomised and controlled. Further, the field veterinary practitioner and ID Lelystad were blinded to the identity of the trial tuberculin combinations and the tuberculin PPDs, respectively. The practitioner was also not aware that the control and one trial tuberculin combination were identical. Although the study was conducted over a period of 8 months, we do not believe that time of year will have adversely influenced the SICTT results. As part of the national TB eradication programme, the SICTT is routinely conducted in Ireland throughout the year. When comparing the rate of lesion disclosure among cattle with varying SICTT responses, Towey and O'Keefe (1996) found some evidence of seasonal differences in multiple animal breakdown herds, but not in single animal breakdown herds. Any temporal effect of skin reactivity is believed to be related to a seasonal risk in exposure rather than seasonal changes in immune response (Martin et al., 2001).

In this study, the potency estimates from the guinea pig bio-assay were imprecise. Assay repeatability is in part due to the inherent variability of tuberculin PPD. Bovine tuberculin PPD has been described as a poorly defined, complex mixture containing more than 100 individual components in various stages of denaturation (Pollock et al., 2001), and is known to vary widely both in protein content and antigenic profile (Tameni et al., 1998). This may explain, at least in part, the variation in estimates of the potency of the ID Lelystad bovine tuberculin PPD that were obtained in this facility during production and in association with the trial (Table 1). However, our results also point to substantial imprecision in the guinea pig bio-assay, for reasons unrelated to the material under evaluation. Widely varying potency estimates (14,950 and 32,180 IU; Table 1) were obtained from duplicate PPD samples of ID Lelystad bovine tuberculin PPD tested in the same laboratory at the same time. In addition, we also found limited agreement between the guinea pig and cattle bio-assays. Using the above-mentioned tuberculin PPD, a potency of 45,003 IU was estimated in the cattle bio-assay. Similar concerns about these bio-assays have been expressed previously (Dobbelaer et al., 1983; Bakker et al., 2005), and it is acknowledged that biological variation is a feature of *in vivo* models. In recognition of this problem, relevant regulations require the fiducial limits of error ( $p=0.95$ ) to be not less than 50% and not more than 200% of the estimated potency, and the estimated potency not less than 75% and not more than 133%, and not less than 66% and not more than 150%, of the stated potency of 20,000 IU/ml for avian and bovine tuberculin, respectively (Anon., 2004). To reduce experimentally induced skin reactions, which can interfere with the bio-assay, Cobb et al. (2001) propose the use of hairless guinea pigs. The requirement to check potency in the bovine bio-assay is a stated requirement in the original Directive (64/432/EEC). However, there is considerable expense and logistic effort associated with routine use of this assay in sourcing, holding and handling a sufficient number of artificially or naturally infected bovine animals. The requirement was removed when the Directive was updated in 2002 (Anon., 2004), presumably due to these difficulties. Moreover, repeated use of the guinea-pig bio-assay, for essentially the same product batch during the manufacturing or licensing process does not appear to be justified, given the above-mentioned problems of assay imprecision.

## 5. CONCLUSION

This study provides reassurance to Irish policy-makers. There would be minimal disruption of the national programme if alternative tuberculin PPDs were used, provided they were of comparable potency within the potency range specified in the EU Directive. Ireland routinely assesses the quality of bovine tuberculin PPD using potency assays with naturally infected cattle, and ongoing use of these quality checks is advisable. In future work, we will compare the SICTT and *post mortem* results in these study animals.

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# AN OUTBREAK OF TUBERCULOSIS AFFECTING CATTLE AND PEOPLE ON AN IRISH DAIRY FARM IN 2005, FOLLOWING THE CONSUMPTION OF RAW MILK FROM A COW WITH TUBERCULOUS MASTITIS

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## ABSTRACT

Bovine tuberculosis (TB) is an ongoing problem in Ireland, and spillover of infection from cattle to people remains an ever-present possibility. This paper describes an outbreak of tuberculosis affecting cattle and people on a dairy farm in 2005, following the consumption of raw milk from a cow with tuberculous mastitis. There were approximately 100 cattle on the 41 ha. farm, as part of an operating dairy and a steer fattening unit. In recent years, the farm had experienced a number of small TB breakdowns in 1993, 1995 (both unconfirmed) and 2004 (confirmed), followed by a significant breakdown in 2005. In this latter breakdown, 38 tuberculin reactors were detected, including 25 calves. Tuberculous mastitis was diagnosed in a 7 yo cow, following the isolation of *Mycobacterium bovis* from a mastitic quarter. Although the milk from this cow was mainly fed to calves, it was occasionally added to the bulk tank. TB was also confirmed in local badgers, with one shared VNTR profile. Five of the six family members were positive to the Mantoux test, and the youngest child, a 4 yo boy, also had clinical findings suggestive of tuberculosis. He has since undergone prolonged treatment. This case demonstrates the infection risk for calves and people associated with a case of tuberculous mastitis. Although the risks are well-recognised, and relevant information for farmers is available, the consumption of raw milk remains prevalent on Irish farms. There seems little doubt that new strategies are needed, in partnership with industry, to address this important issue.

## 1. INTRODUCTION

Bovine tuberculosis (TB; infection with *Mycobacterium bovis*) has been an ongoing problem in Ireland for many years. Prior to national control measures, disease in cattle was common. From 1929 to 1938, it was estimated that gross pathology consistent with tuberculosis was present in 31-33% of cattle slaughtered at the city abattoirs in Dublin (Cotter *et al.*, 1996). A national eradication programme commenced in 1954, in part as a consequence of public health concerns, leading to a substantial reduction in disease prevalence by the mid 1960s (More and Good, 2006). Although subsequent progress has slowed, herd incidence has remained at approximately 5% for some years. The eradication programme is complex (More and Good, 2006), but includes annual testing of all Irish cattle with the single intradermal comparative tuberculin test (SICTT).

There have been substantial changes in the epidemiology of human tuberculosis in Europe, including Ireland. Throughout the 19<sup>th</sup> and early 20<sup>th</sup> century, a substantial proportion of human tuberculosis cases were caused by infection with *M. bovis* (Thoen *et al.*, 2007), generally linked to the consumption of raw cows' milk (Quinn *et al.*, 2006; de la Rua, 2006). In recent years, however, human infection with *M. bovis* has become very uncommon, accounting for only 1.8% of the culture-confirmed cases in Ireland during 2004 (Health Protection Surveillance Centre, 2006).

Spillover of infection from cattle to people remains an ever-present possibility, given the ongoing pool of infection in the Irish cattle population. This paper describes an outbreak of tuberculosis affecting cattle and people on a dairy farm in 2005, following the consumption of raw milk from a cow with tuberculous mastitis.

## 2. CASE HISTORY

### 2.1 The farm

The 41 ha. farm (the index farm) was located in southeastern Ireland. It was divided into four non-contiguous fragments, including three (Fragments 1, 2 and 4, which are grazed by cattle each spring and summer; Figure 1). A final fragment (Fragment 3), of 10 ha., was used exclusively for tillage. The farm was managed solely by the herdowner. Although the farm was an operating dairy, the farmer also fattened homebred steers for sale. In March 2005, there were 100 cattle on the farm, including 38 cows, 32 steers, 8 heifers and 22 calves. The farmer had no other commercial livestock, such as goats or deer, and no cats. A dog had been present on the farm; however, in February 2005, this animal was treated for suspected paraquat poisoning and subsequently died after a road traffic accident.

Farm management was consistent from year to year (Figure 2). The milking cows remained on the home farm (Fragment 1) throughout the year, including a period of housing each winter (from November to March; adult cattle housing). The cows calved in either spring or autumn, and the calves were held with their dam for approximately 1 week following birth. Autumn-born and early spring-born calves were housed (in designated calf housing in batches of 3-4 similar-aged calves, well-separated from other animals) from shortly after birth until late April/early May, then turned out to pasture on Fragment 1 (May to September, designated pasture separate from the milking cows) and Fragment 4 (October to November, post-silage production). Late spring-born calves were added to this group during late spring and summer. During housing and prior to weaning, calves were fed hay, and approximately 1 kg of calf concentrate ration and 5 litres of 'discard' milk per day (from cows immediately post-calving, those with mastitis or high somatic cell count, and those with milk

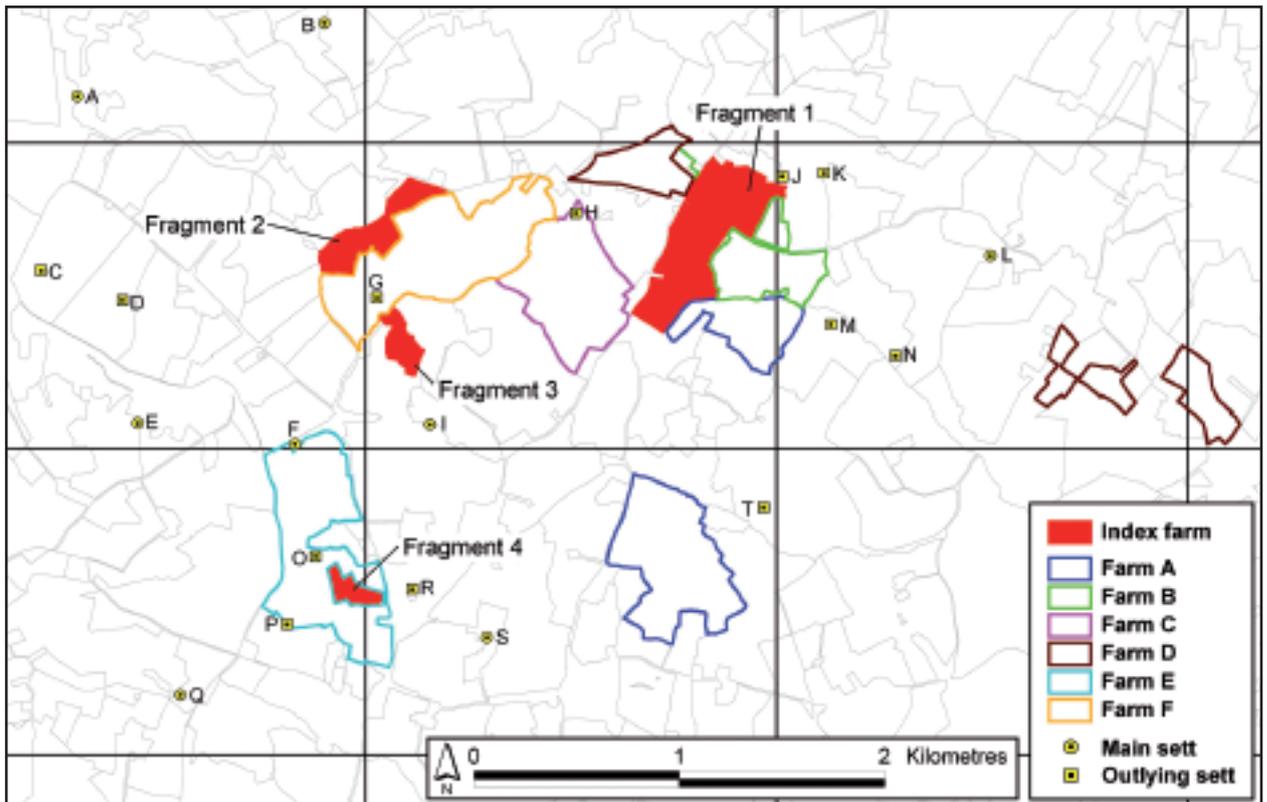


Figure 1. A map of the index farm, including fragments 1 (the home farm), 2 (yearling summer grazing), 3 (tillage only) and 4 (silage production, autumn grazing for calves). The location of six neighbouring farms (A to F) and local badger setts (differentiated by sett type) are also indicated

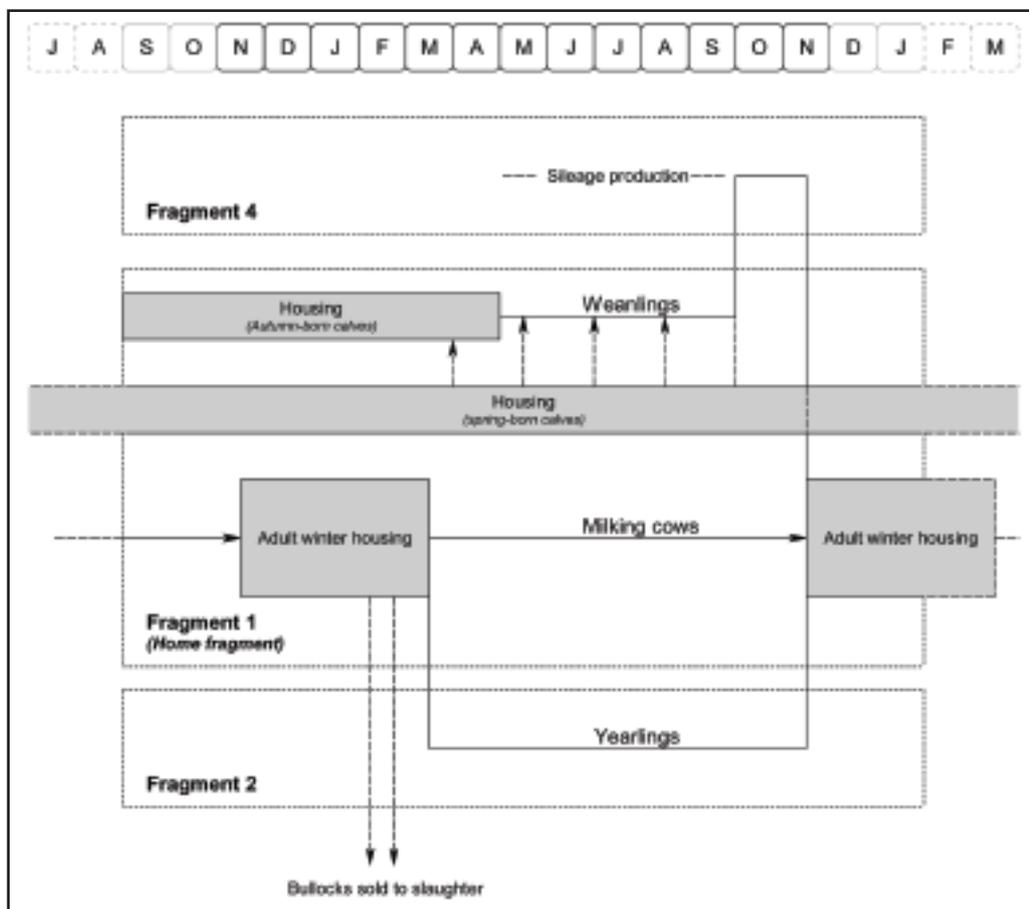


Figure 2. The annual management of cattle on the index farm

withheld due to medicine withhold requirements). Yearling animals were also held in adult cattle housing on Fragment 1, but grazed pasture on Fragment 2 during spring and summer. Older (2 year old) steers were housed for fattening. During winter housing, adult cattle are fed silage and rolled barley (each home-grown) and housed in a line of pens (in order: 2 yo steers, yearlings, dry cows, milking cows) under a common roof. There was ready contact between animals in adjacent pens, but not otherwise.

The farm was maintained as a closed unit; there had been no cattle introductions for six years prior to 2005, and all cows were artificially inseminated. The farm was well fenced and there was no history of contact with any animals from other herds. Animals were moved between Fragments 1 and 2, and between Fragments 1 and 4, on foot and via farm vehicle, respectively. Water was sourced from either a deep sealed well (the southern part of Fragment 1) or mains supply (all other areas), and supplied to water troughs (some less than 28 inches high, not all free-standing). No machinery, housing, crushes or other facilities were shared with other farms, and all slurry and dung spreading was conducted by the herdowner.

Liquid milk was stored in a bulk tank, before collection for processing by a local milk cooperative. Raw (unpasteurised) milk from the bulk tank was consumed routinely by the farm family. A total of 6 people lived on the farm, including the farmer and his wife, a grandparent, and three children (aged 4, 7 and 14).

### 2.2 Tuberculosis in animals

The tuberculosis testing history on the index farm is presented in Figure 3. Between 1989 and 2004, the farm had been restricted during 1993 (with one reactor), 1995 (5), 2003 (1) and 2004 (1); in the latter three years with confirmed infection. The herd experienced a significant TB breakdown, following initial detection on 12 March 2005, with 38 tuberculin reactors including cows (7), 2 yo animals (3 steers), 1 yo animals (2 steers, 1 heifer) and calves (13 autumn-born, 12 spring-born). At the tests in March and June 2005, TB-like lesions were detected on routine gross *post mortem* examination in 13 (48%) of these reactors, including 2 (67%) 2 yo animals and 8 (80%) autumn-born calves and 3 (75%) spring-born calves.

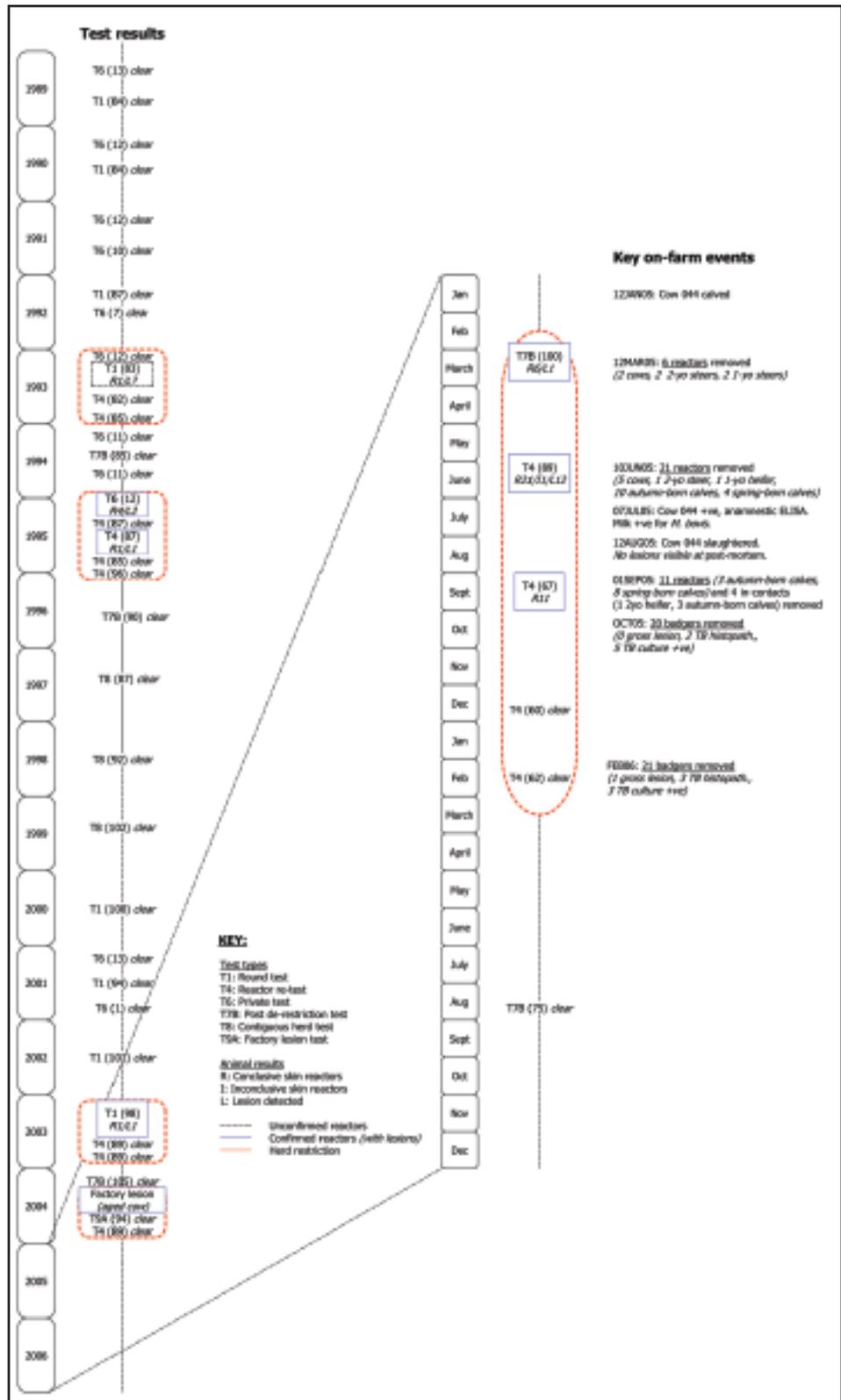


Figure 3. The testing history for tuberculosis on the index farm during 1989 to 2006. The test types include the round test (T1), the inconclusive re-test (T3), the reactor re-test (T4), the high incidence area test (T5C), the private test (T6), the post de-restriction test (T7B), the contiguous herd test (T8) and the factory lesion test (T9B). In this figure, the number of conclusive skin reactors (R), inconclusive skin reactors (I) and lesions detected (L) at each test are also presented. The herd was unable to trade, due to tuberculosis, during the periods encompassed by the red dashed line; further, the presence of unconfirmed and confirmed reactors is indicated by the dashed black and solid blue box, respectively

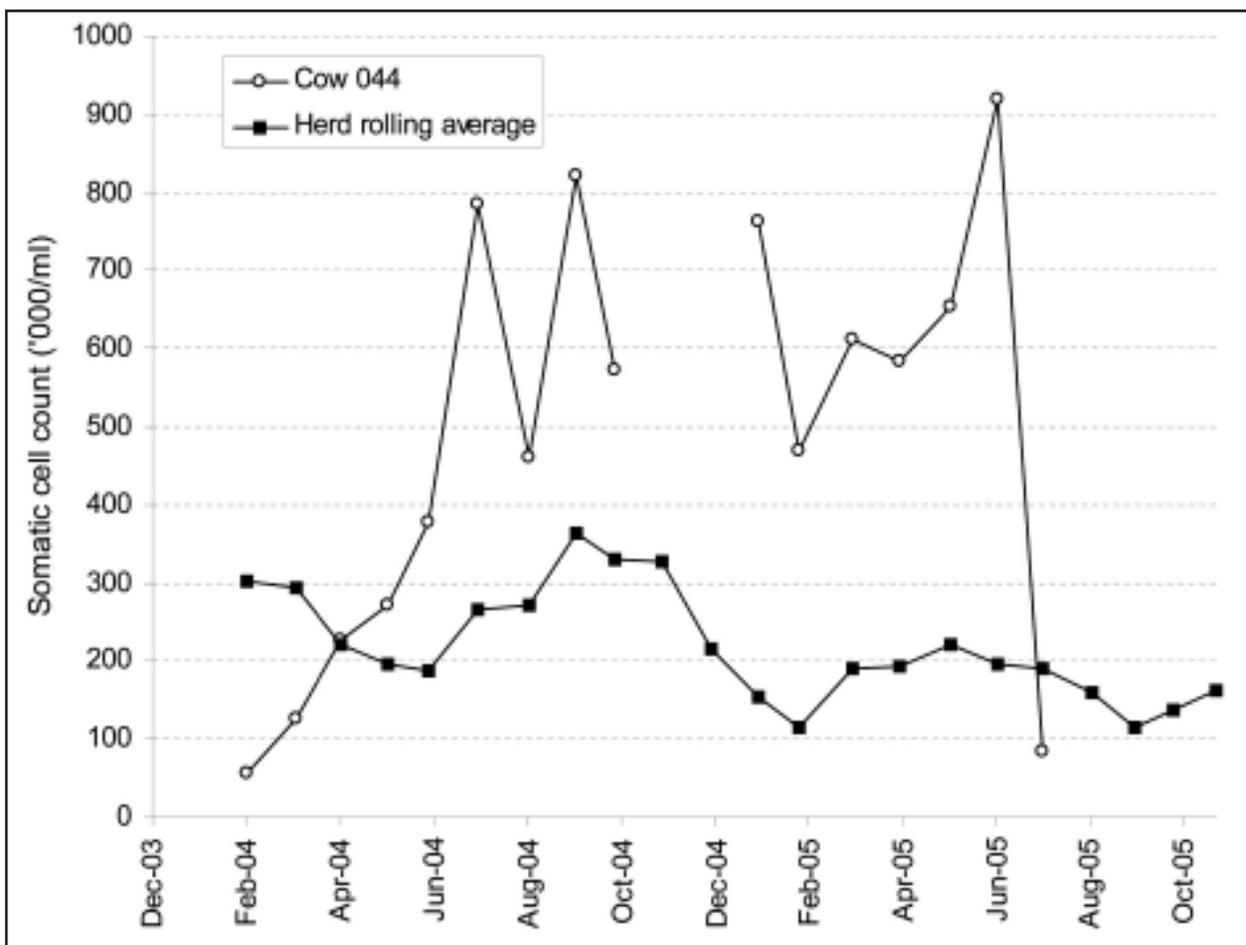


Figure 4. The somatic cell count (SCC) for cow no. 044 and all lactating animals on the index farm (3 month rolling average) during December 2003 to October 2005, based on individual milk recording conducted on a monthly basis. In July 2005, cow no. 044 was tested based on milk collected from the 3 non-mastitic quarters

The 11 reactors detected in September 2005 were removed alive as part of an unrelated tuberculin assay trial. They were subsequently slaughtered in July 2006; at *post mortem*, TB-like lesions were detected in 8 of these animals.

Tuberculous mastitis was diagnosed in a 7 yo cow (no. 044) on 7 July 2005, following the isolation of *M. bovis* from a mastitic quarter. *M. bovis* was not isolated from the three unaffected quarters. The 2005 lactation commenced, at calving, on 12 January 2005. Previously, the 2003/04 lactation extended from 18 August 2003 (calving) to 15 November 2004 (drying-off). As a result of chronic mastitis in one quarter (and an associated high somatic cell count; Figure 4), this cow's milk was mainly withheld from the bulk tank and fed to calves. The quarter was hard on palpation, with the consistency of the milk changing over time between thick and watery. However, on an intermittent basis (cumulatively approximately 3 weeks) during the 2005 lactation, milk from cow no. 044 was added to the bulk tank. This cow had been negative to the SICCT on each of 7 occasions since 2003, but was positive to an antibody-based anamnestic ELISA using bovine purified protein derivative (PPD) antigen on 7 July 2005. This cow was slaughtered on 12 August 2005. Although no detailed *post mortem* was conducted, no lesions were detected in lymph nodes, including the supramammary lymph nodes, during routine abattoir inspection. *M. bovis* was subsequently cultured from a supramammary lymph node.

The locality surrounding the index farm was not considered problematic for tuberculosis. A total of 6 cattle farms (Farms A-F)

had land directly contiguous to fragments 1, 2 and/or 4 of the index farm (Figure 1). Since 1998, there had been two TB breakdowns on Farm F (1 confirmed reactor in 1998/99; 1 unconfirmed reactor in 2003/04), one on Farm B (3 unconfirmed reactors in 2001/02) and none on the remainder.

Badgers were captured in this locality on two occasions, in October 2005 and February 2006. A total of 41 badgers were removed (20 in 2005, 21 in 2006), and all were subjected to *post mortem* examination. One of these animals had gross lesions consistent with TB. Of 22 badgers examined histopathologically, 5 (including 2 captured in 2005 and 3 in 2006) were positive. Of 18 badgers examined microbiologically, 8 (including 5 in 2005 and 3 in 2006) were positive. In total, based on results from histopathology and/or microbiology, 11 of 32 (34.4%; including 35.0% in 2005 and 33.3% in 2006) badgers had evidence of infection.

### 2.3 Tuberculosis in people

Six family members (grandmother, father, mother, 14 year old girl, 2 boys aged 7 and 4) lived on the farm. The father, mother and 14 year old girl had previously been vaccinated using BCG.

In June 2005, Mantoux testing was conducted on all family members, using 2 tuberculin units injected intradermally. The results of this test were as follows: grandmother (no induration), father (14 mm diameter induration), mother (12 mm), 14 year old (8 mm), 7 year old (12 mm) and 4 year old (14 mm). Chest x-rays on all individuals showed no abnormalities.

The 7 year old boy had no evidence of clinical TB and was treated as latent TB with prophylactic isoniazid initially, then rifampicin for a total of 6 months.

The 4 year old boy had two enlarged (approximately 5 mm diameter) lymph nodes in the right anterior triangle of the neck. Biopsy revealed acid-fast bacteria in these lymph nodes, but TB culture was negative. Pathological examination of the lymph nodes on microscopy showed partially opened cystic lesions measuring 1.5 cm in maximum diameter, which contained creamy friable material. There were further features of caseating granulomas and some lymphoid tissue on microscopy, which were highly suspicious of tuberculosis. This child was considered an active case of TB. The initial drug choice (ethambutol, pyrazinamide, rifampicin and isoniazid) was modified to ethambutol and rifampicin, once antibiotic sensitivity results (highlighting partial resistance to isoniazid and pyrazinamide) became available from the culture of milk from cow no. 044. Treatment continued for 13 months. There were no liver or ocular complications from the treatment.

Four months after stopping treatment, a swelling recurred in the same site on the right side of his neck. On excision biopsy, caseating necrosis was seen in a lymph node with surrounding lymphohistiocytic granulomatous reaction. There was no evidence of acid-fast bacteria and TB culture was negative. Full immunological assessment was normal. A differential diagnosis of re-infection, relapse of either *M. bovis*, *M. tuberculosis*, atypical mycobacteria or delayed immune reconstitution syndrome was made. Atypical mycobacteria were essentially excluded by a positive blood quantiferon test, which would confirm the diagnosis of TB but would not discriminate between *M. bovis* or *M. tuberculosis*. Treatment has been restarted with azithromycin, ethambutol, isoniazid, rifampicin and pyrazinamide and is on-going.

The grandmother, parents and 14 year old child had no overt signs of disease, and no treatment was undertaken.

### 2.4 VNTR profiling

VNTR typing was conducted on *M. bovis* isolated from the milk sample (from cow no. 044) and from five badgers captured in October 2005, based on six VNTR loci: QUB11a, QUB11b, ETRA, MIRU26, VNTR4052 and VNTR1895 and using primers and PCR conditions as described by Roring *et al.* (2004). Although *M. bovis* was isolated from a further three badgers in February 2006, VNTR typing is not available. No bacteria were cultured from the human cases.

Three different VNTR profiles were identified (i: 11 4 6 5 4 4 based on the earlier loci sequence, ii: 11 4 7 6 3 4, iii: 10 3 7 5 4 4). The isolates from the milk and from two badgers (captured at setts J and S, see Figure 1) were each VNTR profile i. Different VNTR profiles (ii and iii) were found in two badgers captured at sett N. VNTR profile iii was also identified in a badger captured at sett H.

## 3. DISCUSSION

This paper reports an outbreak of bovine TB in cattle and people following the consumption of raw milk on an Irish dairy farm, which clearly demonstrates the infection risk for calves and people associated with a case of tuberculous mastitis. A wide range of measures are in place to minimise transmission between animals and people, and infection is now very rare. However, these measures do not address practices such as on-farm pasteurisation, which remain the responsibility of individual farmers. The case highlights the importance of this on-farm measure.

During 2005, a substantial number of calves and people became infected following the consumption of milk from cow no. 044 (there is no evidence suggesting additional cases of tuberculous mastitis on the index farm). Of 16 and 12 calves born during autumn 2004 and spring 2005, 13 (81.3%) and 12 (100%), respectively, were subsequently identified as TB reactors between June and September 2005. Similarly, 5 of 6 family members were positive on the Mantoux test in June 2005. The 2005 spring- and autumn-born calves each received infected milk on an almost continuous basis between birth and weaning. Due to milk quota restrictions, extended feeding of whole milk was undertaken in this herd. Generally, two cows (including cow no. 044) contributed to the discard milk, and calves were weaned at various ages between 5 and 8 months. On 10 June 2005, lesions were detected in 3 spring-born calves (at most, 4 months of age), which highlights the degree to which this milk was infectious. This finding is supported by information from the human cases. The family collected milk from the bulk milk tank, and consumed it without pasteurisation. During 2005, they will have had only very limited exposure to the milk from cow no. 044, because it was rarely added to the bulk tank, and will have been substantially diluted in any case. It is not possible to determine when cow no. 044 first became infected, although it should be noted that this cow had been consistently negative when tested using the SICTT on seven occasions since 2003. Although a substantial increase in the somatic cell count was observed during the latter third of the 2003/04 lactation (Figure 4), there is no indication that this cow was infectious until her 2005 lactation.

The consumption of raw milk does not fully explain the transmission of infection among cattle within the index herd. In addition to the 25 milk-fed calves, there were a further 13 cases in older animals, including milking cows (7 animals), steers (three 2 yo animals, two 1 yo animals) and a heifer (1 yo). Cow no. 044 may have been the index case during this outbreak. Pulmonary lesions were not detected, however, only a very limited examination is possible at abattoir post mortem inspection. The immunological profile of high antibody levels and an absence of skin reactivity to tuberculin has been associated with progressive disease and possible respiratory shedding of *M. bovis* (Welsh *et al.*, 2005). This animal remained with each of the other milking cows (including 6 TB cases) throughout the year, but did not have direct contact with the younger stock, either whilst grazing or in housing. It is very unlikely that the younger animals had been infected during a previous lactation (for example, in 2004) since other cases would have been expected; further, extensive testing had been conducted during this period. Other alternatives are also feasible (for example, a number of animals infected independently from a common source). Although the initial transmission components remain uncertain, cow no. 044 played a key role in the later transmission of infection to the calves and the family.

The TB outbreak during 2003 to 2005 in the index herd was the result of either residual infection or introduction from wildlife, although the latter seems more likely. The index farm had last experienced a confirmed TB outbreak in 1995, and it is possible that one or more animals, including the aged cow with lesions detected

at slaughter in 2004, may have been infected (but remained anergic) during the intervening period. Note that cow no. 044 was born in 1998, three years after this earlier outbreak. Similarly, a diverse range of *M. bovis* strains, suggesting complex infection dynamics, are prevalent in local wildlife. Three different *M. bovis* strains were found in the locality, including strains with two different VNTR profiles in badgers from the same sett. The *M. bovis* isolate was identical from cow no. 044 and from badgers from two setts, including one adjacent to Fragment 1 (the home farm). This information provides no indication of the direction of transmission (badgers to cattle, cattle to badgers) nor can it distinguish whether both species were exposed to an independent common source. Nonetheless, earlier work has highlighted the importance of badgers in the epidemiology of bovine tuberculosis in Ireland (Griffin *et al.*, 2005). There is no evidence to support introduction of infection through purchased infection and as a result of spread from neighbouring farms. No cattle had been introduced onto the index farm for 6 years prior to 2005. Further, there was a high level of biosecurity on the index farm, and no opportunity for direct contact with cattle on neighbouring farms. The area was not a TB 'hot-spot'. This herd experienced a further TB breakdown in 2007, following a positive herd test on 16 August 2007. At this test, 4 SICTT reactors were identified, including one cow with milary TB. It is currently unclear if the 2007 breakdown is due to residual recrudescence or further wildlife involvement.

Bovine infection with *M. bovis* has been eliminated or substantially reduced throughout Europe, and, as a consequence, is generally not considered a substantial zoonotic risk. Nonetheless, public health concerns have recently been raised in the UK following the resurgence of *M. bovis* infection in cattle (Evans *et al.*, 2007; Jalava *et al.*, 2007), and it is recognised as an ongoing zoonotic risk in other industrialised countries, including Canada (Fanning *et al.*, 1991; Liss *et al.*, 1994) and New Zealand (Baker *et al.*, 2006). Although *M. bovis* remains prevalent in the Irish cattle population (More and Good, 2006), many measures are in place to limit exposure to the human population. In particular, infected animals are removed early in their clinical course, and milk is pasteurized before sale. Nonetheless, spill-over of infection is still possible. This case highlights the risks associated with the consumption of raw milk. In this family, TB has had a very significant impact on the health of two young children. These risks are well-recognised (Anon., 2003; Buckley *et al.*, 1998), and relevant information for farmers is available (Food Safety Authority of Ireland, 2005). It is of concern, therefore, that raw milk consumption remains prevalent on Irish farms. In a survey of 230 liquid milk suppliers in 8 Irish counties, families on 84% of farms reported the consumption of unpasteurised milk (Buckley *et al.*, 1998). There seems little doubt that new strategies are needed, in partnership with industry, to address this important issue.

#### 4. ACKNOWLEDGEMENTS

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# AN ALL-ISLAND APPROACH TO MAPPING BOVINE TUBERCULOSIS IN IRELAND

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## ABSTRACT

Bovine tuberculosis (TB) remains an important animal health issue throughout the island of Ireland, which includes the jurisdictions of Northern Ireland and the Republic of Ireland. A comparison of the differing experiences within these two jurisdictions may be instructive, noting the differing approaches to TB control over many years. In this paper, we have used geographic information systems (GIS) to explore the spatial patterns of TB in the whole island over an 11 year period using techniques that incorporate methodologies of both point-process and polygon-based visualisation without the need to conform to the conventional limitations imposed by political or administrative boundaries. All active farms with cattle in Northern Ireland and the Republic of Ireland between 1994 and 2006 ('the study years') were compiled into a single spatial coverage, and the number of tuberculosis tests and the number of disclosed tuberculosis standard reactor animals were summarised by farm for each of the study years. Two different GIS methodologies were employed to visualise the spatial patterns in tuberculosis over time, including density (kernel smoothing) and thematic mapping. Using each method, we present the cattle population, the reactor population and the relative risk surface during each study year. This is the first time that data from the island of Ireland have been collated to examine spatial patterns of the cattle population and of bovine tuberculosis across the whole island. This project demonstrates the value of cross-border projects in analysing cattle population and notifiable animal disease data. Whilst this study was restricted to a visual representation of an all-island problem, the techniques used can be expanded and developed in many ways, the ultimate aim being to assist in future collaborative informed policy making.

## 1. INTRODUCTION

Bovine tuberculosis (TB) remains an important animal health issue throughout the island of Ireland, which includes the jurisdictions of Northern Ireland and the Republic of Ireland. In Northern Ireland, the control of TB commenced in 1935, with the slaughter of clinically affected animals, and a compulsory eradication scheme was established in 1959 (Abernethy *et al.*, 2006). In the Republic, eradication efforts commenced in 1954 (More and Good, 2006). These programmes are currently directed by European Council Directive 64/432, as amended (Anon., 1964). Further, each is underpinned by laboratory and epidemiological support and research (for example, Denny and Wilesmith, 1999; Pollock and Neill, 2002; Griffin *et al.*, 2005; Costello *et al.*, 2006). Reactive badger removal is conducted as part of the control programme in the Republic of Ireland, but not Northern Ireland.

There have been similarities, but also differences, in eradication measures for bovine tuberculosis in Northern Ireland and the Republic of Ireland, which share a lengthy common border. During the 1950s and early 1960s, progress throughout the island was good, leading to a substantial decrease in animal incidence. However, in both jurisdictions, eradication has proved elusive. A range of factors have been identified as constraints to eradication, as discussed previously (Abernethy *et al.*, 2006; More and Good, 2006).

Geographical Information Systems (GIS) enable data to be visualised and examined spatially. At a simple level, data representing locations of interest or an event can be visualised in space as point maps. Data occupying an area such as a county or electoral division can be represented as a polygon with a defined shape. Count data can be assigned to these shapes and visualised through colouring or shading as a choropleth map (Cromley and Cromley, 1996). Disease data is commonly recorded at a point level and then assigned to an area and represented as a choropleth map (for example, More, 2006; Centers for Disease Control and Prevention, 2007).

The aim of this project is to use GIS to explore the spatial patterns of TB in the whole island over an 11-year period using techniques that incorporate methodologies of both point-process and polygon-based visualisation without the need to conform to the conventional limitations imposed by political or administrative boundaries.

## 2. MATERIALS AND METHODS

In total, 198,156 point locations representing all active farms with cattle in Northern Ireland and the Republic of Ireland between 1994 and 2006 were compiled into a single spatial coverage. The technique used for determining the point representation for farms differs between Northern Ireland and the Republic of Ireland:

- The Department of Agriculture and Rural Development, Northern Ireland (DARDNI) uses a system whereby the point location of the home farm is recorded in the Animal and Public Health Information System (APHIS), the national database for animal disease and movement control.
- In the Republic of Ireland, the Land Parcel Identification System (LPIS), a spatial database created by the Department of Agriculture, Fisheries and Food (DAFF) to manage European Union Area Aid claims, contains the location of the farm areas claimed by 95% of all farms. The centre of gravity or centroid of the largest fragment of land of each farm is calculated and used as a point representation of that farm.

There were certain discrepancies between the northern (Northern Ireland) and southern (Republic of Ireland) data through time before 1999. The LPIS data were first compiled in 1999. Herd numbers that changed or went dormant between 1994 and 1998 do not exist in the southern spatial database.

The number of tuberculosis tests and the number of disclosed tuberculosis standard reactor animals were summarised by farm for each of the study years. In each administration, a standard reactor at the single comparative intradermal skin test is defined, in accordance with Annex A of Directive 64/432/EEC (Anon., 1964), as

'a positive bovine reaction which is more than 4 mm greater than the avian reaction'.

Two different GIS methodologies were employed to visualise the spatial patterns in tuberculosis over time and are described, as follows:

The first method involved transforming the point locations representing farms from Cartesian coordinates (X, Y) into a continuous surface. This technique is known as kernel smoothing and uses a bivariate probability density function (or kernel) to allocate a density distribution at each location, based on the selected bandwidth or search radius (Bailey and Gatrell, 1995). Two surfaces were generated for each year, one representing the number of animals tested (Figure 1) and one the number of standard reactors (Figure 2). The output values for these surfaces were per square kilometre. The disease surface (standard reactors) was then divided by the population surface (number of animal tests) to create a relative risk surface for each year (Figure 3). This work was conducted using ArcGIS 9.1 (ESRI, Redlands, CA, USA). The reactor and population surfaces were separately generated (using the Spatial Analyst extension - kernel density) using a 15 kilometre search radius and a grid size of 250 metres. A 10 kilometre search radius was used for the enumerator raster surface to eliminate the edge effect associated with dividing raster surfaces of matching extents. Then, the relative risk surface was calculated (using 3D Analyst, Raster Math, Divide function), and the output surface was masked to a coverage of the coast of the island.

The second method involved the generation of a uniform surface of 5,662 hexagons covering the area of the island of Ireland, each hexagon having a cross-sectional width of 5 km (a circle with a diameter of 4.3 km would fit inside a hexagon). Hexagons were generated using a custom script in ArcGIS 9.2 (ESRI, Redlands, CA, USA). Whole hexagons were clipped to the outline of the island. Each hexagon was assigned a unique identification number (ID), and all farm points were associated with hexagons using a point in polygon analyses. Data were summed by hexagon ID in Microsoft Access (Microsoft Corporation, Redmond, WA, USA) and joined back into the hexagon coverage in the GIS. Dividing an area into hexagons or triangles (a hexagon being derived from 6 triangles) is more efficient than using squares (White *et al.*, 1992). All neighbouring cells are equidistant from a centre cell in all directions. In a grid consisting of squares, there is distance decay where the horizontal and vertical distance to neighbouring cells is less than the diagonal distance (Nekola and White, 1999). All farms were assigned to the hexagon in which their point representation fell. The animal test and standard reactor information associated with all farms were then summarised for each hexagon and displayed as thematic maps (Figures 4 and 5). A measure of relative risk was represented by dividing the summarised disease data with the summarised population data in each hexagon and expressed as a percentile (Figure 6).

### 3. RESULTS

The density maps are presented in Figures 1-3, and the thematic maps in Figure 4-6. The location of non-agricultural land (predominantly mountain and/or bog) is evident in Figures 1 and 4.

## 4. DISCUSSION

This is the first time that data from the island of Ireland have been collated to examine spatial patterns of the cattle population and of bovine tuberculosis across the whole island. Disease statistics are usually aggregated and displayed by administrative boundaries, which may obscure any underlying spatial patterns spanning boundaries. Additionally, until now there have been differences in both the calculation and presentation of disease statistics in each jurisdiction, thereby limiting comparison. As illustrated in Figure 3, a high level of animal-level TB risk was present in south Co. Armagh (Northern Ireland) and Co. Monaghan (Republic of Ireland) during 1998. Using smoothed surfaces or fixed sized area units to represent disease in a population makes it very straightforward to discern localised patterns in space and time, especially in the context of attempting to represent data from two adjoining countries with a shared non-biosecure border.

The maps highlight some of the differences in TB experience between the two jurisdictions. As illustrated in Figure 6, there has been some improvement in animal-level TB risk in the Republic of Ireland throughout the period 1996 to 2006. Within this period, the situation was worst in 1998, with TB risk highest in the border counties, including Co. Monaghan. In 2006, TB risk was at a lower level, but remained widely dispersed, throughout the Republic of Ireland. In Northern Ireland, Figure 6 highlights the increased TB risk during 1998 to 2002, particularly in counties Down and Fermanagh. By 2006, substantial improvements in TB risk had been achieved throughout Northern Ireland, although TB risk remained higher in this jurisdiction compared to the Republic of Ireland.

Farms in both Northern Ireland and the Republic of Ireland are subject to varying levels of fragmentation. The extent of fragmentation is highly varied throughout the country with farms in the Republic having an average of 4 fragments of land. In this study, we have represented farms as points, which does not take this fragmentation issue into account. However, it should not cause any significant concerns with analyses conducted at an all-island level. In addition, for the analysis performed, the data were further consolidated into larger units (hexagons), or smoothed over large areas (kernel density analysis). These two techniques also have the added advantage of anonymising the data, thereby making it impossible to identify individual farms.

The kernel density maps (Figure 3) should be interpreted with caution, as it may appear that there is almost no disease in certain areas. This is because it is a spatial relative risk illustration of positive cattle to population. The display intervals reflect the very high incidence in some areas, while high cattle density in other areas may mean that there are positive cases but a relatively low incidence when these are compared to the underlying population. The process of smoothing reduces output precision to an area of at least the size of the kernel bandwidth. This limits its usefulness to identifying generalised large-scale trends at the expense of detecting localised clustering. In contrast, the hexagon maps are conceptually simple. There is no extrapolation or interpretation. The output is a spatial summary at a defined level that depends on the size of the hexagon grid. With this method both large scale and small scale trends can be seen visually.

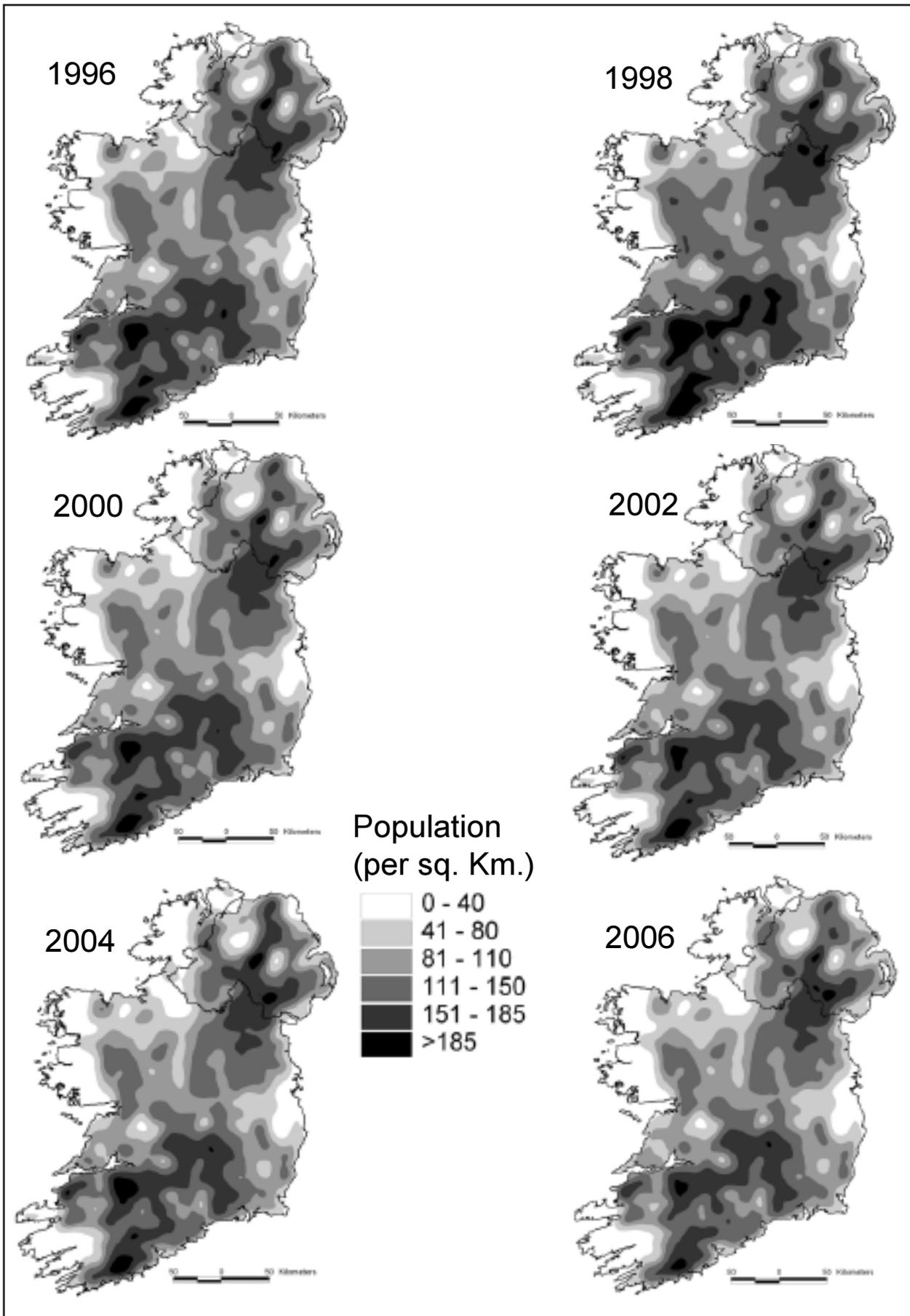


Figure 1. Density map of the TB-tested cattle population each year on the island of Ireland for the years 1996 to 2006

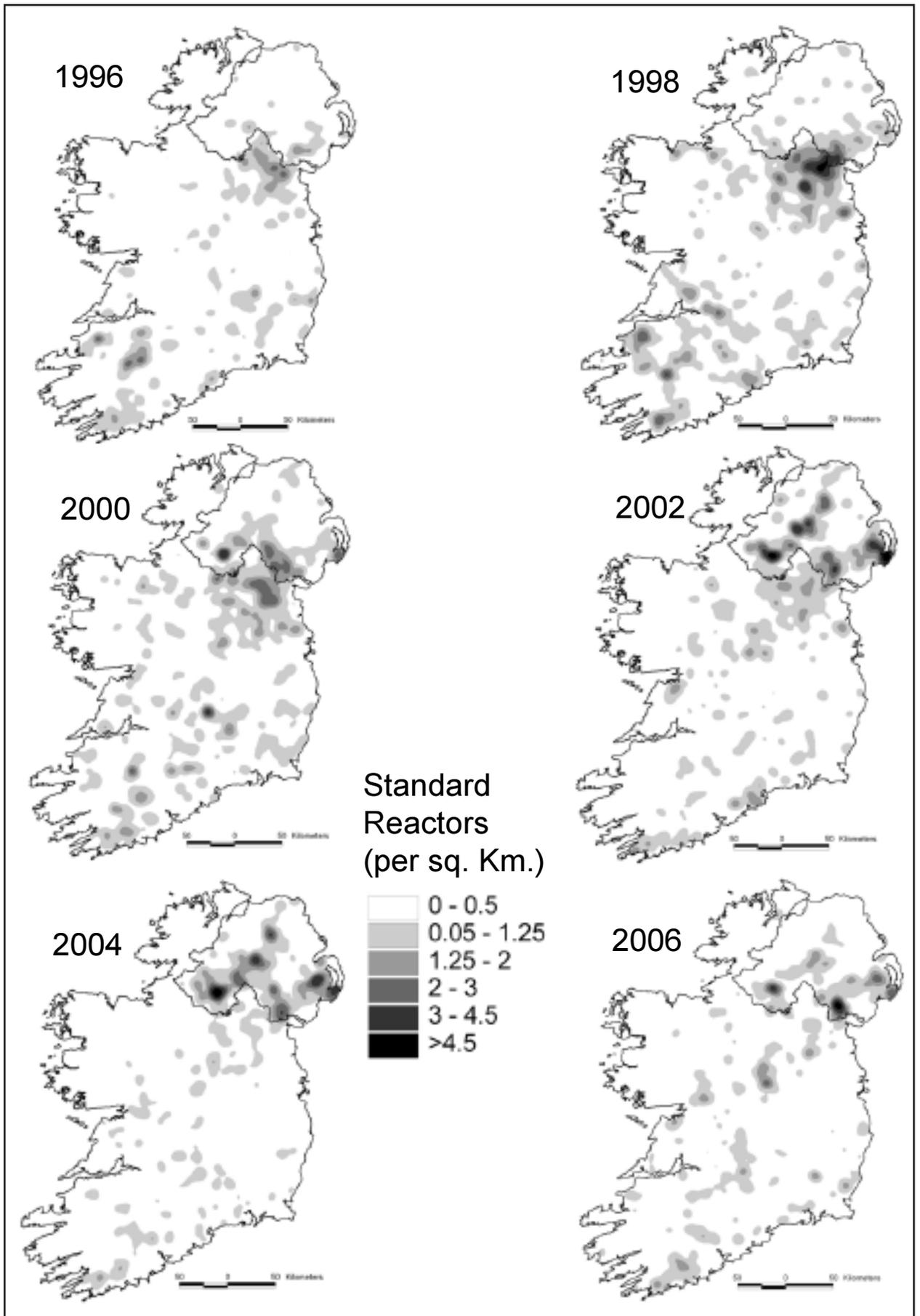


Figure 2. Density map of TB standard reactors detected each year on the island of Ireland for the years 1996 to 2006

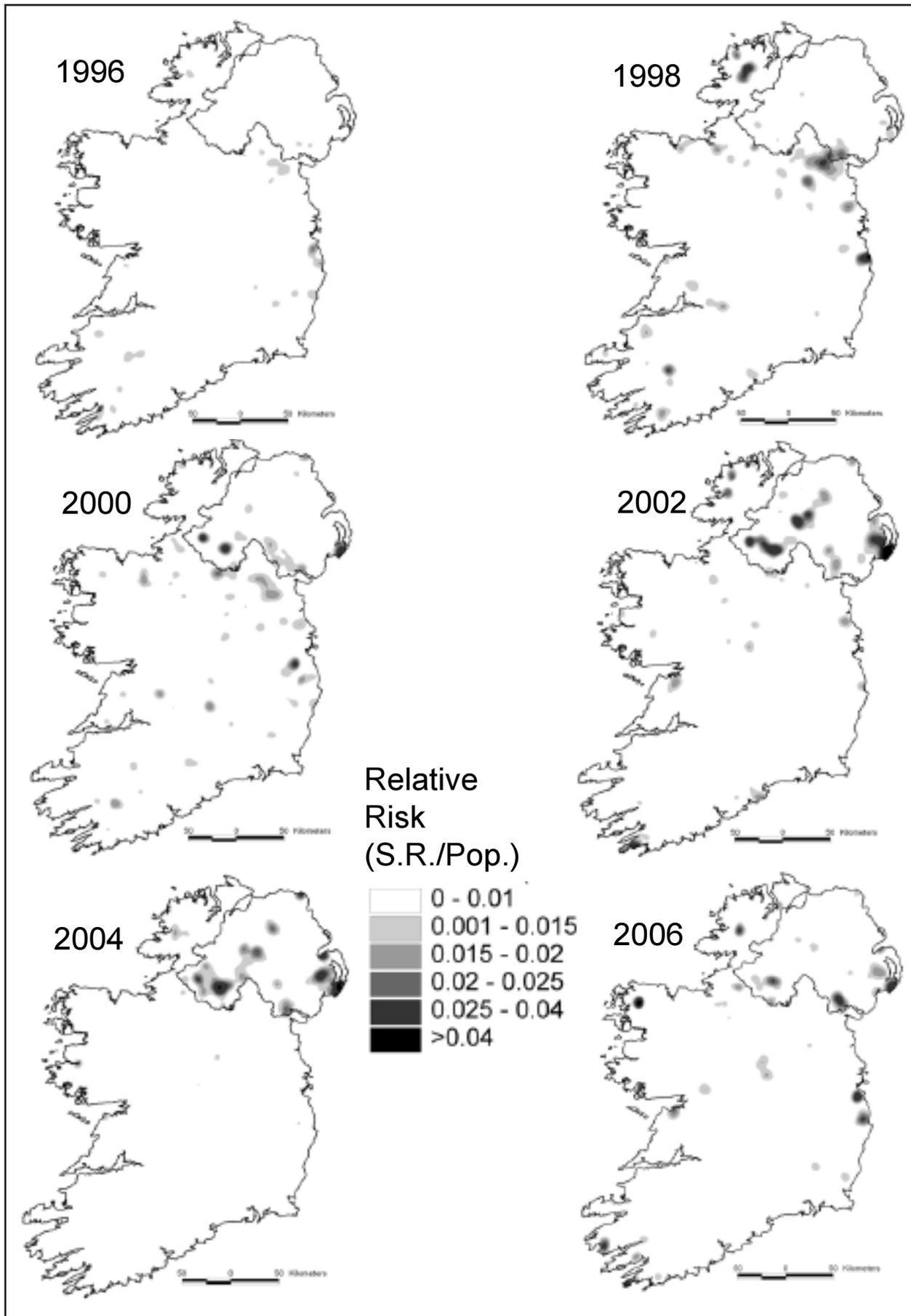


Figure 3. Density map of animal-level TB risk each year on the island of Ireland during 1996 to 2006. Animal-level TB risk was calculated each year as a relative risk surface after overlaying the density map of TB standard reactors over the density map of cattle population tested for TB

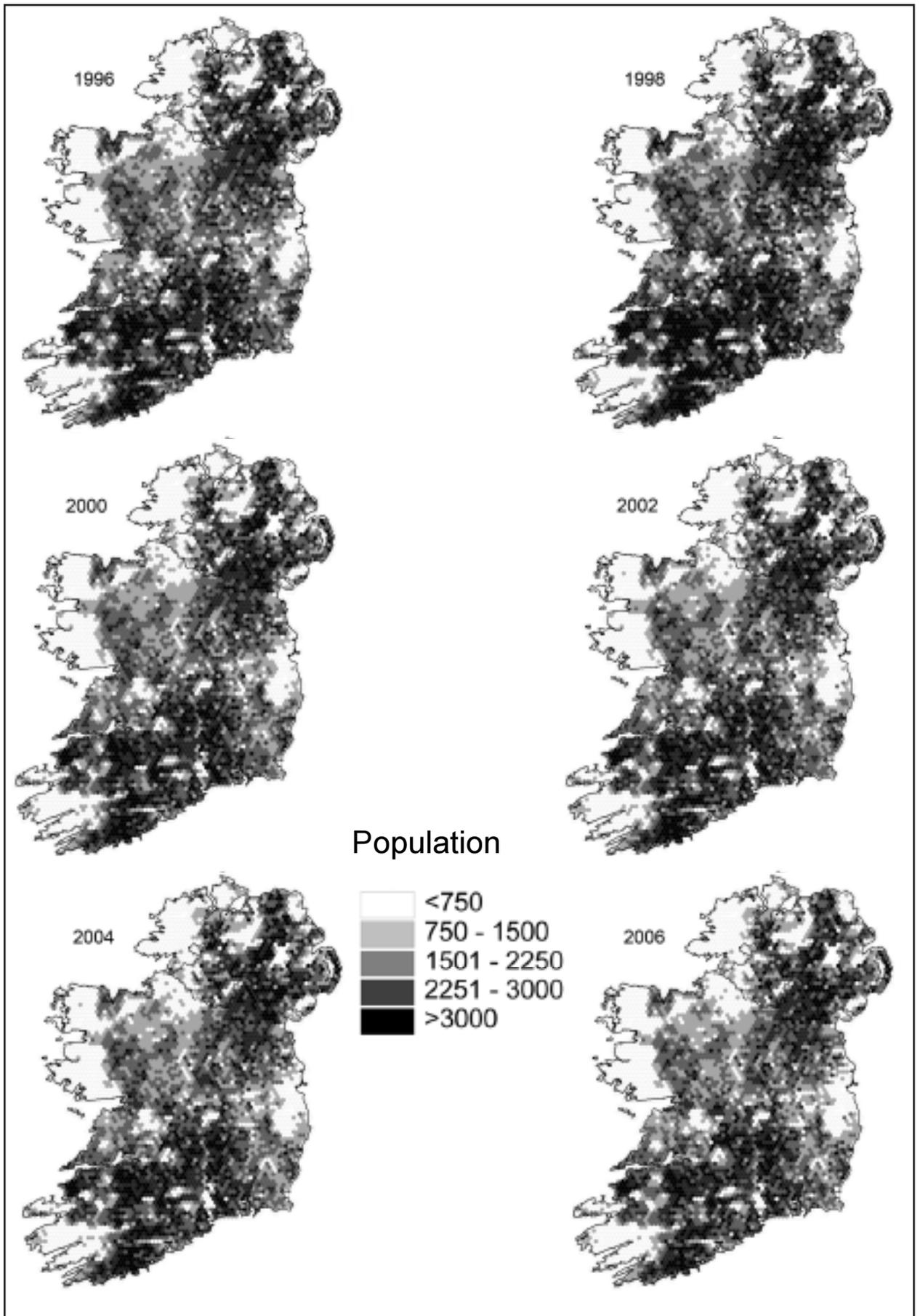


Figure 4. Thematic map of the TB-tested cattle population each year on the island of Ireland from 1996 to 2006. Cattle population data from each farm were assigned to the relevant hexagon, based on the location of its point representation

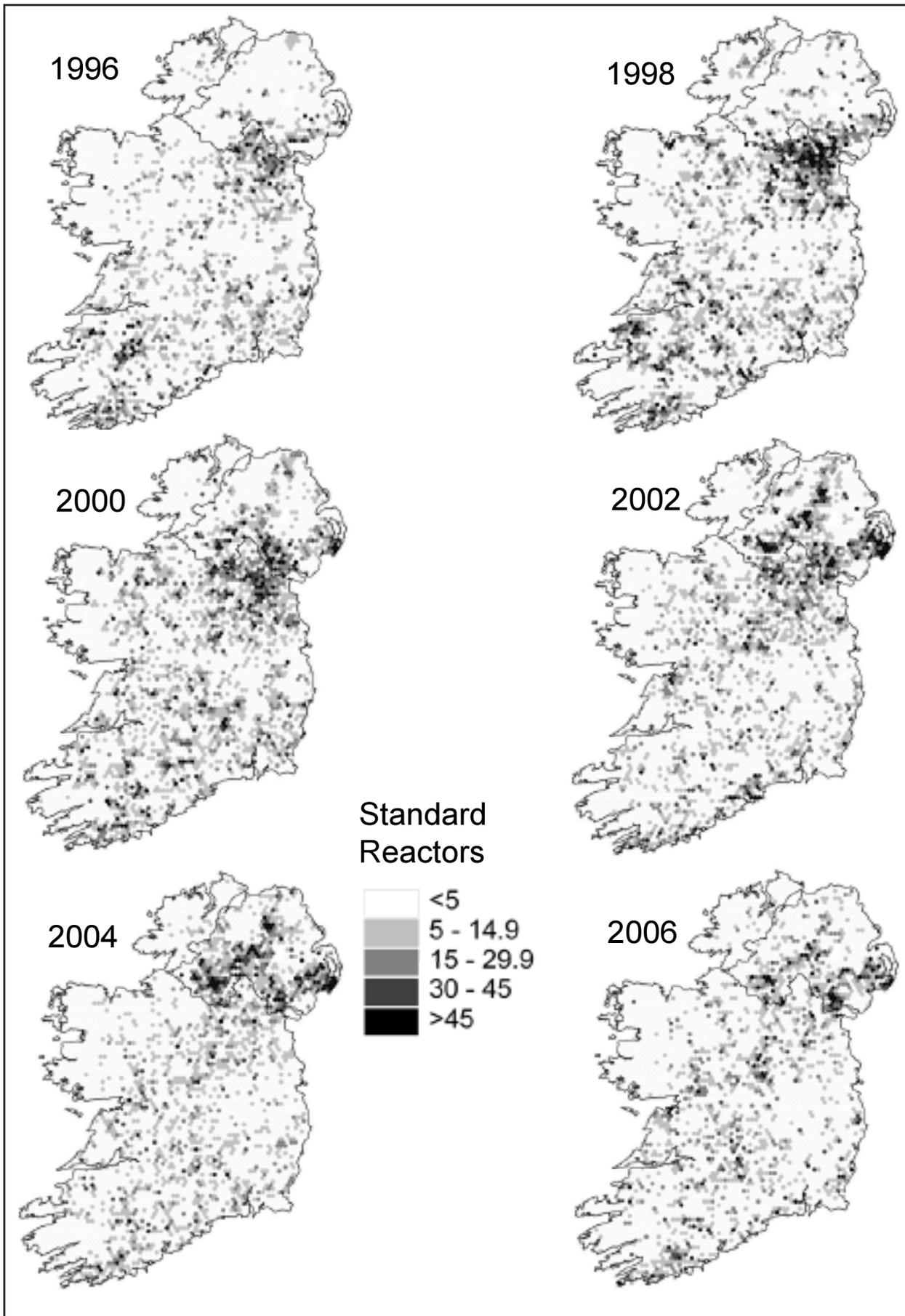


Figure 5. Thematic map of TB standard reactors detected each year on the island of Ireland from 1996 to 2006. TB reactor data from each farm were assigned to the relevant hexagon, based on the location of its point representation

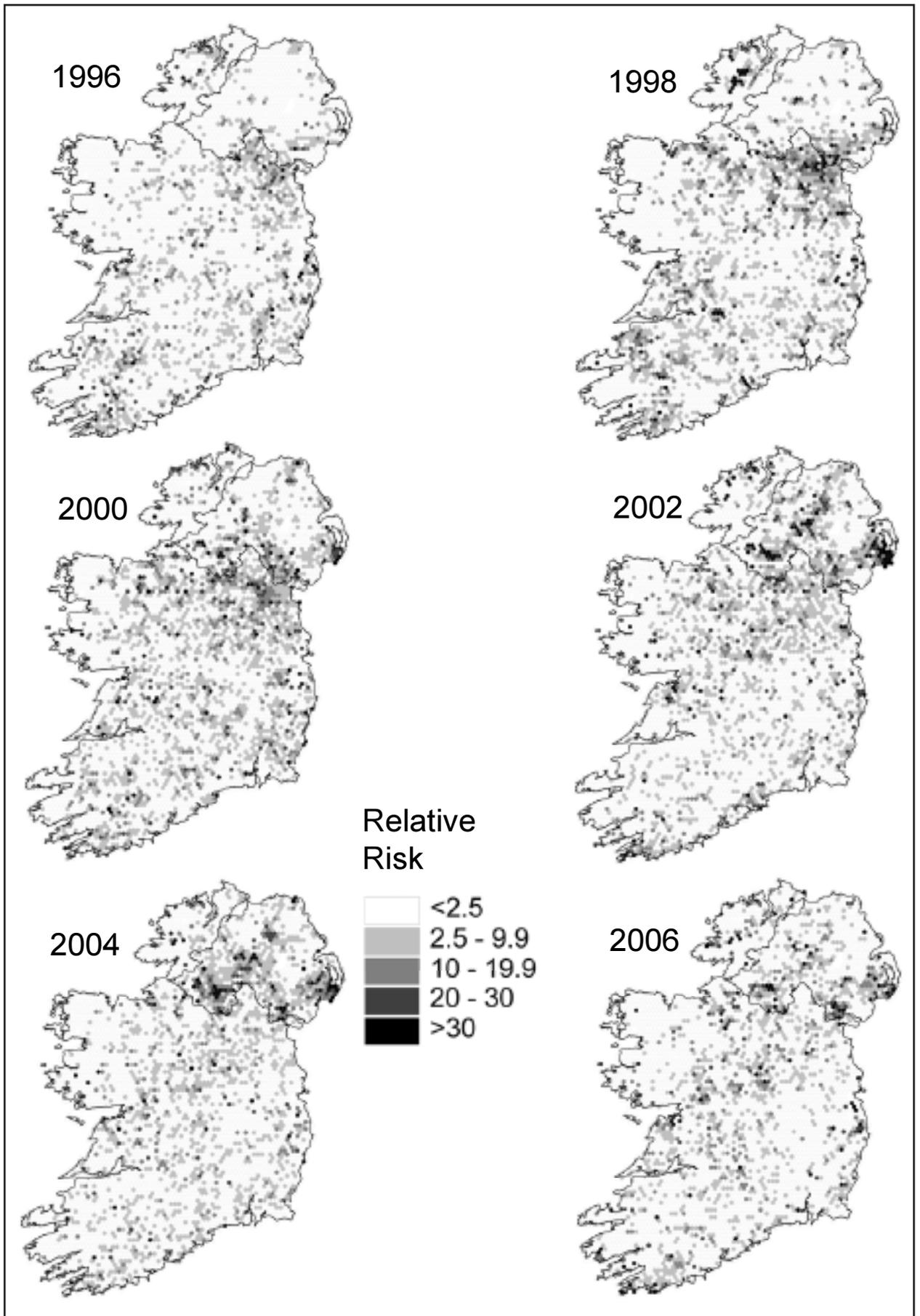


Figure 6. Thematic map of animal-level TB risk each year on the island of Ireland from 1996 to 2006. Animal-level TB risk was calculated each year after dividing the summarised disease data with the summarised population data in each hexagon and expressed as a percentile

## 5. CONCLUSIONS

This project demonstrates the value of cross-border projects in analysing cattle population and notifiable animal disease data. It is hoped that it sets a valuable precedent which can be applied to other animal diseases, as well as a more-detailed evaluation of bovine tuberculosis, particularly in border counties. Whilst this study was restricted to a visual representation of an all-island problem, the techniques used can be expanded and developed in many ways, the ultimate aim being to assist in future collaborative informed policy-making.

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## MAKING FERTILITY RECORDS TALK

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### ABSTRACT

The analysis of herd management records allows for accurate assessment of the current status of the herd, a crucial decision making tool to implement effective change. Monitoring of such changes to ensure their effectiveness is essential to the success of any programme, while participation in discussion groups allows for peer comparisons, a key factor in motivating herd management change. The aim of this review is to evaluate the effectiveness of fertility reports to improve dairy herd performance. Two sample reports are included.

### INTRODUCTION

Intensively managed dairy herds must achieve fertility targets to ensure long-term economic viability, and costs associated with poor fertility have been highlighted in many studies<sup>1,2,3</sup>. Integrated computerised programmes for fertility, health and production facilitate herd management<sup>4</sup>. The analysis of herd management records allows for accurate assessment of the current status of the herd, a crucial decision making tool to implement effective change. Monitoring of such changes to ensure their effectiveness is essential to the success of any programme. Furthermore, participation in discussion groups, allows for peer comparisons, a key factor in motivating herd management change.

### REPRODUCTION EFFICIENCY OF CATTLE HERDS

Reproductive efficiency in cattle herds is dependent on high submission and conception rates to service. In Ireland, our reliance on grass-based management systems dictates that the vast proportion of our dairy cows calve in spring-time. Individual cows should calve within a pre-defined calving season in order to maximize the economic output of the herd, optimizing milk production from spring and early summer grass growth, and enabling maximal growth rates of beef calves following turnout to grass, resulting in heavier calves at weaning and longer postpartum periods for re-breeding.

Seasonal calving patterns are greatly affected by the proportion of cyclic cows within the herd at the start of the breeding season. An increased interval from calving to first oestrus is associated with reduced conception rate to first service, and cows that have not cycled by 60 days post-partum have a higher risk of being culled than those that have displayed oestrus<sup>5</sup>. Indeed, prolonged post-partum anoestrus is a major limitation of reproductive efficiency in both beef<sup>6</sup> and dairy<sup>7</sup> herds. A number of factors including negative energy balance and body condition, nutrition, suckling, the incidence of disease and the use of exogenous hormones influence the length of the calving to conception interval.

Poor management is a key difficulty in Irish dairy herds and while oestrous detection rates of 90% have been reported in a New Zealand study<sup>8</sup>; the average oestrous detection rate in the Northern Ireland has been estimated to be 70%<sup>9</sup>. More worryingly, a Northern Irish study conducted by White and Sheldon<sup>10</sup> reported that 20% of cows submitted for service had progesterone concentrations > 5 ng/ml, indicative of the presence of active luteal tissue, and were clearly incorrectly presented for insemination. Similarly, McCoy *et al.*<sup>11</sup> reported that 12% of cows

submitted for service had high progesterone concentrations and indeed, the two farms with the highest number of incorrectly staged cows had the poorest conceptions rates over the past three years, highlighting the consequence of inaccurate heat detection. Thus, the reproductive efficiency of herds utilizing artificial insemination is further confounded by the need to accurate heat detection.

Coincident with increasing milk yields, conception rates in dairy cattle are declining by between approximately 0.5 and 1% per year worldwide. This negative relationship between increasing milk yield and fertility is well described<sup>12,13</sup>, and is more evident in multiparous than primiparous cows<sup>14</sup>. The average conception rate to first service in a Northern Irish study was 37%, and ranged from 21 to 66%, indicating considerable farm variation<sup>9</sup>. While, analysis of the Teagasc DairyMIS herds indicated that the situation is less extreme in the Republic with one study suggesting that 48% of cows become pregnant to the first service<sup>15</sup>. Caution must be taken while interpreting this seemingly good result, as this was based on pregnancy diagnosis, not calving rate. At any rate, conception rates, in Irish dairy cattle are decreasing at a rate of between 0.5 to 0.9% per year, with calving interval increasing by approximately one day per annum<sup>16</sup>. As the proportion of Holstein genes increase in the national herd, herds become larger, labour more expensive, and off-farm employment more frequent, it is imperative that we assess, monitor and aim to improve our dairy herds fertility performance to ensure economic performance.

### COMPUTERISED FARM RECORDS

The quality of the records is likewise important; the old adage applies, "rubbish in, rubbish out". It cannot be emphasised enough, incomplete or inaccurate records lead to erroneous assessments and ineffective advice. Farm records should include cow identities and age, calving dates, dates and times of all observed heats, date of services, bull and inseminator used, dates bull ran with the cows, details of reproductive examinations, including pregnancy tests and synchronisation treatments. Most importantly, sufficient numbers of animal events are needed for accurate evaluation and effective decisions making.

Calculation of fertility indices is possible with the use of spreadsheets or more sophisticated software, such as InterHerd, DairyWIN and Kingswood Herd Management. However, with the development of additional services from the Irish Cattle Breeding federation (ICBF), fertility reports are now available to all farm subscribed to HerdPlus. In time, data generated from HerdPlus will allow the collation of national statistics to evaluate cattle fertility statistics. The target indices for dairy herds in two different management systems are presented in Table 1.

Table 1. The target fertility indices for Irish dairy herds for either a seasonal grass based, moderate yielding herd and for higher genetic merit herds

	Seasonally calving grass-based herd	High genetic merit herd
Calving Interval (days)	365	400
Calving to first service (days)	≥42	60 - 100
Submission rate (21 days; %)	90	low
Calving to conception interval (days)	82	100 - 140
Conception rate to single service (%)	60	40
Overall pregnancy rate (%)	95	90?
Mean no. of services per cow per year	1.4	2
Culling rate for infertility (%)	< 5	< 10
Short repeat interval (0-17 days; %)	5 to 10 %	5 to 10 %
Normal repeat intervals (18-24 days; %)	> 65 %	> 65 %
Abnormal repeat intervals (25-35 days; %)	< 10 %	< 10 %
Missed repeat intervals (36-48 %)	< 10 %	< 10 %
Long repeat intervals (> 48 days; %)	< 10 %	< 10 %
3 to 6 week ratio	6:1	6:1

## CONCLUSIONS

The use of herd management programmes ensures that fertility indices are measurable, and can be used for decision making to implement management changes, thus, enabling monitoring the effectiveness of these changes and their effects on herd profitability. Collation of individual herd data, within discussion groups and nationally, enables peer comparisons, a key motivator for farm improvements.

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## FERTILITY INVESTIGATION – CASE 1

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Herd Owner: FFR 0001  
 Investigation: Dairy herd fertility  
 Farm visits: 5<sup>th</sup> September and 1<sup>st</sup> November 2007  
 Report: 14<sup>th</sup> November 2007

### OVERALL ASSESSMENT

Herd fertility good, certainly well above the average for Irish dairy farms, with the intervals from calving to first heat, first service, conception and calving very good on average, but spread exists in calving and breeding pattern, resulting in the need for extended supervision for calving cows and increased time heat detecting. Furthermore, the high proportion of late calving cows will be dried off earlier in lactation leading to a significant loss of milk production. The low percentage of cows submitted for service by 42 days, 63% compared with the aim of 90%, and repeat interval analysis suggests that some cows are submitted to service are either not in heat or not cycling. Increased attention to heat detection should improve this. Heifer fertility has not been addressed in this report.

Conception rates are good, but conception rate to AI is 21% less than to the bull, despite the similar age profiles and the number of days in milk for both groups. Indeed, the cows bred to AI are mainly the early calving cows and hence should have a better chance of going in calf. Attending to the accuracy of heat detection is required to improve this and adherence to the AM/PM rule for AI. Serving cows too early after calving is resulting in a 40% decrease in conception rate. While a few cows have gone in calf before day 42, it is best to avoid serving cows before 42 days after calving. Early and mid season calving cows have better conception rate to 1<sup>st</sup> service than late calvers, as late calvers are served too early after calving (average 36 days), decreasing their chance of going in calf to first service. Finally older cows have lowered conception rates to first service (18% v 64%) but they are mainly part of the late calving group, and hence lowered conception rate is expected.

### AIM FOR HERD

To reduce the length of the calving season with the aim to calve 90% of cows in first 8 weeks of calving season

### RESULTS

Parameter	Result	Target	Comment
2007 calving season	15 weeks	12 weeks	Spread in calving season leading to increased need for supervision at calving
2008 calving season	14 weeks	12 weeks	Predicted improvement for 2008 expected, but still greater than aim of 12 wks
% cows calving in the 6 wks before breeding	41%	20%	Too many cows are calving late in the breeding season, this puts pressure on these cows to go back in calf quickly and also contributes to the spread in the calving pattern
Calving to 1 <sup>st</sup> heat	40 days with 63% cows by 42 days	40 days with 90% cows by 42 days	Excellent average interval from calving to first heat, first service and conception, but spread exists. Only 63% of cows are detected in heat by 42 days after calving, indicating some cows are being missed or perhaps are not cycling; 40% cows received 1 <sup>st</sup> service by day 60, and only 60% cows in calf by day 83 after calving. The predicted calving interval varies from 306 to 441 days, with only 63% cows due to calve within 365 days. This will lead to cows being dried off early, along with increased time required for supervision at calving and for heat detection. Identify cows not in heat by 42 days, and not served by 60 days after calving for close attention and vet examination
Calving to 1 <sup>st</sup> service	63 days	60 days	
Calving to conception	77 days	83 days	
Predicted calving interval	357 days	365 days	
Submission rate (24d)	73%	90%	Recommendations should improve this
Submission rate (42d)	100%	98%	Excellent
Conception rate to 1 <sup>st</sup> service	57%	50%	Very good
Conception rate to subsequent services	57%	60%	Adequate
Pregnancy rate (4 wk)	54%	50%	Very good
Pregnancy rate (8 wk)	83%	90%	Reasonable, but should improve if recommendations followed
No. services per cow	1.7	1.4	Too many services per cow. See recommendation 5
Not in calf rate	4%	Less than 5%	Excellent

## HEAT DETECTION

Repeat Intervals	Short (0-17d) %	Normal repeat (18-24d) %	Abnormal (25-35d) %	Missed (36-48%) %	Long (>48d) %
Target	5 -10	>65	<10	<10	<10
Actual	18	54	21	3	5

Heat detection efficiency (finding cows in heat) is very good, however, too many cows are having short cycles and abnormal length of cycles. This often means that some cows are incorrectly identified as being in heat. Recommendation 1 should be followed to improve this.

## RECOMMENDATIONS

1. Aim to conduct heat detection 4 times daily for at least 30 minutes, at 6 and 10am and 6 and 10pm, while the cows are in field, in addition to observation during walking to and from parlour. This will maximise the chances of detecting cows in heat. Be clear as to which cow is selected in heat; she should be standing to be mounted by another. Do not assume that the cow mounting is in heat (although she is usually around the time of heat). Consider using tail paint or other heat detection aids to help with heat detection. We can give more advice, if interested. Always follow the AM/PM rule when submitting cows for AI.
2. To increase submission rate, spend 3 weeks prior to the planned start of the breeding season, conducting intensive heat detection. Any cow, calved more than 42 days, that is not seen in heat in this 3 week period should be examined by a vet.
3. Consider using strategic prostaglandin injections to increase submission rate in the first two weeks of the breeding season and hence reduce the length of the calving season (explained in Appendix 1).
4. Cows, calved more than 42 days, that are not seen in heat by Day 24 of the breeding season, and cows not served by 60 days after calving should be examined by a vet.
5. Do not serve cows until at least 40 days calved (they have a 40% less chance of going in calf compared with those served after 42 days). This will increase conception rate to first service and decrease the number of services each cow requires to go in calf, lowering costs of AI.

## APPENDIX 1

### Using prostaglandin to increase submission rate

1. Only select cows calved by Feb 14<sup>th</sup>, with no abnormal discharges or disease. Cows calved after Feb 14<sup>th</sup>, may not be cycling and hence will not respond to prostaglandin injection. Based on our predictions, about 70% of the herd will have calved by Feb 14<sup>th</sup> next year.
2. Assume the breeding season will start on 5<sup>th</sup> April 2008, similar to 2007.
3. For cows seen in heat between 14<sup>th</sup> to 20<sup>th</sup> March, give nothing. These cows should cycle in first week of the breeding season between April 4<sup>th</sup> and 12<sup>th</sup>. Serve when in heat in April.
4. For cows seen in heat between 21<sup>st</sup> and 27<sup>th</sup> March, give one injection of prostaglandin on April 3<sup>rd</sup>, these cows should come in heat between 5<sup>th</sup> to 10<sup>th</sup> April, Serve when in heat.
5. For cows seen in heat between 28<sup>th</sup> March and 3<sup>th</sup> April, give one injection of prostaglandin on April 10<sup>th</sup>. These cows will come into heat between April 12<sup>th</sup> and 18<sup>th</sup>, and serve at this April heat.
6. 90% of cows selected for this programme should come in heat in first 14 days of breeding season. This improves submission rate, and should help shorten the calving season in 2009.
7. If a cow has not been seen in heat between 14<sup>th</sup> March and 10<sup>th</sup> April, you can consider giving them a prostaglandin injection on April 10<sup>th</sup>. Approximately 60% of these should show heat between April 12<sup>th</sup> and 18<sup>th</sup>, and should be served when they do.

Prostaglandin is sold under the trade names of Estrumate/Prosolvlin/Lutalyse, these must be obtained from your vet and used under their direction.

NB. if you suspect that **cows are not cycling** correctly after calving, this treatment will have **very poor** response rates.

Finally, this programme is very much dependent on **excellent heat detection** for the 3 weeks prior to the breeding season and for the first 2 weeks of the breeding season. Aim to heat detect at a minimum for 5 times daily during this period at 6 and 10am, 12 noon, and 6 and 10pm for a minimum of 30 minutes on each occasion. Be very clear which cow is in heat and record all mounts. The **definitive sign for heat being that the cow stands to be mounted**; the cow mounting is usually close to being in heat, in heat or just gone out of heat. Aids such as tail paint can be used to help heat detection. Submit for service using the AM/PM rule.

## FERTILITY INVESTIGATION – CASE 2

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Herd Owner: FFR 0002  
 Investigation: Dairy herd infertility  
 Farm visits: 21<sup>st</sup> November 2007  
 Report: 1<sup>st</sup> December 2007

### OVERALL ASSESSMENT

Herd fertility is generally very problematic, certainly well below the average for Irish dairy farms, with the intervals from calving to first heat, first service, conception and calving very poor on average. It is important to bear in mind that the milk production of this herd is well above the national average (10,000l per 305 day lactation), and so we would certainly expect poorer fertility in these high genetic merit cows compared with herds with more moderate yielding cows.

We would recommend that this herd aims to achieve a 400 day calving interval, as achieving an interval of 365 days would be impractical with such high yielding cows. We would suggest that the herd is divided into spring and autumn calving with cows that calve late allowed to slip from spring to autumn and vice versa. For reasons discussed during the farm visit, it would be difficult to expect heifers to calve at 24 months; the aim would be to calve heifers down for the first time at 30 months, and hence to be bred between 19 to 21 months. To optimise herd efficiency, we would suggest that heifers should calve at the start of the calving period, and should be allowed to slip by one month per year. Once they are determined to be late calvers within that calving period, they should be allowed to slip to the following breeding season.

Very importantly, massive spread exists in calving and breeding pattern, resulting in the need for extended supervision for calving cows and increased time heat detecting. The high proportion of cows not in calf at the end of the breeding season means that non pregnant cows are being carried over to the following year, and additionally, a decreased number of heifers are being produced, leading to loss of revenue from selling high genetic merit replacement heifers. The low percentage of cows submitted for service by 60 days (9%) and by 85 days (24%), compared with the aim of 90% by 85 days (to maintain a 400 day calving interval), and results from repeat interval analysis suggests that some cows submitted to service are either not cycling or are not in heat. Increased attention to heat detection should improve this, and strategic veterinary exams to determine whether cows are cyclic or not.

Conception rates are poor (21% to first service and 30% to all services). However, conception rate to AI is only 4% less than to the bull, suggesting that management of AI is not a factor in the poorer fertility. Late calvers also have a much lower chance of going in calf than early and mid calvers (11% to first service versus 33% for early calvers and 20% for mid calvers). Cows are not served too early on this farm and hence this should not be a factor in the poor fertility. Finally, older cows have lowered conception rates to first service (18% v 64%) but they are mainly part of the late calving group, and hence lowered conception rate is expected.

Heifer fertility is generally good, suggesting the management of the cows could be optimised.

We would recommend nutritionist advice for the herd. During our visit, questions were raised with regard to the high body condition of the dry cows. Calving cows down in high body condition score results in poor dry matter intakes following calving and increased loss of condition in the first 6 weeks of lactation. Cows should not lose more than 0.5 units condition score during this period. A greater loss indicates increased negative energy balance, and is associated with poorer fertility.

### AIM FOR HERD

To divide cows into spring and autumn calving patterns to ensure more focussed times for calving and breeding supervision, and increase the overall pregnancy rate by the end of breeding season

## RESULTS

Parameter	Result	Target	Comment
2007 calving season	30 weeks	12 weeks in two periods	Spread in calving season leading to increased need for supervision at calving and spread in breeding season
2008 calving season	29 weeks	12 weeks in two periods	Similar pattern predicted for 2008
% cows calving in the 6 wks before breeding	61%	20%	Too many cows are calving late in the calving season and into the breeding season; this puts pressure on these cows to go back in calf and also contributes to the massive spread in the calving pattern
Interval from calving to 1 <sup>st</sup> heat	106 days with only 9% in heat by day 60	60 days with 90% cows by 60 days	Very poor average interval from calving to first heat, first service and conception, massive spread exists, only 9% of cows are detected in heat/served by 60 days after calving, and only 24% by day 85, indicating cows are being missed or may not be cycling. The predicted calving interval is 413 days and varies from 348 to 515 days, with only 42% cows (that went in calf) due to calve within 400 days. Such spread in calving means that time for calving supervision and heat detection is required almost all year around. It also means that with only a few cows due in heat at any one period, they will be harder to detect in heat. Similarly, because these are high yielding cows, heat periods will be short and less intense, making it even more difficult to detect in heat. Identify cows not in heat by 60 days and not served by 85 days after calving for vet exam to determine normality
Interval from calving to 1 <sup>st</sup> service	106 days with range from 36 to 234 days	85 days	
Interval from calving to conception	133 days with range from 65 to 235 days	115 days	
Predicted calving interval	413 days with range from 348 to 515 days	400 days	
Conception rate to 1 <sup>st</sup> service	21%	50%	
Conception rate to subsequent services	36%	60%	
Pregnancy rate (4wk)	4%	50%	Focusing on improving the interval from calving to first heat detection, and first service will improve pregnancy rates for each calving period
Pregnancy rate (8wk)	17%	90%	
No. services per cow	2.4	2	Too many services per cow. Due to low end of season pregnancy rate, the number of services per conception is very low. Indication of poor conception rates
No. services per pregnancy	3.3	2	
Not in calf rate	36%	Less than 10%	Very poor. This needs to be addressed

## HEAT DETECTION

Repeat Intervals	Short (0-17d) %	Normal repeat (18-24d) %	Abnormal (25-35d) %	Missed (36-48%) %	Long (>48d) %
Target	5 - 10	>65	<10	<10	<10
Actual	2	48	17	13	21

Heat detection efficiency (finding cows in heat) is less than the target, too many cows are having abnormal cycles (inaccurate or early embryonic loss) and too many cows are identified as having missed cycles. Additionally, a very high proportion of cows having been identified as having long cycles. This may indicate a number of issues: 1) cows have been missed, 2) cows misidentified as in heat or 3) cows have experienced embryonic loss.

## RECOMMENDATIONS

1. We would recommend that this herd aims to achieve a 400 day calving interval, as achieving a calving interval of 365 days would be impractical with such high yielding cows. We would suggest that the herd is divided into spring and autumn calving with cows that calve late allowed to slip from spring to autumn and vice versa. For reasons discussed during farm visit, it has been suggested that it would be difficult to expect heifers to calve at 24 months; the aim would be to calve heifers down for the first time at 27 to 30 months, and hence to be bred between 18 to 21 months. To optimise herd efficiency, we would suggest that heifers should calve at the start of the calving period, and should be allowed to slip by one month per year. Once they are determined to be late calvers within that calving period; they should be allowed to slip to the following breeding season.
2. Seek advice from nutritionist with regard to a possible change to total mixed ration, to ensure that the cows are being provided with a balanced diet. Monitor body condition score at drying off, at calving and after 6 weeks of the breeding season for individual cows. Aim to calve cows down at condition score of 3 to 3.25. Cows should not lose more than 0.5 units body condition in first 6 weeks of lactation. A greater loss indicates that cows are experiencing too much negative energy balance, leading to poorer dry matter intakes after calving. These cows will have increased problems cycling normally and have difficulty going back in calf.
3. Extended intervals from calving to first service, results from the repeat interval analysis and the high proportion of cows not in calf at the end of the season suggests that oestrous cows are being missed or that there is a very high proportion of cows not cycling after calving. Attention to heat detection will be very important to improve this situation. Aim to conduct heat detection 4 times daily for at least 30 minutes, at 6 and 10am and 6 and 10pm, while the cows are in field, in addition to observation during walking to and from parlour. This will maximise the chances of detecting cows in heat. High genetic merit cows have shorter heat periods (often as short as 6 hours) and decreased intensity of heats (few number of mounts per heat period), thus care is needed with selection of cows as in heat. Also bear in mind that the spread that exists in the calving and breeding pattern means that very few cows are due in heat on any given day. Hence with a small sexually active group (cows coming in, in and going out of heat), the chances of detecting cows in heat are lower:
  - Consider using heat detection aids such as tail paint or Kamar heat detection aids to help with heat detection. Bearing in mind the spread in the cows, we would recommend the Kamar heat detection aids compared with the tail paint. Kamar can be placed on individual cows from 50 days after calving, if cows are not detected in heat by 70 days then she should be submitted for a veterinary examination.
  - Alternatively, a vasectomised bull with a chin ball to indicate oestrous cows is a consideration. However, if you do decide to go this route, ensuring that the bull is not producing viable semen every year is important. Although these bulls do not produce viable semen, they are essentially entire bulls from a behaviour point of view. Care would be needed with regard to children on the farm. We can give more advice, if required. This would be a very good option considering the spread in the calving and breeding pattern. The bull can overcome the problem with small sexually active groups, increasing the probability of detecting cows in heat.
4. To improve the intervals from calving to first heat and to first service, aim to detect 90% of cows in heat by 70 days post calving and to serve 90% of the cows within 85 days after calving. Bear in mind that high yielding cows will experience more anoestrus and increased numbers of abnormal cycles compared with more average cows. Any cow, calved more than 70 days, or not served by 85 days, should be examined by a vet and advice followed. The use of strategic prostaglandin (PG) could be considered to increase the number of cows in heat in a given period of time. Cows should only be given PG after a veterinary examination to determine they have a corpus luteum present. Please request more advice if interested.
5. Conception rate to first service is poor (21%) although cows are not served early in lactation. Conception rate to subsequent services improves (36%). Attention to nutrition and being definite that cows presented for service are in heat is important. Conception rate following AI is only 4% less than natural service which indicates management of AI is good.



# GLOBAL TRENDS IN MILK QUALITY: IMPLICATIONS FOR THE IRISH DAIRY INDUSTRY

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## ABSTRACT

The quality of Irish agricultural product will become increasingly important, with the ongoing liberalisation of international trade. This paper presents a review of the global and Irish dairy industries, considers the impact of milk quality on farm profitability, food processing and human health, examines global trends in quality and explores several models that are successfully being used to tackle milk quality concerns. There is a growing global demand for dairy products, fuelled in part by growing consumer wealth in developing countries. Global dairy trade represents only 6.5% of global production, and demand currently outstrips supply. Although the Irish dairy industry is small, by global standards, approximately 85% of annual production is exported annually. It is also the world's largest producer of powdered infant formula. Milk quality has an impact on human health, milk processing and on-farm profitability. Somatic cell count (SCC) is a key measure of milk quality, with a SCC not exceeding 400,000 cells/ml (the EU milk quality standard) generally accepted as the international export standard. There have been ongoing improvements in milk quality among both established and emerging international suppliers. A number of countries have developed successful industry-led models to tackle milk quality concerns. Based on experiences from a range of countries, it is likely that problems with effective translation of knowledge to practice, rather than incomplete knowledge *per se*, are the more important constraint to national progress towards improved milk quality.

## 1. INTRODUCTION

Global markets have been critically important to Irish agriculture for some years. In these, but also domestic, markets, competition will intensify as a result of ongoing moves towards liberalisation of international trade. In this setting, Irish agricultural product cannot hope to compete on price alone, and quality will become increasingly important to Ireland's ability to successfully compete into the future (More, 2007).

An understanding of global competitors, and of global trends in milk quality, will play an important role in the efforts of industry, at all levels, to strategically plan for the future. As a contributor to this process, this paper presents a review of the global and Irish dairy industries, considers the impact of milk quality on farm profitability, food processing and human health, examines global trends in quality and explores several models that are successfully being used to tackle milk quality concerns.

## 2. THE GLOBAL AND IRISH DAIRY INDUSTRIES

### 2.1 Global milk production

#### a. World dairy production

In 2006, world dairy production reached 644 million tonnes, from cattle (541 million tonnes; 84%), buffalo (12.5%, mainly from India and Pakistan), goats (1.9%), sheep (1.3%) and other (0.3%). Almost all countries produce milk for local consumption. However, the cost of production varies greatly depending on factors including labour costs, animal genetics, on-farm technology, and fodder and water availability (Blayney et al., 2006). In 2006, the largest cows' milk producers included the EU25 (142 million tonnes, 26.2%), the US (82.8, 15.3%), India (38.5, 7.1%; a further 52.5 million tonnes of buffalo milk was produced), China (27.5 [2005 figure], 5.1%), Brazil (24.7, 4.6%), Russia (15, 2.8%), New Zealand (14.8 [2005 figure],

2.7%), Ukraine (14.1, 2.6%), Argentina (10.8, 2.0%), Australia (10.4; 1.9%) and Mexico (10.5, 1.9%). Within the EU25, Ireland was the 8<sup>th</sup> largest producer of cows' milk (5.1 million tonnes, 0.95% of global production), behind Germany (28 million tonnes), France (24.3), United Kingdom (14.6), Poland (12.1), Italy (11.3), Netherlands (10.8) and Spain (6.1) (International Dairy Federation, 2006).

There has been strong and sustained growth in global dairy production, leading to a ten- and one-year rise of 18.6% (from 543 million tonnes in 1996) and 1.9% (from 632.3 million tonnes in 2005, respectively) (International Dairy Federation, 2006). This growth is mainly concentrated in China, India and the Americas (Argentina, Brazil, Mexico, USA). China has experienced very rapid growth in dairy production, with production doubling between 1990 and 2000, then again between 2000 and 2004 (Fuller et al., 2007). Between 2004 and 2005, cow numbers and milk production increased by 10% and 21%, respectively (International Dairy Federation, 2006). Argentina, Brazil and Chile have achieved self-sufficiency in milk production, and each is now focused on exports. In 2006, a long-term trend of increasing milk production in Australasia was adversely affected by adverse weather conditions (drought in Australia, unusually wet and cold conditions in New Zealand) (International Dairy Federation, 2006).

#### b. World dairy demand

There is a growing global demand (an increase of 3% globally, but more than 10% in some developing countries, and 15% in China) for milk and other dairy products. Global competitiveness is also fuelling new uses for milk-based ingredients, rising demand for cheese variety, an increase in niche product markets and increased product shelf life (Blayney et al., 2006; Anon., 2007a). The very sharp rise in world dairy prices since late 2006 (Berry and Hogan, 2007) was driven, in large part, by the strong global demand for dairy products, leading to record prices (exceeding €0.35c/l) for manufacturing milk in Ireland (Lavery, 2007). By early 2008, the price spike had peaked for commodities such as milk powders and butter, with market prices rapidly returning to more normal levels (Anon., 2008).

In wealthy countries, there have been substantial shifts in demand for dairy products. In the EU, the demand for cheese and other milk products (such as fresh cream, specialised milk protein for the food industry and other dairy ingredients) has risen, and butter consumption has fallen. Approximately 40% of milk within the EU is now consumed as cheese (Anon., 2006a). In the US, milk consumption is falling (concurrent with a rise in the consumption of carbonated drinks) (Huth et al., 2006), whereas butter consumption has remained steady (Henning et al., 2006). In recent years, there has been a substantial drive to retain market share in the face of non dairy substitutes. Functional foods (such as probiotic milks, yogurts and fermented dairy drinks) represent one strategy to capitalise on growing consumer awareness of the role of dairy components in health and vitality. There has also been a rapid technological advances in dairy processing (Figure 1), particularly the use of membrane technology (allowing the separation of milk components) for industry applications (Henning et al., 2006). A key outcome of this process, milk protein concentrates (principally liquid or spray-dried milk protein) is increasingly used as a food ingredients (for example, in frozen desserts, bakery and confectionary products) and for pharmaceutical use (Bailey, 2003; Blayney et al., 2006). A general

shift towards non-dairy substitutes has also been avoided, due to the rising price of substitute fats and proteins (Anon., 2007a).

In low-income countries, dairy products, including dry milk powders, remain luxury goods for many consumers (Blayney et al., 2006). Therefore, in Africa, the Americas and Asia, demand is fuelled in large part by increasing consumer wealth. *Per capita* milk consumption is rising, but often from a very low base (Fuller et al., 2007; Anon., 2007b). There has been a marked change in dietary patterns throughout Asia, as a consequence of higher incomes and changing consumption patterns (Berry and Hogan, 2007), leading to shifts towards 'western' foods including dairy products (Fuller et al., 2006; Pingali, 2006). Growing consumer income is also driving increased milk consumption in China (where there was an increase of 18% in 2006), India (a 6% increase), the Russian Federation and the Ukraine, and an increasing global demand for high-quality dairy products, particularly cheese (International Dairy Federation, 2006). In a recent study, Fuller et al. (2007) has highlighted the influence of education, advertising and convenience, as well as the increasing sophistication of the retail sector, in the growth of milk products in the Chinese market.

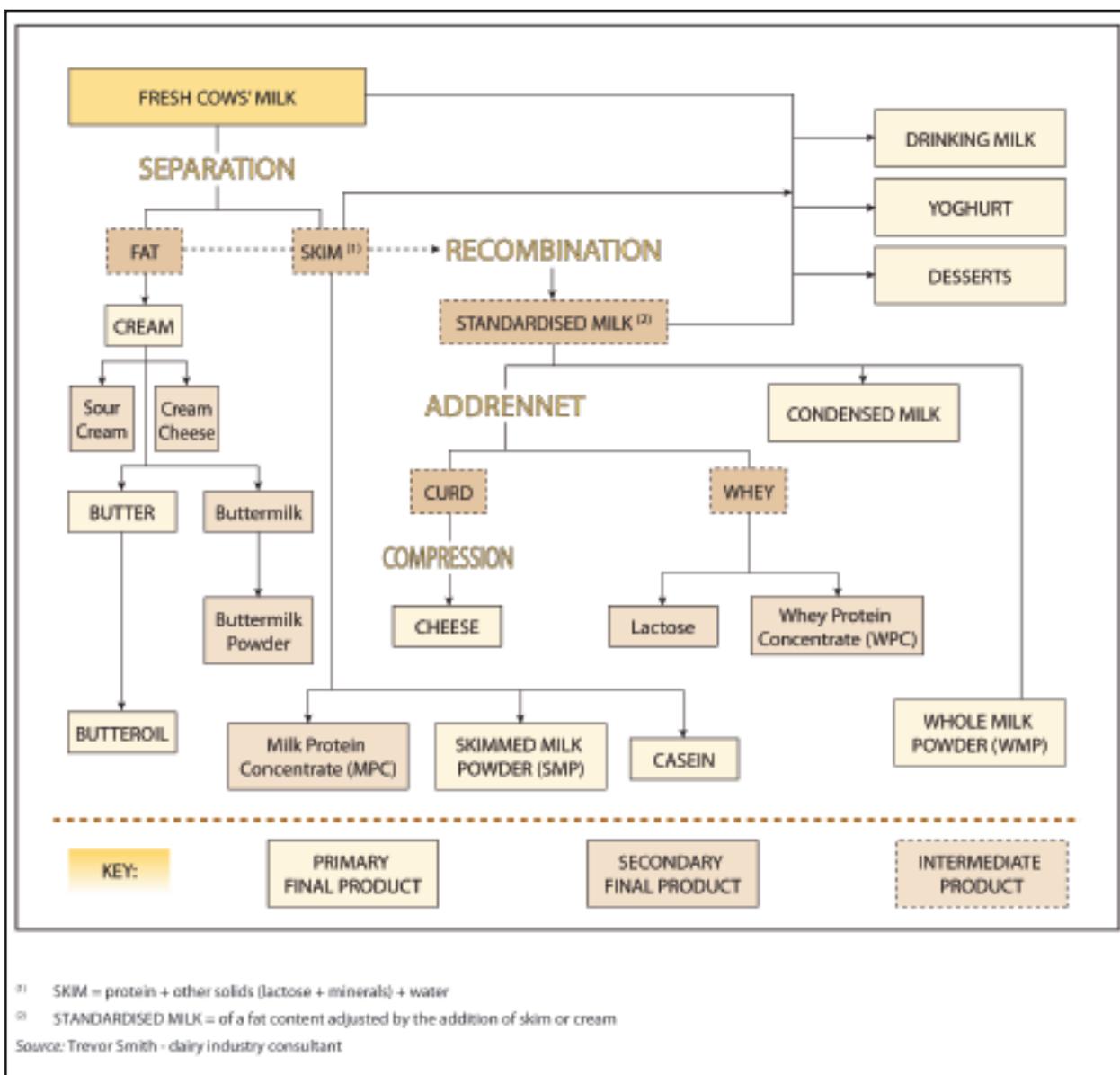


Figure 1. The conversion of milk, by a range of processes, into a variety of dairy products and food ingredients. From Anon., 2006a

### c. World dairy trade

Until fairly recently, the world dairy trade was considered a secondary market for the disposal of surplus commodities. In recent years, however, the trade has been facilitated by improved refrigeration and transportation technologies, and is being increasingly influenced by increasing global demand for dairy products (Blayney et al., 2006). The international dairy trade has been dominated for many years by the European Union (with 30% of global dairy trade) and Australasia (New Zealand, 32%; Australia, 12%) (Anon., 2007a). In broad terms, the EU focuses on the export of quality cheese to nearby traditional markets and to North America, whereas Australia and New Zealand, with low-cost milk production and active international marketing, are prominent suppliers of cheese and milk powder to Asian markets. New Zealand, in particular, is highly responsive to changing global demand (Blayney et al., 2006).

In 2006, 41 million tonnes (milk equivalents) were traded internationally, representing 6.5% of global dairy production. Milk powder is by far the most-commonly traded product (whole milk powder, 1.74 million tonnes in 2005; skim milk powder, 1.05) (International Dairy Federation, 2006). New Zealand is the largest exporter, followed by the EU and Australia, with lesser amount from Poland, Argentina and (for skim milk) the US. Milk powder is imported by a range of countries in Asia, Africa, the Middle East and Latin America (Anon., 2007b). There has been a steady growth (about 1% annually) in global trade in cheeses (1.58 million tonnes in 2005), from the EU and increasingly from Australasia. Japan, the US, the EU and Russia are key importing markets. The EU is facing increasing competition from other suppliers, including Argentina, in the Russian market (International Dairy Federation, 2006). The international butter market (0.9 million tonnes in 2005) is dominated by New Zealand and the EU, supplying Russia, the Middle East and North Africa.

Supply has been unable to match global demand for dairy products, for several reasons. The EU has become less influential in global markets, in part as a result of EU expansion (noting the specific exclusion of within-EU movement within the definition of 'world dairy trade'), limits to dairy production due to quota and environmental restrictions, and the suspension of all dairy export subsidies. Further, drought conditions have led to reduced milk production in Australia (Anon., 2007b), and there has been increased domestic production among countries that had previously imported (particularly Brazil, China, EU, USA) (International Dairy Federation, 2006). As a consequence, a number

of new international suppliers have emerged, including Argentina, Brazil, India, China and the Ukraine. There has been rapid export growth from Argentina (in 2006: 7% annual increase in dairy production, 40% annual increase in dairy exports) and Brazil (2.5%, 30%), and these countries have the potential to become major dairy exporters (Anon., 2007a). An increased demand for dairy products throughout Asia is likely to be met by several countries in South America (Argentina, Brazil, Chile), as well as Australia and New Zealand (Beghin, 2006). China is likely to remain a net importer of dairy products into the foreseeable future (Anon., 2007a), with demand outstripping the steady increase (19% in 2005) in local dairy production (Berry and Hogan, 2007). Prior to 2007, India had emerged as an important exporter of dairy products, particularly milk powder. However, exports were banned in early 2007, in an effort to stabilise domestic milk prices (Anon., 2007a).

### 2.2 The Irish dairy industry

In 2006, the Irish dairy industry produced 5.1 million tonnes of milk, equivalent to 0.95% of global dairy (cow) production (International Dairy Federation, 2006). As such, Ireland is a small global dairy producer. However, the industry plays a critical role to the national economy, accounting for approximately 3% to national gross domestic product (Anon., 2006b). Approximately 85% of annual production is exported, to a value of €2.1 billion and representing approximately a quarter of all food exports, to markets including countries in mainland Europe (38% of total exports), the UK (23%), North America (13%), Africa (13%) and Middle and Far East (8%). In 2007, the key outputs from the processing industry included butterfat (147,000 tonnes), cheese (136,000), SMP (skim milk powder)/BMP (butter milk powder) (88,000), choc crumb (45,000), WMP (whole milk powder) (38,000) and casein (40,000). Since 2005, there has been a marked increase in production of cheese and skim milk powders, and a decrease in choc crumb and casein (Anon., 2007c). Critically, Ireland is the world's leading producer of infant nutrition products, producing 15% of the world's powdered infant formula (Anon., 2007c). Three of the world's top four infant formula milk manufacturers (Numico, Wyeth Nutritional and Abbott Laboratories) operate in Ireland, generating approximately €506 million with an output in 2005 of approximately 112,000 tonnes of powdered infant formula (from 50,000 tonnes of milk powder and 13,200 tonnes of skim milk). In 2005, the formula milk sector was valued at over US\$10 billion globally, with a predicted growth in world consumption of 8.3% *per annum* in volume terms and 5.7% in value terms (Mooney, 2006).

#### In summary

In 2006, world dairy production reached 644 million tonnes, up by 18.6% since 1996 and 1.9% since 2005. The EU is the largest milk producer, followed by the US, India, China and Brazil. The growth in milk production is mainly concentrated in China, India and the Americas. 6.5% of global production is traded across national borders. There is a growing global demand for dairy products (approximately 3% annually), fuelled in large part by growing consumer wealth in developing countries. Global competitiveness is also fuelling new uses for milk-based ingredients, rising demand for cheese variety, an increase in niche product markets and increased product shelf life. Supply from traditional exporting countries (the EU, Australasia) has not kept pace with demand, leading to record international milk prices and the emergence of new suppliers. In global terms, the Irish dairy industry is small, producing 5.1 million tonnes (0.95% of global production). However, the industry exports approximately 85% of annual production and is a major contributor to the national economy. The industry is also the world's largest producer of powdered infant formula.

### 3. THE IMPORTANCE OF MILK QUALITY

#### 3.1 Definition

Raw milk quality encompasses criteria relating to composition (butterfat, crude protein, lactose, milk solids etc) and hygiene (total bacterial count, somatic cell count). Of these, somatic cell count (SCC) is the most important single indicator of milk quality, reflecting the health status of the mammary gland and the risk of non-physiological changes to milk composition (Hamann, 2005). It is also the key component of national and international regulation for milk quality (van Schaik et al., 2002). An udder quarter is considered healthy if it has an SCC < 100,000 cells/ml and is free of mastitis pathogens (Dohoo and Meek, 1982; Hamann, 2005). An elevated SCC is indicative of mastitis (inflammation of the mammary gland), generally caused by presence of infectious microorganisms (Hamann, 2005).

In response to consumer demands, the processing industry also has a growing interest in additional milk quality parameters relating to environmental considerations, animal welfare and food safety and traceability (Andersen, 2007; Nousiainen et al., 2007; Refsholt et al., 2007).

#### 3.2 The impact of milk quality on farm profitability

There are a range of economic consequences from clinical and subclinical mastitis, relating to treatment, production losses, culling and changes in milk quality (Hasala et al., 2007). Collectively, these factors have a substantial impact on the farm business. To this point, however, there has been little consistency among a range of studies in the reported costs of mastitis and the benefits from mastitis management. This variation partly reflects regional differences, for example in labour costs. In addition, Hasala et al. (2007) highlight important methodological differences between reported studies, which make comparison difficult. To overcome this difficulty, these authors propose an economic framework to consistently assess the economic effects of mastitis and mastitis management.

Increased somatic cell counts are associated with reduced milk yield. Estimates of milk loss from high SCC range from 0.3 to 1.8

l/cow/day, depending on the stage of lactation and SCC level (Hortet and Seegers, 199; Green et al., 2006). A slightly lower reduction in yield was measured, after accounting for the effect of dilution on SCC among high-yielding dairy cows (Green et al., 2006). There appears to be no loss of milk yield in cows with SCC up to approximately 100,000 cells/ml; therefore, economic benefits from driving cow SCC below this level are unlikely (Green et al., 2006).

#### 3.3 The impact of milk quality on milk processing

Milk quality has a substantial, adverse impact on milk processing. Mastitis is associated with an influx of inflammatory cells (hence, 'high somatic cell count' milk), and increased activity of heat-stable proteases and lipases, leading to a breakdown of casein and milk fat (Santos et al., 2003; Barbano et al., 2006). Herds with mastitis problems are also at increasing risk of antibiotic residue violation, as a result of increased antibiotic usage (Ruegg and Tabone, 2000; van Schaik et al., 2002).

There are a range of adverse effects from the use of high SCC milk in the production of cheese, including reduced curd firmness, decreased cheese yield, increased fat and casein loss in whey and compromised sensory quality (Ma et al., 2000). When used in the production of cottage cheese (made from acid coagulation of milk, rather than rennet), high SCC count milk was also associated with increased proteolysis during refrigerated storage (Klei et al., 1998). These effects would adversely affect the yield of milk protein concentrate (MPC), which consist of casein-type and whey proteins (Blayney et al., 2006). Mastitis also affects the quality of pasteurised liquid milk and reduces its shelf life (Ma et al., 2000).

#### 3.4 The impact of milk quality on human health

There is no evidence that high cell count milk is directly associated with adverse effects on human health (National Mastitis Council, 2001). However, high cell counts are associated with increased indirect risks, including poor farm hygiene, antibiotic residues and the presence of pathogenic organisms and toxins in milk. Heat-stable enterotoxins produced by *Staphylococcus aureus* in milk from infected cows has been implicated in cases of food poisoning (Anon., 2005a).

#### In summary

Milk somatic cell count is a key measure of milk quality, reflecting the health status of the mammary gland and the risk of non-physiological changes to milk composition. It is also the key component of national and international regulation for milk quality udder health and the prevalence of clinical and subclinical mastitis in dairy herds. Milk quality is important, with impacts on human health, milk processing and on-farm profitability:

- *Farm profitability:* There are a range of economic consequences of mastitis and mastitis management, relating to treatment, production losses, culling and changes in milk quality. Increased SCC is associated with reductions in milk yield.
- *Milk processing:* High SCC milk adversely affects cheese production, as a result of reduced curd firmness, decreased milk yield, increased fat and casein loss in whey and compromised sensory quality. High SCC milk also affects the quality of pasteurised liquid milk and reduces its shelf life.
- *Human health:* High cell count milk is associated with indirect risks to human health, as a result of poor farm hygiene, antibiotic residues and the presence of pathogenic organisms and toxins in milk.

### 4. GLOBAL TRENDS IN MILK QUALITY

#### 4.1 Legislative issues

Within the European Union, Council Directive 92/46/EEC of 16 June 1992 (with subsequent amendments) lays down the health

rules for the production and placing on the market of raw milk, heat-treated milk and milk-based products. These include a requirement that raw milk has a somatic cell count not exceeding 400,000 cells/ml, based on the geometric average of monthly samples over a period of three months (Anon., 1992). All dairy

products sold in the European market (both local and imported) must meet these standards. As provided in Commission Decision 96/360/EC (Anon., 1996), Ireland applies an adjusted calculation method (weighting the SCC results of November to February) to account for seasonal variations in production levels, and where excesses have a physiological basis and cannot be ascribed to a disease of the udder. The EU SCC rules are applied in a number of other countries, including Norway, Switzerland, Australia and New Zealand (Norman et al., 2000), whereas the USA and Canada have national penalty limits of 750,000 (van Schaik et al., 2002) and 500,000 (Norman et al., 2000) cells/ml, respectively. In the USA, efforts have been made to reduce the national penalty limits from 750,000 to 400,000 cells/ml (Adkinson et al., 2001; Anon., 2005b), but without success. The European rules have essentially been adopted as the international export standard.

## 4.2 National progress

### a. Established international suppliers

There has been a progressive fall in somatic cell counts among established international suppliers, particularly in Europe and Australasia. In Norway between 1994 and 2000, there was a 44% reduction in the rate of mastitis treatment and a significant reduction in the national bulk milk somatic cell count (BMSCC) (Anon., 2005c). In 2004, the geometric SCC mean was 115,000 cells/ml (Østerås and Sølverød, 2005). Among other Scandinavian countries, similar levels were recorded in Finland, but higher levels in Sweden (less than 200,000 cells/ml) and in Iceland and Denmark (less than 250,000 cells/ml) (Anon., 2007d). In Australia, there has been a fall in SCC since the late 1990s; in 2004, the average BMSCC was 204,000 cells/ml, and 94.6% and 70.8% of the national milk supply was below 400,000 and 250,000 cells/ml, respectively (Brightling et al., 2005). Higher cell counts were recorded in the United States (van Schaik et al., 2002) and Canada (Sargeant et al., 1998), which reflects higher regulatory limits on milk quality (Berry et al., 2006).

In Ireland, milk production is highly seasonal with 75% of milk supplied during April–September, and 55% and 79% of dairy calves are born in February–March and January–April, respectively (Berry et al., 2006). Based on monthly bulk SCC data from 3 Irish milk processors, SCC declined between 1994 and 2000, but has subsequently risen from 2000 to 2004 (geometric mean: 250,937 cells/ml; 52% of tests exceeded 250,000 cells/ml). High SCC herds, which tended to be smaller, contributed disproportionately to the overall mean cell count of processed milk (Berry et al., 2006).

### b. Emerging international suppliers

Among emerging dairy suppliers, there has been a rise in milk quality as a consequence of industry investment and a focus on export success. To illustrate, consider dairy producing countries in South America. In the 1970s and 1980s in Chile, unofficial information suggests that the average BMSCC was >500,000 cells/ml. Since the mid-1990s, there has been substantial investment in the dairy industry to improve production systems, milk quality and milk products. Further, a scheme of penalty and bonus payments was introduced in 1993, based on BMSCC and bacterial counts. By 2000, the average BMSCC had fallen to 330,000 cells/ml (Tadich et al., 2003). Until the early 1990s in Argentina and Brazil, the development of standards for milk safety and quality was managed by government. Although these standards were rigorous, government often did not have the capacity to rigorously enforce compliance. Following deregulation in 1990, there was substantial industry reform including the imposition of private milk standards for both the farm and processing sectors. In 2005, Argentina exported 184,000 tonnes of whole milk powder and 47,000 tonnes of cheese (International Dairy Federation, 2006), and exporters now exceed international standards in quality, hygiene, safety and traceability (Farina et al., 2005). In Brazil, the industry has mainly focused on local demand (Anon., 2007a), where quality demands have been lower. UHT milk, which dominates the liquid milk market in Brazil, can be made from lower quality raw milk provided stabilisers are used (Farina et al., 2005).

#### In summary

The EU milk quality standard (SCC not exceeding 400,000 cells/ml) is generally accepted as the international export standard. Among established international suppliers, particularly in Europe and Australasia, there has been a progressive fall in somatic cell counts. In Norway, the national BMSCC (bulk milk somatic cell count) is 115,000 cells/ml; in Ireland, this figure is 250,937 cells/ml. Among emerging dairy suppliers, there has been a rise in milk quality as a consequence of industry investment and a focus on export success. Exporters from Argentina now exceed international standards in the quality, hygiene, safety and traceability of dairy products.

## 5. TACKLING MILK QUALITY CONCERNS

### 5.1 Constraints to progress

Mastitis research has been conducted for many decades (Noordhuizen and Hogeveen, 2005), and many aspects of mastitis are now very well-understood (Radostits et al., 2007). The 5 point mastitis control programme was first devised in 1970, and remains the basis for infectious mastitis control. A further 5 points, specifically addressing the control of environmental mastitis, were added later (Radostits et al., 2007). The US National Mastitis Council produce a ten-point recommended mastitis control programme, which includes:

- Establishment of goals for udder health
- Maintenance of a clean, dry, comfortable environment
- Proper milking procedures
- Proper maintenance and use of milking equipment
- Good record keeping

- Appropriate management of clinical mastitis during lactation
- Effective dry cow management
- Maintenance of biosecurity for contagious pathogens and marketing of chronically infected cows
- Regular monitoring of udder health status
- Periodic review of mastitis control programme (Anon., undated).

Problems with effective translation of knowledge to practice, rather than incomplete knowledge *per se*, are likely to be the more important constraint to national progress towards improved milk quality (Doherty, 2007; Valeeva et al., 2007). In support of this view:

- There are variable levels of on-farm compliance with well-recognised mastitis management practices (Olde Riekerink et al., 2005; van der Zwaag et al., 2005);
- Very substantial progress in mastitis control has been achieved in several countries, particularly in Scandinavia, based on the application of existing knowledge (Østerås and Sølverød, 2005);

- Anon., 2007d);
- In a national intervention study in England and Wales, there were significant reductions in clinical mastitis and somatic cell counts following the implementation of well-specified mastitis control plans in problem herds. These authors concluded that *'there may be sufficient knowledge to reduce the current incidence of mastitis ..., but that its application, and also further education, knowledge transfer and motivation may remain essential to achieving improved mastitis control'* (Green et al., 2007); and
- In recent years, somatic cell count problems have been resolved on many farms in Ireland following a detailed farm investigation and follow-up support (O'Grady and More, unpublished).

### 5.2 Examples of national mastitis control programmes

#### a. The Netherlands

A national programme to tackle mastitis in the Netherlands was recently established (Uier Gezondheids Centrum Nederland, UGCN, <http://www.ugcn.nl/>; the Dutch Udder Health Centre), funded by the Dutch Dairy Board (Productschap Zuivel, PZ; an industry organisation) and coordinating by GD-Animal Health Services Deventer under a steering committee, comprising farmers (Dutch Organisation for Agriculture and Horticulture; LTO, Land-en Tuinbouw Organisatie Nederland), industry (Dutch Dairy Association; NZO, De Nederlandse Zuivel Organisatie) and the Dutch Dairy Board. The programme commenced with an initial situation assessment followed by field implementation, based on an understanding of the current situation, implementation of new tools, and international best-practice in mastitis control (van der Zwaag et al., 2005). The programme is being implemented by a multidisciplinary team, through a series of veterinary practices. A wide range of tools are being used, based on best-practice in other countries, including the use of a 'milk mirror' (a once-yearly specialist farm visit), structured and nationally-consistent protocol, a monthly mastitis update for veterinarians and monthly financial feedback to farmers (money saved from reduced mastitis) (van der Zwaag et al., 2005).

#### b. Australia

Australia's national mastitis and cell count control programme, Countdown Downunder, was created in 1998 to help farmers meet new quality standards, improve farm profitability and protect export markets (Anon., 2001). The programme was instigated following the implementation of EU Directive 92/46/EEC (Anon., 1992) and the implementation of industry-wide targets seeking 90% and 100% of the milk supply from Australian dairy farms with BMSCC <250,000 and <400,000 cells/ml, respectively (Anon., 2001). After the first 5 years of the programme, just under 94% of herds achieved a cell count of less than 400,000 cells/ml (Brightling et al., 2005). The current phase of the programme (2004-2007) is focusing on the translation of the knowledge and skills of the whole farm team (farmers and advisers) into continuous improvement and risk management on farm (Brightling et al., 2005).

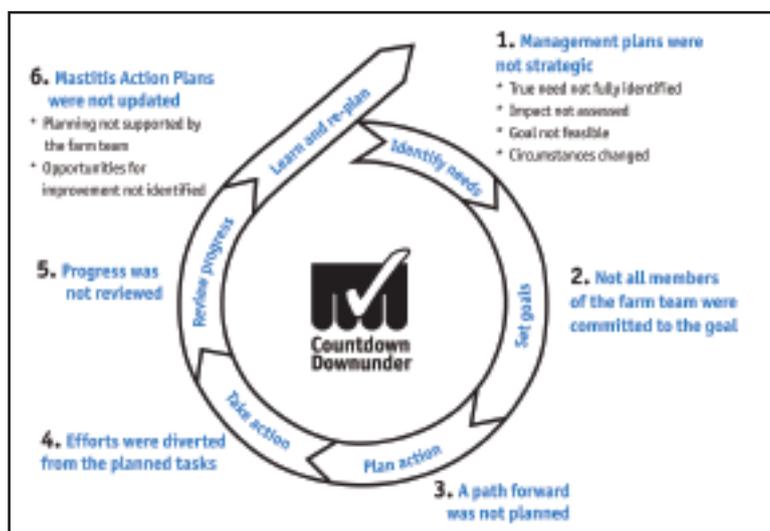


Figure 3. Stalling points, and potential reasons for stalling, on the action planning cycle. From Nettle et al. (2006)

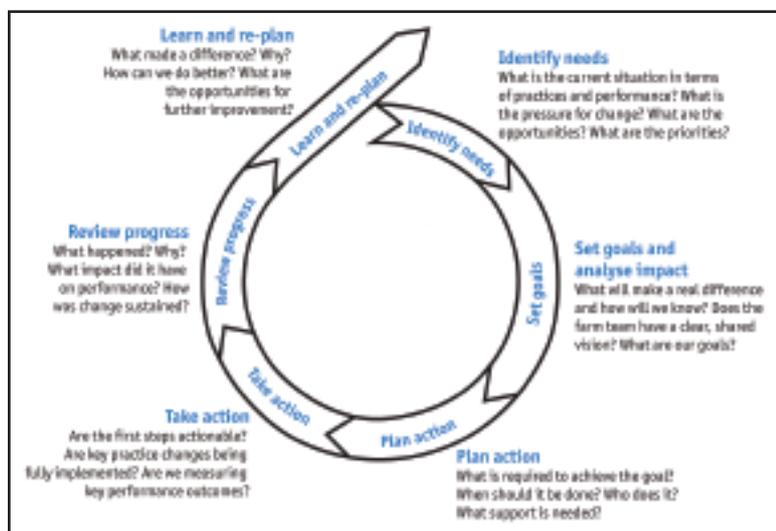


Figure 2. The action planning cycle, as used in the Countdown programme. Adapted from Nettle et al. (2006)

The Countdown programme has been built around the concept of capacity-building which, in simple terms, is about increasing the abilities and resources of individuals, organisations and communities to manage change (Anon., 2004). It is now considered a more effective means of extension delivery to support change, compared with both the transfer of technology, 'top-down' approach, and the 'bottom-up' approach based on farmer participation and group extension methods (Nettle et al., 2003). Capacity-building is an area of active research (Macadam et al., 2004; including the establishment of a Cooperative Venture for Capacity Building, with the aim to build capacity to enable rural industries to become more sustainable and competitive), and detailed resources are available (McKenzie, 2007).

The Countdown programme focuses on the capacity of farmers to address (that is, make strategic and progressive improvements to) mastitis and milk quality. To achieve this, they need a good understanding of the principles underpinning mastitis control, the skills and confidence to achieve best practice on farm, and resources and services to support change on farms (Brightling et al., 2005). The programme is built around the six steps of the action planning cycle, which includes identifying needs, setting goals, planning action, taking action, reviewing progress, and learning and re-planning (Nettle et al., 2006; Figure 2).

A broad range of resources have been developed to support these steps, including farmer short courses, farm guidelines, mastitis action plans, mastitis focus reports and milk quality awards. The purpose of the short courses has been to stimulate change on-farm, by repeatedly challenging farmers to 'close to gap' between current and best practice, by encouraging the use of triggers for the early detection of udder health problems, by promoting a team approach between farmers and their dairy advisors, and helping farmers to be comfortable about using the services of farm advisors

(McKenzie, 2007). The action planning process has the potential to stall at a number of points on the action planning cycle, as highlighted in Figure 3. Based on recent research (Nettle et al., 2006), support for sustainable change on-farm is reliant upon:

- Mastitis action plans that fit the needs of the farm business;
- Jointly-agreed goals by all members of the farm team with day-to-day responsibility for udder health and milk quality; and
- Regular review of the farm situation by farm managers (Nettle et al., 2006).

#### In summary

Based on experiences from a number of countries, it is likely that problems with effective translation of knowledge to practice, rather than incomplete knowledge *per se*, are the more important constraint to national progress towards improved milk quality. A number of national programmes have now been developed to address milk quality issues, including an industry-led programme in Australia called Countdown Downunder. This programme has been built around the concept of capacity-building, which, in simple terms, is about increasing the abilities and resources of individuals, organisations and communities to manage change. The Countdown programme is built around the six steps of the action planning cycle, which includes identifying needs, setting goals, planning action, taking action, reviewing progress, and learning and re-planning. A broad range of resources have been developed to support these steps, including farmer short courses, farm guidelines, mastitis action plans, mastitis focus reports and milk quality awards.

## 6. CONCLUSIONS

The Irish dairy industry is well-positioned to benefit from the increased global demand for dairy products. Milk quality will increasingly contribute to competitive advantage for the Irish dairy industry, for a range of reasons relating to human health, milk processing and farm profitability. A number of countries have achieved substantial improvements in milk quality, highlighting models to tackle milk quality concerns. Ireland would greatly benefit from an industry-led programme, with defined objective national targets, focusing on the capacity of farmers to make strategic and progressive improvements to mastitis and milk quality.

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## POST HOC ASSESSMENT OF EXTERNAL VALIDITY AND PRECISION OF FIELD SAMPLES USED TO SURVEY THE IRISH CATTLE POPULATION FOR JOHNE'S DISEASE

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### ABSTRACT

We generally rely on a sample, rather than a census, to gain an understanding of characteristics of animal populations. The value of the sample as a reflection of the population of interest is measured in terms of external validity and precision. A study conducted to investigate the sero-prevalence of Johne's disease in Irish cattle. Following sampling errors during the collection of 1,000 serum samples, the current study was conducted to assess the external validity and precision of two field datasets (605 samples selected randomly, 295 selected opportunistically). Limited prior knowledge was available about the population with respect to Johne's disease. Therefore, we used a range of methods to conduct a *post hoc* assessment of external validity (spatial distribution, nearest neighbour method, kernel density plots) and precision. Based on this *post hoc* assessment, results from the randomly selected samples would provide an externally valid, albeit relatively imprecise, estimate of national disease prevalence, and of the disease prevalence in three of the four provinces (Munster, Leinster and Connacht) and in beef and dairy herds.

### 1. INTRODUCTION

We generally rely on a sample, rather than a census, to gain an understanding of characteristics of animal populations. The value of the sample as a reflection of the population of interest is measured in terms of external validity and precision. External validity refers to the accuracy with which a sample represents the population of interest (Greiner and Gardner, 2000), and differences between the sample and its target population reflect the level of sampling bias (Dohoo et al., 2003). When using sample data to describe population characteristics, sampling bias is the primary threat to the external validity of a study (Johnson et al., 2004). To overcome this concern, samples are generally collected randomly (Norman and Streiner, 2003). However, there are situations where there are changes to the sampling frame as the study progresses. These would include mail surveys, where changes may be required according to the number of non-respondents (Johnson et al., 2004). Consequently, the external validity of the study can alter as the study progresses. A second measure of survey performance is precision, where precise sample estimates have minimal variation around the true value from the target population. Precision is directly related to sample size, where generally, increasing sample size gives increased precision (Dohoo et al., 2003).

Statistical methods to assess sampling bias require prior knowledge about the target population, which can make these techniques impractical in some circumstances (Dohoo et al., 2003). To be of value, sampled data must reflect population characteristics, even when little is known of this latter population. Methods such as population density measurements have been found accurate and precise methods to remove error bias (Krebs, 2001). Further, Geographic Information System (GIS) technology provides methods to analyse the distribution of populations (Nodtvedt et al., 2007; Stevenson et al., 2000).

A sampling error occurred during collection of samples to investigate the sero-prevalence of Johne's disease (JD) in Irish cattle, which resulted in approximately a third of the data being collected opportunistically, rather than randomly. This created concern over the potential for sampling bias in the data set. As data

collection is expensive, a *post hoc* analysis of both external validity and precision was considered necessary to ascertain if the samples could be usefully used for the purpose intended. The purpose of the study was to assess the external validity and precision of the two field datasets (selected randomly and opportunistically), and to assess the level of sampling bias if the opportunistic and random field datasets were combined.

### 2. MATERIALS AND METHODS

#### 2.1 The data

In Ireland, all cattle herds have a unique herd number and are registered in the national Animal Health Computer System (AHCS). As part of the national brucellosis eradication programme, blood is collected annually from all cattle (females and entire males) greater than 1 year old. In 2003, brucellosis sampling was conducted on approximately 132,000 herds. In this study, our reference population included a subset of these herds; specifically the 97,455 (breeding) herds where at least one home-born calf had been registered in 2003.

A simple random sample of 1,000 herd numbers ('the proposed dataset') was selected from the reference population, using computer-generated random numbers. This sample size is sufficient to estimate a national herd level prevalence of 10%, with a 95% CI and a precision of 2%. Arrangements were then made, through the national brucellosis testing laboratory, to collect all sera from each selected herd. A computer programme was used to notify staff when relevant samples were available. Between June and November 2005, the sera from 644 herds (so-called 'random field dataset') were collected in this way. However, a computer error occurred in mid-November, and no further samples were collected using this approach. Once the error was detected, sera from a further 367 herds were collected opportunistically during early winter 2005 to make up for the earlier missed samples. Samples in this 'opportunistic field dataset' were selected by laboratory staff as brucellosis samples came in, without any formal methodology or stratification of the sampling. These datasets were checked for

entry errors, including multiple entries. Duplicate entries for four herds (1 in random dataset, 3 in opportunistic dataset) were removed. A further three datasets were generated ('generated datasets' A, B and C), using the random number selection in the Animal Movement extension of Arc View (version 2.4), to provide a comparison group (with an equivalent number of herds) to the random, opportunistic and combined field datasets, respectively.

## 2.2 Data analyses

### a. The spatial database

In Ireland, herd numbers are geo-referenced to digitised parcels of land, constructed for calculating EU land based farming aid. The geo-referenced farm database does not include farms that do not manually complete an application for farming aid, including those that were automatically eligible, and those where a claim for farming aid was not made. In this study, the position of each farm was based on the centre of the largest land fragment. Mapping was conducted using ArcVIEW 9.1 (ERSI, Redlands, CA, USA).

### b. Post hoc assessment of external validity

We visually compared the spatial distribution of the random and opportunistic field datasets. Then, we used the nearest neighbour method (ArcVIEW 9.1) on the field (random, opportunistic and combined) and three generated datasets to determine the degree of clustering in each (high: neither dispersed or clustered; medium: dispersed but possibly random; low: <5% likelihood that clustering is randomly distributed; very low: <1% likelihood that clustering is

randomly distributed). Nearest neighbour ratios and qualitative outputs from ArcVIEW were reported. The nearest neighbour analysis was restricted to a rectangular area or 'window' (Figure 1) that incorporated as much of Ireland (but as little sea or Northern Ireland) as possible. We also developed a kernel density plot (ArcVIEW 9.1) for each data set, except the combined field and generated datasets, to further examine sample distribution within the window. The kernel density plot was conducted using a 10km search radius, with a 100m grid. Results are presented as points per square kilometre.

Table 1. The total numbers of herds and the number of geo-referenced herds, in total and within the target window, in each of the field and generated datasets

	Total	Geo-referenced	
		In total	Within target window
<b>Field datasets</b>			
Random	644	605	387
Opportunistic	367	295	187
Combined	1011	900	574
<b>Generated datasets</b>			
A	605	605	381
B	295	295	172
C	900	900	533

### c. Post hoc assessment of precision

We calculated the precision of the proposed dataset sample (n=1000) and of each field (n=644, n=367) dataset, at different prevalence levels and given a 95% confidence level. Precision was displayed as margin of error and was calculated using:

$$L = \sqrt{\frac{1.96^2 \times pq}{n}} \quad (1)$$

where L=precision, p=prevalence, q= 1-p and n=sample size.

We determined the percentage of herds within each of the 26 counties, based on data from all breeding herds (n=94,261), the random field dataset (n=644), the opportunistic field dataset (n=367) and the combined field datasets (n=1011). The original datasets were stratified by province (4 categories: Connacht, Leinster, Munster, Ulster), county (26) and enterprise type (3: dairy, beef, mixed). Enterprise type was determined based on the proportion of beef and dairy breeds among mature cows in each herd (beef: >66% beef breeds; dairy: >66% dairy breeds; mixed: all other herds). The strata-level distribution of herds was compared between datasets using the chi-square test.

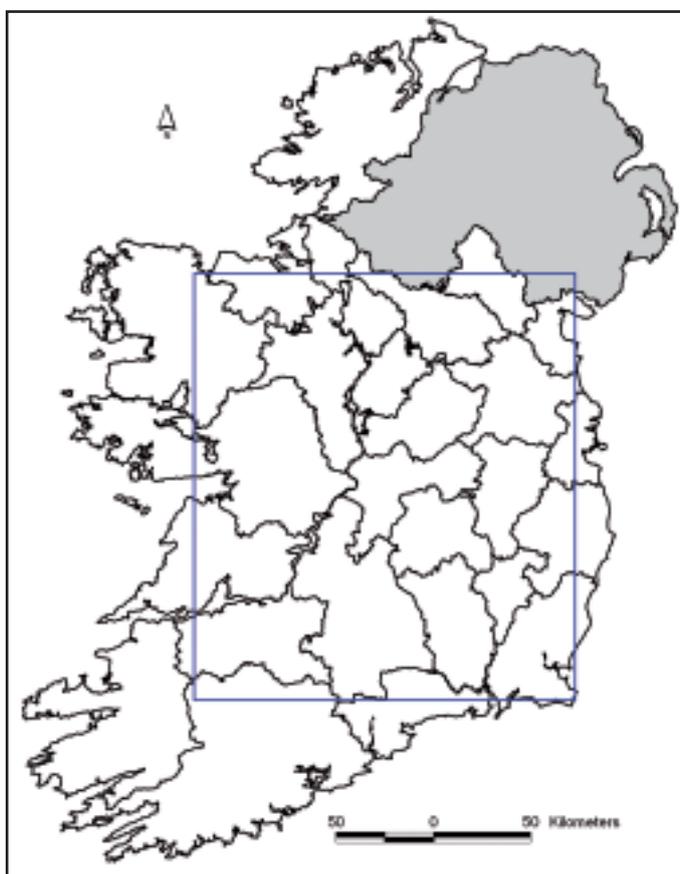


Figure 1. The rectangular area or 'window' that was used during the nearest neighbour analysis. The window incorporates as much of Ireland (but as little sea or Northern Ireland) as possible

### 3. RESULTS

#### 3.1 The datasets

During 2003, there were 97,455 (breeding) herds in Ireland where at least one home-born calf had been registered. Of these, 90,807 (93.2%) were geo-referenced, including 58,285 (59.8% of all breeding herds) located within the target window. Table 1 presents the total number of herds, the number geo-referenced in total and within the target window in each of the field and generated datasets.

#### 3.2 *Post hoc* assessment of external validity

##### a. Visual assessment

The distribution of all geo-referenced cattle herds across the country was visually homogeneous, except for areas obviously not suitable for grazing, such as lakes, bogs, forest and upland areas. Herds in the opportunistic field dataset (n=295) were distributed in clusters across the country, whereas those in the random field dataset (n= 605) were evenly dispersed (Figure 2).

##### b. Nearest neighbour analysis

Based on results of the nearest neighbour analysis, herds in the field datasets were more clustered than those in the generated datasets (Table 2).

##### c. Kernel density plots

Areas of higher sampling density are present in the kernel density plots of the opportunistic field dataset and to a lesser degree the random field dataset, but not of the equivalent generated datasets (Figure 3).

##### d. Herd distribution

The percentage of herds in each county, based on data from the national database and from each of the three field datasets, is presented in Figure 4. There was a significant difference between the county distribution of herds in the national dataset and the random field dataset compared with the opportunistic field dataset ( $p < 0.001$ ), but not between the national data set and the random field datasets ( $p = 0.576$ ).

The percentage of herds in each province and of each enterprise type, based on data from the national database and from the random and opportunistic field datasets, is presented in Table 3. This table also presents the ratio of percentages, comparing each field dataset with the national database. There were significant differences in the ratio of percentages between the two datasets, both by province and by enterprise type (each  $P < 0.001$ ).

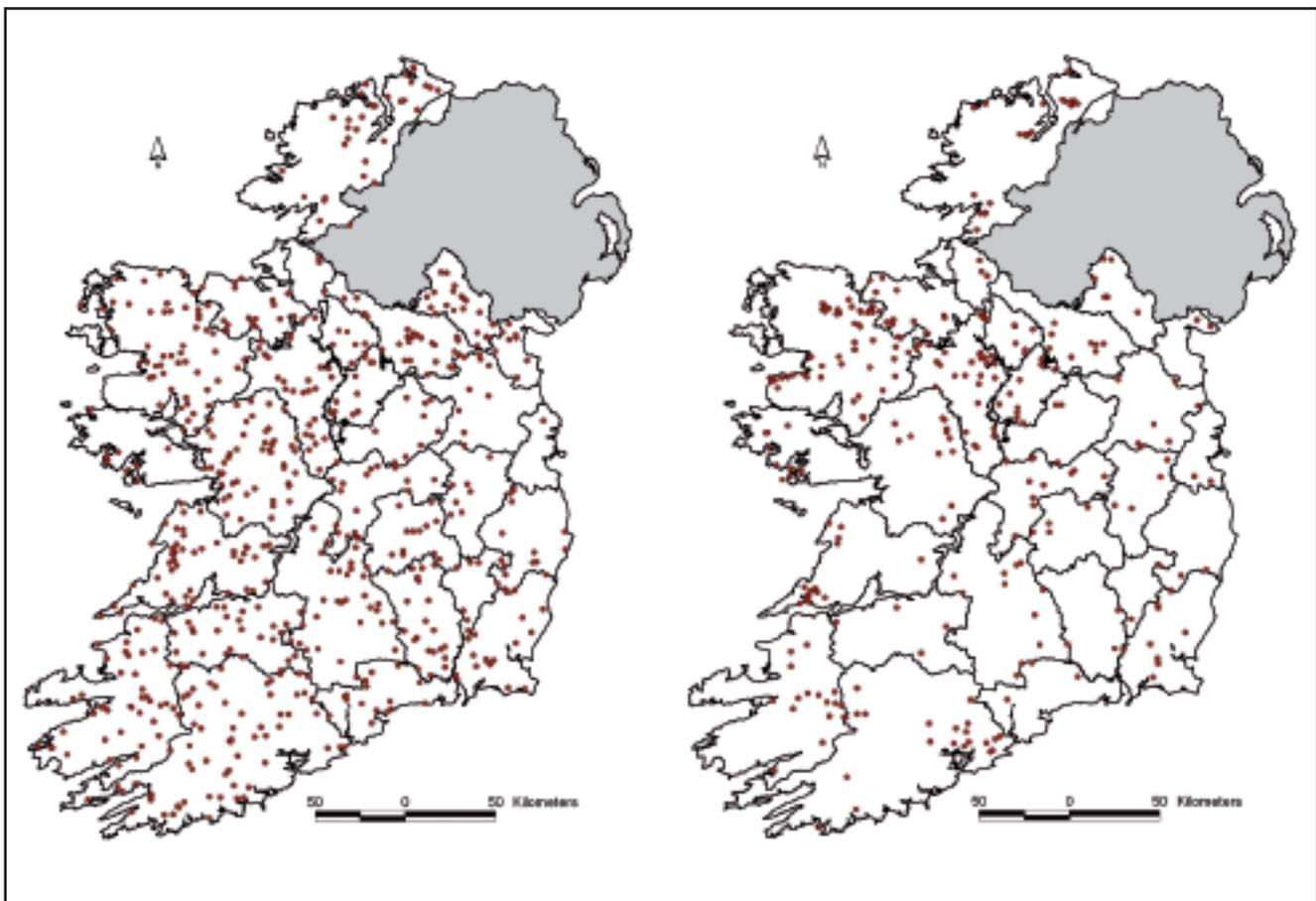


Figure 2. Distribution of geo-referenced herds in the random (left; n=605) and opportunistic (right; n=295) field datasets

Table 2. Assessment of clustering of farms in each of the field and generated datasets, based on the nearest neighbour analysis

	Nearest neighbour analysis	
	Ratio	Qualitative interpretation <sup>a</sup>
Field datasets		
Random	0.94	Low
Opportunistic	0.83	Very low
Combined	0.93	Very low
Generated datasets		
A	1.01	High
B	0.96	Medium
C	0.98	High

<sup>a</sup> Chance that observed spatial pattern could have occurred at random

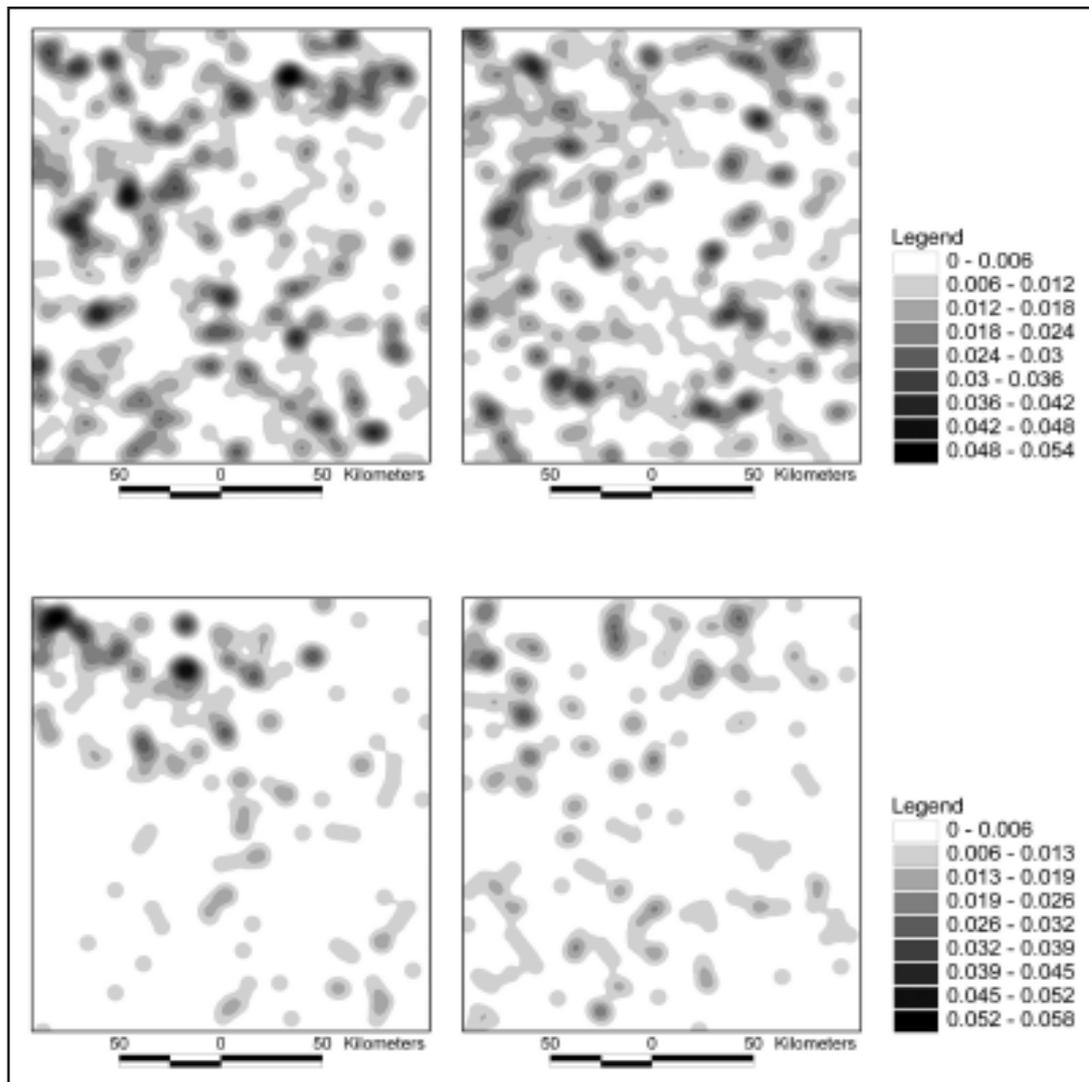


Figure 3. Kernel density plots of herds in:  
 • (top) the random field (left) and generated A (right) datasets within the target window (each representing 605 farms)  
 • (bottom) the opportunistic field (left) and generated B (right) datasets within the target window (each representing 295 farms)

Table 3. Percentage of herds in the field datasets and the national database, and the ratio of percentages in selected datasets, by province and enterprise type

Strata	Percentage of herds			Ratio of percentages	
	Within the random field dataset (X)	Within the opportunistic field dataset (Y)	All breeding herds % (Z)	X/Z	Y/Z
<b>Province <sup>ab</sup></b>					
Connacht	28.2%	23%	31%	0.92	0.74
Leinster	22.2%	48%	22%	1.00	2.16
Munster	37.5%	20%	34%	1.10	0.58
Ulster	12.1%	10%	13%	0.93	0.76
Total number of herds	645	335	94,261		
<b>Enterprise type <sup>ab</sup></b>					
Dairy	26%	10%	29%	0.90	0.36
Beef	71%	88%	70%	1.02	1.26
Mixed	2%	1%	1%	2.47	1.38
Total number of herds	642	358	94,261		

<sup>a</sup>Significant difference between the proportion in each strata sampled for the random and opportunistic samples ( P <0.001)  
<sup>b</sup>Not all herds could be allocated a breed or province strata, therefore total numbers of sampled herds differ in this part of the analysis

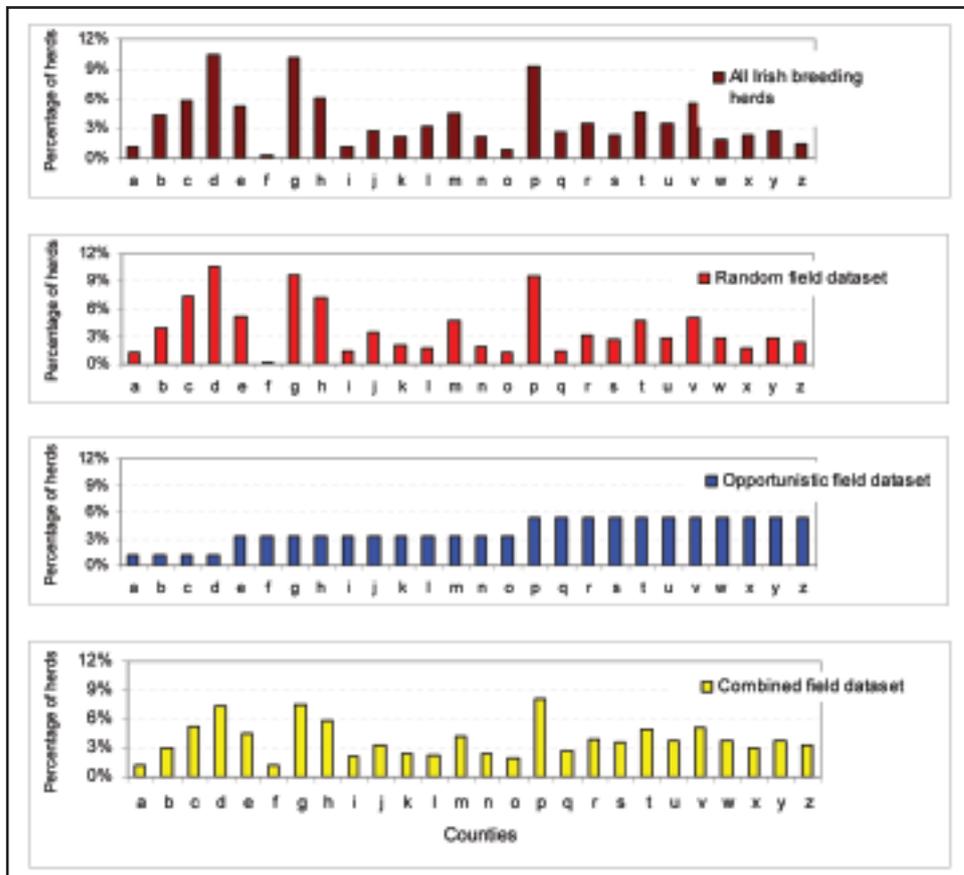


Figure 4. The percentage of herds in each county is graphed for four datasets; 'all Irish breeding herds, the random, opportunistic and combined field datasets.' Counties are alphabetised from Carlow to Wicklow, and labelled from A to Z in that order

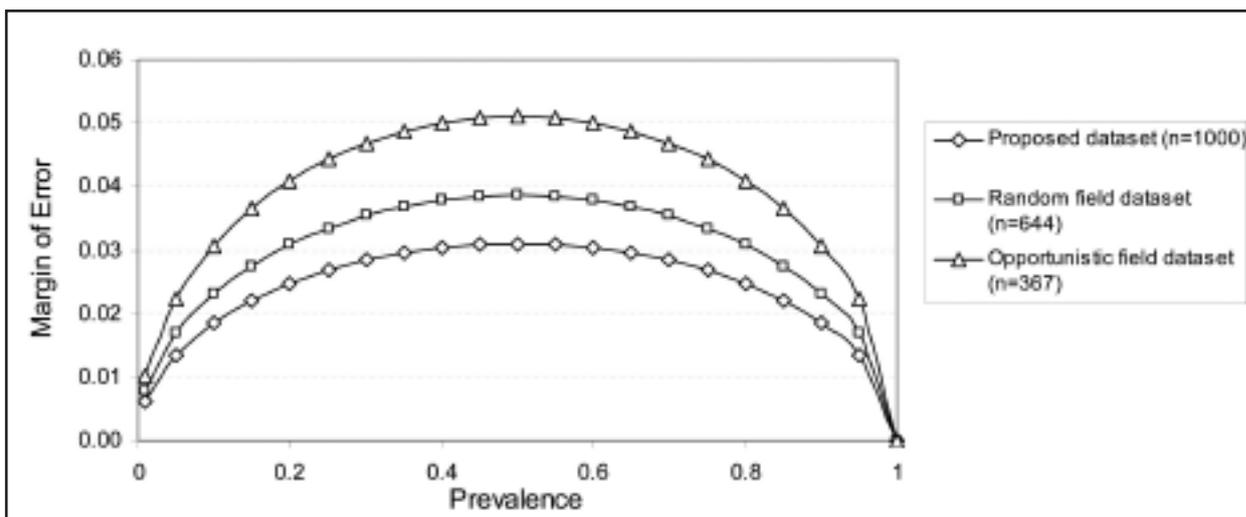


Figure 5. The margin of error with varying prevalence and sample size of the proposed and actual field data sets involved in the survey

### 3.3 Post hoc assessment of precision

The margin of error varies with prevalence and sample size, in both the generated and field datasets (Figure 5). There is an increase in the margin of error as sample size decreases, particularly with prevalence between 30% and 70%.

## 4. DISCUSSION

This paper applies practical methods for *post hoc* assessment of the external validity and precision of field samples, before data analysis is attempted. In the current study, these methods were used to compare the external validity and precision of several datasets, collected from the same population, but using different sampling strategies. *Post hoc* analysis of data suitability is generally assessed following data analysis, by checking confidence intervals, standard deviations to assess the amount of variation within a sample, or looking at 'diagnostics' such as the normality of residuals when model building (Dohoo et al., 2003). However, when external validity is in question following data collection, but prior to sample analysis, this is not a suitable approach.

External validity concerns the ability to extrapolate study results from the sample to the broader reference population. This issue is particularly important in prevalence surveys, such as the Johne's disease survey on which the current work was based. In this study, we used a range of methods to assess the external validity of the two field datasets. Further, random datasets were generated, to facilitate robust comparison. In our work, we have focused on GIS methods, noting that these methods did not need prior knowledge of the prevalence of disease surveyed. This was important, given that there was little data on the national prevalence of Johne's disease prior to the start of this work. Nearest neighbour analysis provided a transparent and useful method to compare the distribution of each data set to the target population. Density plots proved useful to further explain the outcome of the nearest neighbour analysis.

There were substantial differences between the opportunistic field dataset and the national database, highlighting problems of sampling bias with the opportunistic field dataset. This was most clearly seen in the artificially even distribution of the proportion of herds selected from each county in the opportunistic sample. Similarly the proportion of cattle types were skewed towards higher numbers of beef cattle in the opportunistic field dataset,

which essentially would not accurately represent the level of disease prevalence in dairy cattle across the country. The nearest neighbour and density analyses further confirmed what was suggested by the descriptive analysis. These findings were consistent with the widely accepted practice that when data is collected in an opportunistic manner it does not follow the conventional random sampling frame considered necessary to produce reliable inferences about a population (Jannink et al., 1995; Norman and Streiner, 2003).

Based on each of the methods used, the random and target populations were similar. Therefore, disease prevalence in the random field database is likely to provide a reliable estimate of disease prevalence in the target population.

Due to sample size constraints, imprecise prevalence estimates would be obtained following separate analysis of each of the two field datasets. Clearly, these estimates would be more precise if the two datasets were combined. Combining the two field datasets in this study resulted in a roughly averaged value of the two; showing that one field dataset would bias the other were the two combined. However, based on the *post hoc* assessment conducted here, it is clear that the random and opportunistic field datasets should not be combined as they do not share the same demographic profile. Results from the opportunistic field dataset will be biased due to being clustered in certain areas and occurring in a different proportion by county and enterprise to the rest of the herds in the country. The difference in the proportion of beef to dairy herds between the random and opportunistic field datasets may be a result of the bias in the opportunistic dataset towards sampling a comparatively lower number of herds from Munster, which characteristically has a high proportion of Ireland's dairy herds. Overall, the results from the opportunistic field dataset will need to be interpreted with caution as they do not appear to represent the target population of Irish breeding herds.

Based on this *post hoc* assessment, results from the randomly selected samples would provide an externally valid, albeit relatively imprecise, estimate of national disease prevalence, and of the disease prevalence in three of the four provinces (Munster, Leinster and Connacht) and in beef and dairy herds.

## 5. ACKNOWLEDGEMENTS

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## HERD AND WITHIN-HERD IBR PREVALENCE AMONG IRISH HERDS SUBMITTING BULLS FOR ENTRY TO A PERFORMANCE TESTING STATION

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### ABSTRACT

Infectious Bovine Rhinotracheitis (IBR), caused by Bovine Herpes Virus 1 (BoHV-1), may result in various clinical consequences, including severe respiratory disease and conjunctivitis, venereal disease and reduced reproductive performance and abortion. This paper presents the serosurveillance findings from an intake of bulls into a performance testing station in Ireland during November 2007. In this study, we have sought to determine the herd and within-herd IBR prevalence in 53 Irish beef herds, risk factors for infection in these herds, and challenges faced in achieving freedom from BoHV-1 infection among bulls entering the performance testing station. IBR status could be determined for 41 herds, with 30 (73.2%) herds infected. Within these latter herds, the mean within-herd IBR prevalence was 28 ( $\pm$  20)%. Multivariate exact logistic modeling revealed increasing numbers of contiguous herds and decreasing percentage of males within the herd as significant risk factors for infected herd status. These findings highlight the high prevalence of IBR in those Irish beef herds that submitted bulls to this performance testing station, and raise concerns regarding IBR control nationally. A number of countries in Europe have moved, or are moving, towards freedom from infection. This will have important implications for Ireland, given the importance of live cattle export to Europe, and international standards in semen production.

### 1. INTRODUCTION

Infectious Bovine Rhinotracheitis (IBR), caused by Bovine Herpes Virus 1 (BoHV-1), may result in various clinical consequences, including severe respiratory disease, venereal disease and reduced reproductive performance and abortion. Like other herpes viruses, BoHV-1 also results in lifelong latent infections. The virus may be spread within cattle populations via contact, aerosol, fomites and via infected semen, ova or embryos (Muytkens *et al.*, 2007).

There are substantial economic consequences associated with clinical disease (Castrucci *et al.*, 2000). In addition, IBR infection has emerged as an important issue in the international trade of live animals and some animal products. As an international standard, all semen used in artificial insemination must be sourced from IBR seronegative bulls (de Ruigh *et al.*, 2006). Further, IBR has been eradicated from a number of countries within Europe (including Austria, Denmark, Finland, several Italian provinces, Norway, Sweden and Switzerland). In some other countries (France, Germany, the Netherlands), eradication programmes are in place. In all cases, eradication strategies have been based on a foundation of improved herd and regional bio-security, in conjunction with test and culling (European Food Safety Authority, 2006). IBR status has emerged as a barrier to within-community trade, with EU Directives (64/432, 88/407 and 93/60) allowing member states to stipulate requirements to be met for the importation of cattle, semen and embryos (Noordegraaf *et al.*, 2000). In some countries where infection is endemic, the use of marker vaccination has been introduced to reduce herd prevalence, whilst still allowing the differentiation between wild virus exposure and vaccination. In Ireland, only the use of marker vaccines is permitted, however, there is currently no national IBR control programme.

In early 2007, an outbreak of clinical Infectious Bovine Rhinotracheitis (IBR) occurred at a bull performance testing station in Ireland. This performance testing station was being used to identify bulls for future use as artificial insemination (AI) sires. The outbreak resulted in substantial economic losses, including a loss of potential for genetic gain within the Irish beef sector. As a result, the facility was temporarily closed and biosecurity measures were revised. From late 2007, a number of measures were addressed, both prior to (farm-of-origin serosurveillance, pre-entry isolation) and following (testing station biosecurity) entry. Results from pre-entry serosurveillance were used to assess infection risk in each herd-of-origin (source herd). This paper presents the serosurveillance findings from the bull intake to this testing station in November 2007. In this study, we have sought to determine the herd and within-herd IBR prevalence of all source herds, risk factors for infection in these herds, and challenges faced in achieving freedom from BoHV-1 infection among bulls entering the test station.

### 2. MATERIALS AND METHODS

#### 2.1 The study farms

The study farms include all Irish farms that sought to submit bulls for entry to a bull performance testing station during November 2007 bull intake. These herds each contained at least one high genetic merit bull, 6-9 months of age, as identified using objective genetic methods. Further, each herd keeper had agreed to a serological assessment of the health status of their herd.

## 2.2 Sample collection

During November 2007, local veterinarians conducted all sampling on the study farms. A clotted serum sample was obtained from each candidate bull. Veterinarians were asked to collect further samples from each herd, drawing from the following groups of animals in decreasing order of preference: the dam of each candidate bull; those in very close contact with the candidate bull (up to, but no greater than 40% of samples collected); those, in the opinion of the veterinarian, most-likely to be infected with IBR if present in the herd, including older animals, animals with contact during the last 12 months with cattle in other herds such as at shows, marts, fields on the farm boundary (up to, but no greater than 40% of samples collected); and other animals in the herd, starting with those that might have had some level of contact with the candidate bull and its dam (the balance of samples). This strategy was devised to maximise confidence in the chances of establishing freedom of infection due to IBR. Sample size was determined based on calculations to substantiate freedom from infection (Cameron and Baldock, 1998). We assumed a minimum expected prevalence of infection of 10 %, if infection were present, with a test sensitivity and specificity of 99% and 99.7%, respectively.

## 2.3 Laboratory testing

Clotted serum samples were sent to the Central Veterinary Research Laboratory (Department of Agriculture, Fisheries and Food [DAFF], Celbridge, Co Dublin, Ireland). All samples were tested in duplicate for the presence of IBR antibodies using a commercial gB IBR ELISA (HerdChek® Infectious Bovine Rhinotracheitis (IBR)/Bovine Herpesvirus-1 (BHV-1) gB Antibody ELISA Test Kit, IDEXX Europe B.V, The Netherlands). The sensitivity and specificity of this assay was previously estimated at 99% and 99.7%, respectively (Kramps et al., 1994). In those herds where gB positive animals were identified, up to 12 gB positive samples were retested using a commercial gE ELISA (HerdChek® Infectious Bovine Rhinotracheitis (IBR)/Bovine Herpesvirus-1 (BHV-1) gE Antibody ELISA Test Kit, IDEXX Europe B.V, The Netherlands) to differentiate vaccination and exposure to wild type virus. Serological test results were classified as either positive or negative. A severe interpretation was applied, and inconclusive ELISA results were reclassified as positive.

## 2.4 Data collection

The local veterinarian collected a range of data, including herd number, herd vaccination status, animal identification, and animal status (candidate bull, dam, other animal from the herd). Using DAFF's Animal Identification and Movement System database (AIM), we determined the total number of animals present in each study herd on the date of sample collection, and data about each of these animals, including signalment (date of birth, breed and sex) and movement (date of entry into herd, if applicable). Using this database, we also identified all inward cattle movements, either from marts or private premises, into each study herd from 1<sup>st</sup> January 2007 until the date of sample collection. The number of herds contiguous to each of the sample farms was calculated using ESRI Arcview 3.2 (Redlands, California, USA), based on 2007 data in DAFF's Land Parcel Identification Scheme (LPIS). These latter data were missing for two study herds.

## 2.5 Data management and analysis

Data were managed in Microsoft Excel and Access (Microsoft Corporation, Redmond, WA, USA), and analysed using Stata® version 10 (Stata Corp, College Station, TX, USA), Freecalc version 2 and Survey Toolbox version 1.04 (AusVet Animal Health Services,

Australia), and ESRI Arcview 3.2 (Redlands, California, USA). Paper-based farm and serological data were manually entered in Excel, then managed in Access as a herd and animal-level database. The location of each study herd was mapped using Arcview, based on the centroid of the largest fragment of each farm. For the two herds without LPIS data, the centroid of the relevant district electoral division was used to represent farm location.

Herds with at least one animal with a gB positive, gE negative result were classified as vaccinated and not considered in further analyses.

The probability of freedom from infection was determined using Freecalc. Using the sample results from each herd, we calculated the probabilities of observing such a result under the null (that infection is present) and alternative (that the population is free from infection) hypotheses (Cameron and Baldock, 1998). We assumed a within-herd prevalence of 10% or greater, if infection were present, a test sensitivity and specificity of 99% and 99.7%, respectively, and type I and II errors at 0.05. Using these criteria, herds were classified as either infected (probability of null hypothesis <5%, probability of alternative hypothesis >95%) or not (>95%, <5%). In some herds, insufficient samples were collected, and no conclusion about infection status could be made. For those herds classified as infected, we estimated true within-herd prevalence using the true prevalence function of Survey Toolbox. The above-mentioned assay sensitivity and specificity were used.

Univariable and multivariable analyses were conducted on the 41 herds classified as either infected or non-infected, using exact logistic regression (Stata exlogistic) and herd as the unit of interest. The outcome of interest was herd infection status. A number of independent variables were considered including herd size, average herd age, percentage of herd male (MALE), percentage of herd pure-bred, percentage of herd home-bred, closed herd since the beginning of 2007, number of contiguous herds (CONTIG), number of bought in cattle since the beginning of 2007, from farms or from marts (MART07). Variables were treated as continuous if a plot of the log odds of a herd being infected against the midpoints of categorical variables (built using the quartiles of the continuous data) was approximately linear. The variables MART07, CONTIG and MALE all appeared to be linearly related to the log odds and were kept as continuous variables. The other remaining independent variables were categorized prior to analysis, after developing histograms and choosing either clearly defined categories or divisions into quartiles based on biological plausibility. To limit the number of predictors in the model we used univariate screening, so that variables with  $p < 0.20$  at the univariate level became candidates for the model. We then used a backward-selection procedure based on a mid P-value of 0.05. Finally we tested terms that were excluded at the initial screening stage for inclusion in the final model ( $p < 0.05$ ). No interaction terms were considered in the model because of the small sample size.

### 3. RESULTS

#### 3.1 Descriptive analysis

A total of 1,462 serum samples (73 candidate bulls, 72 dams, 1,317 cohort animals) were collected from 53 study herds. Six herds (179 samples) had vaccinated for IBR. Among the 47 herds (1,283 samples including 65 candidate bulls, 64 dams, 1,154 cohort animals) that did not vaccinate, 257 (20.0%) samples were gB positive, including 4 (6.2%) candidate bulls, 19 (29.7%) dams and 234 (20.3%) cohort animals. The age-specific IBR prevalence and number of animals in each age category among the 1,283 cattle from 47 non-vaccinated herds is presented in Figure 1. Descriptive information about the 53 study herds is presented in Table 1.

#### 3.2 Infection status and within-herd prevalence

Among the 53 study herds, 30 were infected, 11 were not and infection status of 12 herds was not determined, either due to vaccination (6 herds) or an insufficient number of animals sampled (6 herds) (Figure 2). The geographic distribution of these herds, by infection status, is presented in Figure 3. Among herds with known infection status, herd IBR prevalence was 73.2%. The mean within-herd prevalence in the 30 infected herds was 28% (SD 20 %) (Figure 4).

#### 3.3 Multivariable analysis

Unconditional associations between infection status and either categorical or continuous independent variables are presented in Tables 2 and 3, respectively. In the final exact logistic regression model (Table 4), MALE and CONTIG were significantly associated with herd infection status.

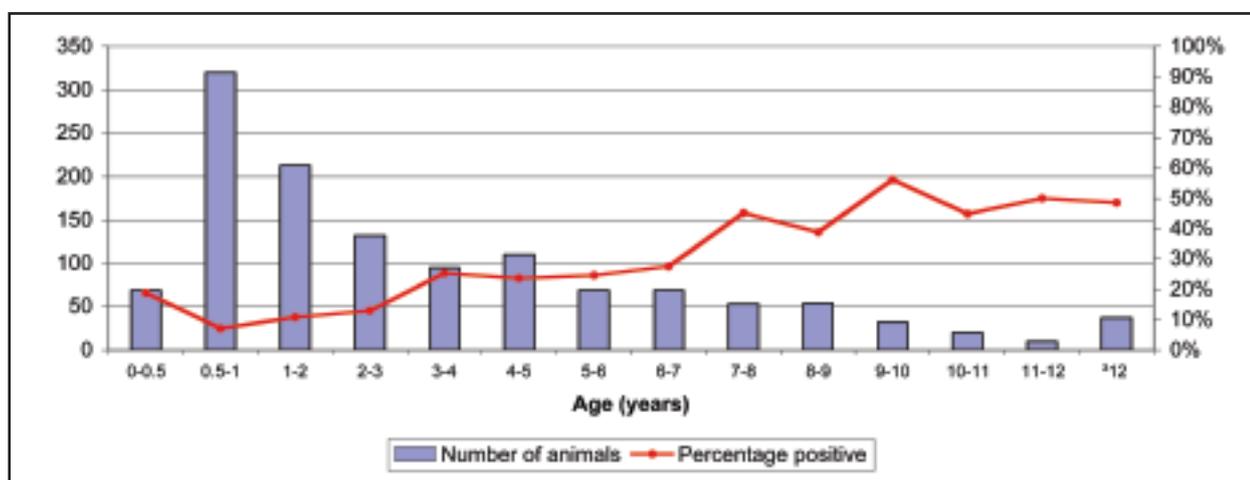


Figure 1. The age-specific IBR prevalence and number of animals in each age category among 1,283 cattle from 47 non-vaccinated study herds in Ireland during November 2007

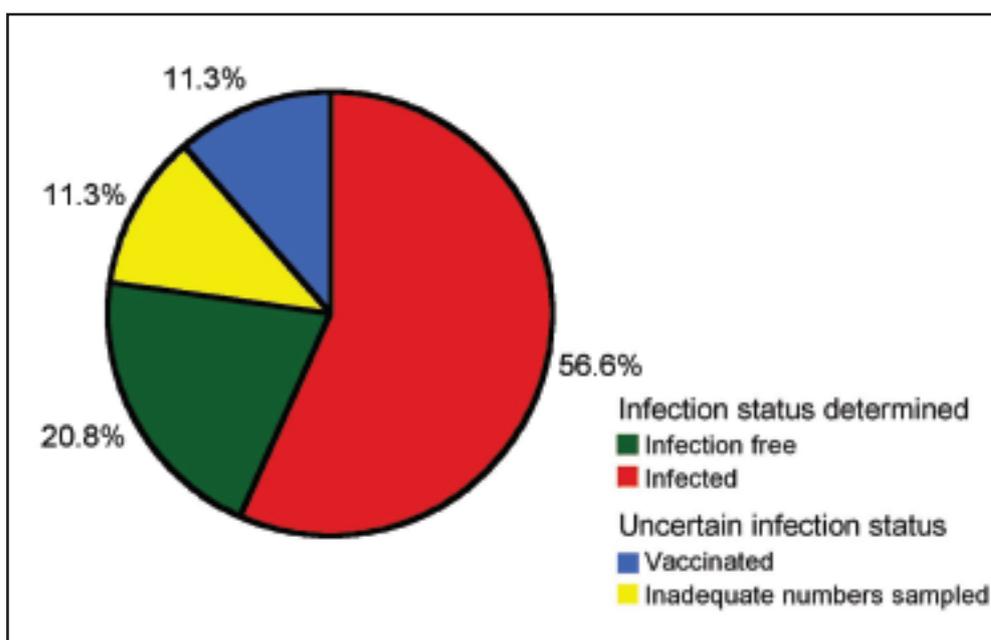


Figure 2. The estimated IBR infection status of the 53 study herds in Ireland during November 2007

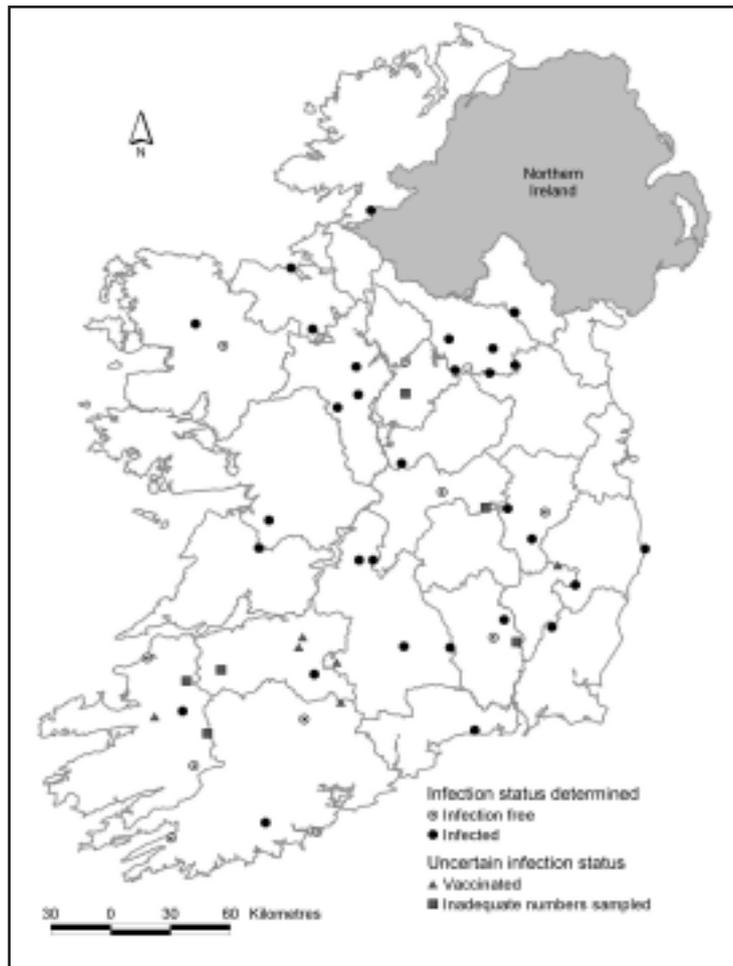


Figure 3. Geographic distribution of the 53 study herds, by infection status

Table 1. Descriptive information about the 53 study herds

Variable	Mean	Standard deviation	Range
Herd size	77.9	± 65.0	4 - 320
Number sampled per herd	27.6	± 11.5	5 - 50
Number of animals bought in 2007	7.6	± 10.2	0 - 51
Number of contiguous herds	14.9	± 10.6	2 - 50

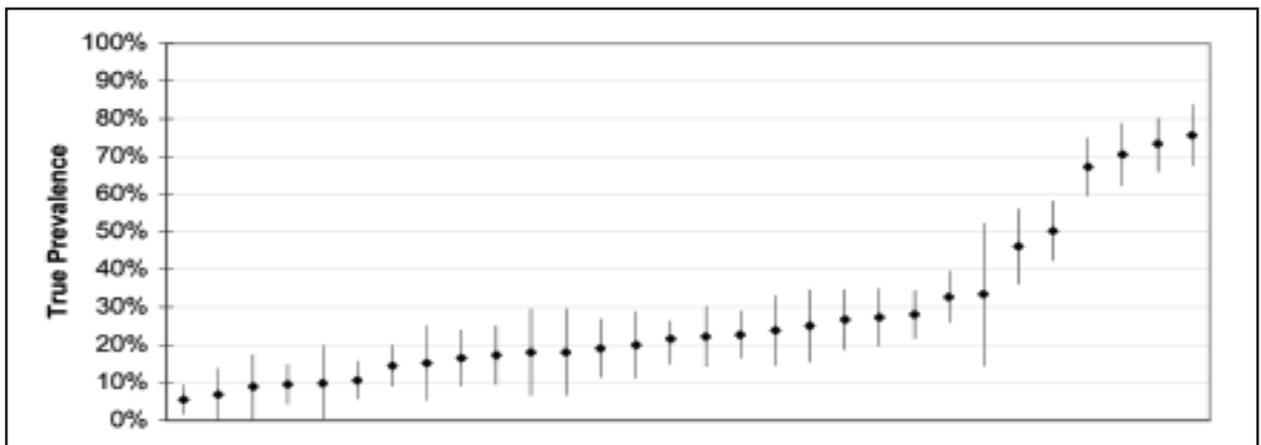


Figure 4. The within herd true IBR prevalence for 30 infected study herds in Ireland during November 2007. The prevalence estimate and 95% confidence limits for each herd are represented by a dot and vertical line, respectively

Table 2. Unconditional associations between categorical independent variables and infection status of 41 study herds in Ireland during November 2007

Variable	Herd infection status			P-value
	Non-infected (%) (n = 11 herds)	Infected (%) (n = 30 herds)	Total (%) (n = 41 herds)	
Herd size				
1) 4-32 animals	18	30	27	0.2256
2) 33-55 animals	45	17	24	
3) 56-88 animals	27	23	24	
4) 89-320 animals	9	30	24	
Number of farm-bought cattle during 2007				
1) 0 animals	45	33	37	0.6000
2) 1-2 animals	18	23	22	
3) 3-5 animals	9	27	22	
4) 5-22 animals	27	17	20	
Closed herd '07				
No	27	17	20	0.6582
Yes	73	83	80	
Percentage purebred				
1) 0-50%	27	40	37	0.6795
2) 51-90%	27	30	29	
3) 91-100%	45	30	34	
Average herd age				
1) 1.77-3.01 years	27	27	27	0.2612
2) 3.02-3.40 years	18	27	24	
3) 3.41-3.75 years	45	17	24	
4) 3.76-4.98 years	9	30	24	
Percentage homebred				
1) 80-100%	55	30	37	0.2720
2) 15-79%	45	70	63	

Table 3. Unconditional associations between continuous independent variables and infection status of 41 study herds in Ireland during November 2007

Variable	Non-Infected (n=11)		Infected (n=30)		P-Value
	Median	Range	Median	Range	
Number of mart bought animals during 2007	0	0 – 5	2	0 – 21	0.066
Number of contiguous herds	11	3 – 16	12	3 – 50	0.067
Percentage male (%)	25	13 – 40	23	6 – 34	0.072

Table 4. Variables conditionally associated with herd infection status of 41 study herds in Ireland during November 2007, based on results from an exact logistic regression model

Variable	Odds ratio	95% Confidential Interval		P-value
		Lower	Upper	
Percentage male (%)	0.88	0.77	1.00	0.040
Number of contiguous herds	1.13	1.01	1.33	0.042

## 4. DISCUSSION

### 4.1 Herd and within-herd prevalence

IBR is prevalent in Irish cattle herds. In this study, among herds with known infection status, herd IBR prevalence was 73.2%. Further, infected herds were located throughout the country (Figure 3). Such information from Ireland has not previously been reported (Ackermann and Engels, 2006). These results concur with levels of infection prior to establishment of national control in other countries, such as Belgium, Italy Spain and the Netherlands. For example, a herd prevalence of 67% (Boelaert *et al.*, 2000) and 97% (Solis-Calderon *et al.*, 2003) was reported from Belgium and Mexico, respectively.

### 4.2 Sampling strategy

The study farms are likely to be representative of beef herds in Ireland from which high genetic merit animals are sourced. Within such herds, IBR risks may be increased as a result of practices such as bull showing. However, 54% of these herds contained less than 70% purebred animals, indicating that these herds may have a mixture of enterprises. Therefore, they may also be representative of commercial beef enterprises. In this serosurvey, the sampling strategy and severe test interpretation placed on inconclusive results was designed to maximise the detection of IBR within herds supplying this bull performance station. This provided us with some confidence of our assessment of herdlevel freedom from infection, but may have resulted in possible overestimation of within herd prevalence. Our classification of herd freedom was based on the assumption that within-herd prevalence would be at least 10%, if infection were present, drawing on our understanding of IBR infection dynamics, and of within-herd transmission of infection following introduction. Note, however, that a single seropositive animal was detected in 4 of the 11 herds that were subsequently classified as free from infection. In each case, the 95% confidence interval for true within-herd prevalence was less than 10%. It is possible that these were true positive results, with the seropositive animal have been recently-infected, recently-introduced or a latent BoHV-1 carrier. If this were true, herd prevalence would in fact be 83.0% (34 positive herds/41 herds where infection status could be assessed). Therefore, these herds would also be at greater infection risk, with implications for safe entry of bulls from these herds into this testing station. Alternatively, these animals may have returned a false positive result, noting that the specificity of the gB ELISA is not perfect.

### 4.3 Risk factor analysis

Two factors were significantly associated with an increased IBR risk in herds, including an increasing number of contiguous herds and a decreasing percentage of male animals within a study herd. The former risk factor could reasonably be linked with levels of biosecurity on the study farms. In previous studies, Boelaert *et al.* (2005) and van Schaik *et al.* (1998) each identified animal purchases as a significant risk to biosecurity. In this study, the number of purchases from markets was initially considered, but was not found to be significant in the final model. This may be due by the relatively small numbers of herds sampled. Further, animals with IBR infection are seropositive for life; therefore, previously exposed animals may mask the impact of herd purchases on the overall herd status. Boelaert *et al.* (2005) also found conflicting results regarding the effect of sex on herd status. In this work, these authors found that animal infection risk was increased in males and with increasing age. We noted a similar age-related trend, however, this was not significant. In Irish beef herds, older animals are more likely to be female, and therefore a decreasing percentage of male animals may be a proxy for increasing age.

### 4.4 Implications for this bull testing station

This study has highlighted the significant challenge faced by this Irish bull performance testing station in the selection and production of high quality sires for the artificial insemination. It raises serious concerns over the continued feasibility of such centres, operating in isolation to create an IBR free herd, when selecting from an endemically infected population, given the substantial economic consequences to bull owners and testing organisations of disease breakdowns.

## 5. CONCLUSIONS

IBR is prevalent and widespread through the Irish cattle population. Any attempts at IBR control are likely to be problematic, given the endemic nature of the infection in Ireland. This study highlights some of the challenges faced when conducting national disease surveillance. Although excellent diagnostic facilities are available for sampling testing, the collection and correlation of farm and animal data is cumbersome and highly labour intensive. Future investment in surveillance will also be needed if national control programmes were to be established. A number of countries in Europe have moved, or are moving, to towards freedom from infection. This will have important implications for Ireland, given the importance of live cattle export to Europe, and international standards in semen production.

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# EQUINE INFECTIOUS ANAEMIA IN IRELAND DURING 2006: AN EPIDEMIOLOGICAL INVESTIGATION TO DETERMINE THE SOURCE OF INFECTION AND MODES OF TRANSMISSION AND SPREAD

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## ABSTRACT

Ireland experienced an outbreak of equine infectious anaemia (EIA) during 2006. This paper presents a subset of a broader investigation of the outbreak, specifically the results of a detailed epidemiological investigation to determine the source of infection and the modes of transmission and spread. A concurrent legal investigation was also conducted. Data were collected about each case and, as relevant, cohort animals on the timing and location of all events that might be relevant to the introduction and transmission of infection. These were collected during discussions with relevant parties, from records and based on observation. We developed detailed timelines, maps and cluster diagrammes to evaluate temporal, spatial and spatio-temporal relationships, and to critically appraise alternative hypotheses concerning introduction, as well as transmission and spread. These were constructed for each case, for each cluster, and for the overall outbreak. 38 cases were identified during the outbreak, linked within 2 clusters, X (21 cases) and Y (17), centred in counties Meath and Kildare, respectively. The probable source of primary infection was identified as hyperimmune plasma, imported from Italy without license. Within cluster X, the modes of transmission and spread were likely to have been iatrogenic transmission (14 cases, including 1 where supporting evidence was lacking), close contact (4) and vector-borne transmission (3). In cluster Y, which is considered in greater detail by More *et al.* (submitted), 16 cases were attributed to nosocomial transmission and 1 to vector-borne transmission. Probable linkages between each of the cluster X cases are presented. These results highlight the need for high standards of hygiene in the administration of medicines, and the danger of using non-registered products. Results from this epidemiological investigation provided 'real-time' information about the behaviour of the infection in Ireland, which contributed to continual fine-tuning of both national and local control strategies, as warranted.

## 1. INTRODUCTION

Equine infectious anaemia (EIA) was confirmed in Ireland on 15 June 2006. Over the following six months, until 10 December 2006, a total of 38 EIA cases were identified. This was the first outbreak of this disease in Ireland with evidence of transmission of infection. Although EIA had previously been diagnosed in Ireland on one occasion, during September 1975, there had been no transmission from the two primary cases (Brangan *et al.* submitted).

EIA is caused by a lentivirus (within the family Retroviridae), and infection is persistent and lifelong. Transmission occurs through the mechanical transfer of blood from an infected horse, either by blood-sucking insects or through the use of contaminated needles or instruments. Transplacental, colostral, lacteal and venereal transmission have also been reported. Viraemia is intermittent and generally associated with acute or chronic clinical signs; therefore, transmission risk is greatest from horses undergoing clinical signs (Sponseller 2003).

This paper presents part of a broader investigation of the EIA outbreak in Ireland during 2006, specifically to identify the probable source of infection and modes of transmission and spread.

## 2. MATERIALS AND METHODS

### 2.1 General

A detailed description of the methodology associated with the national response to the EIA incursion, including field operations

and central coordination, is presented elsewhere (Brangan *et al.* submitted). As mentioned previously (Brangan *et al.* submitted), all horses with a positive result on the agar gel immunodiffusion (AGID) test were considered confirmed EIA cases. All horses suspected of being infected, based on clinical, epidemiological and/or laboratory evidence consistent with EIA, but which were not confirmed by the AGID test, were considered unconfirmed EIA cases.

### 2.2 The epidemiological investigation

A detailed investigation of all confirmed and unconfirmed cases was undertaken by the local Veterinary Inspector (VI), headquarters staff, and staff from the Centre for Veterinary Epidemiology and Risk Analysis (CVERA) at University College Dublin (UCD). During on-farm visit(s), data were collected on the timing and location of all events that might be relevant to the introduction and transmission of infection. Data were collected during discussions with relevant parties, from records and based on observation. We were primarily interested in events (including movement(s), treatment(s), foaling, grazing and stalling history, laboratory data, etc) relevant to confirmed and unconfirmed cases, however, events relating to cohort horses were also considered when relevant. Additional data about each case and relevant cohort animals were collected from local veterinary practices (based on records, interview), horse transporters (records, interview), and from maps (topography, farm fragments). As relevant, data were also collected from hospital records, detailed observation and interview. Photographs were taken to assist during subsequent discussions.

The following temporal data were collected in each case:

- *Infection date*: the date when each case was infected with the EIA agent, when known. If the infection date was uncertain, we

Table 1. Descriptive data about the 38 EIA cases identified during the 2006 outbreak in Ireland

Case number	Coding (Cullinane et al., 2007) <sup>a</sup>	Breed <sup>b</sup>	Sex <sup>c</sup>	Age <sup>d</sup>	Home premise		Infection			Clinical signs			Diagnosis		Date	Death			
					Most-likely infection date	Probable mode of infection <sup>e</sup>	Infection cluster	Clinical presentation <sup>f</sup>	Date of initial signs	Diagnosis premise	Diagnosis date <sup>g</sup>	Confirmed/ unconfirmed <sup>h</sup>	Method <sup>i</sup>						
1	Horse 1	t	m	a	Farm A	Meath	Farm A	Meath	-	A	A	a	9-Jun	Hospital Y	Kildare	12-Jun	c	14-Jun	e
2	Foal 3	t	f	f	Farm B	Meath	Farm B	Meath	-	i	A	a	18-Apr	Hospital Y	Kildare	3-May	c	25-May	e
3	-	t	f	f	Farm A	Meath	Farm A	Meath	1-Mar	i	A	a	23-Mar	Home premise (Farm A)	Meath	14-Jun	c	14-Jun	d
4	Horse 2	t	m	a	Farm B	Meath	Farm B	Meath	-	cc	A	a	4-Jul	Home premise (Farm B)	Meath	4-Jul	c	5-Jul	e
5	Horse 3	t	m	a	Farm A	Meath	Farm A	Meath	-	cc	A	a	11-Jul	Home premise (Farm A)	Meath	12-Jul	c	12-Jul	e
6	Foal 5	t	f	f	Other	Kildare	Hosp. Y	Kildare	13-Jun	n	B	a	17-Jul	Hospital Y	Kildare	19-Jul	c	22-Jul	d
7	Horse 4	t	m	a	Other	Kildare	Hosp. Y	Kildare	13-Jun	n	B	a	21-Jul	Hospital Y	Kildare	19-Jul	c	22-Jul	e
8	Horse 5	t	m	a	Other	Tipperary	Hosp. Y	Kildare	13-Jun	n	B	a	21-Jul	Hospital Y	Kildare	19-Jul	c	22-Jul	e
9	Horse 6	t	m	a	Other	Kildare	Hosp. Y	Kildare	13-Jun	n	B	a	21-Jul	Hospital Y	Kildare	20-Jul	c	24-Jul	e
10	Horse 8	t	g	a	Other	Dublin	Hosp. Y	Kildare	13-Jun	n	B	i	-	Home premise (other)	Dublin	22-Jul	c	26-Jul	e
11	Horse 10	t	m	a	Other	Kildare	Hosp. Y	Kildare	13-Jun	n <sup>l</sup>	B	a	21-Jul	Hospital Y	Kildare	24-Jul	c	25-Jul	e
12	Horse 9	t	m	a	Other	Meath	Hosp. Y	Kildare	13-Jun	n	B	a	21-Jul	Home premise (other)	Meath	24-Jul	c	27-Jul	e
13	Horse 12	t	m	a	Other	Wexford	Hosp. Y	Kildare	13-Jun	n	B	a	25-Jul	Home premise (other)	Wexford	27-Jul	c	29-Jul	e
14	Horse 11	t	m	a	Other	Limerick	Hosp. Y	Kildare	13-Jun	n	B	a	21-Jul	Home premise (other)	Limerick	27-Jul	c	31-Jul	e
15	Horse 13	t	m	a	Farm B	Meath	Farm B	Meath	-	v	A	a	5-Aug	Home premise (Farm B)	Meath	5-Aug	c	7-Aug	e
16	Foal 6	t	f	f	Farm C	Meath	Farm C	Meath	4-Jul	i	A	a	21-Jul	Home premise (Farm C)	Meath	21-Aug	c	25-Aug	e
17	Horse 14	t	m	a	Farm A	Meath	Farm A	Meath	-	v	A	i	-	Home premise (Farm A)	Meath	25-Aug	c	9-Nov	e
18	Foal 7	t	f	f	Farm I	Derry	Farm I	Derry	-	v	B	a	17-Aug	Home premise (Farm I)	Derry	25-Aug	c	28-Aug	e
19	Horse 15	t	m	a	Other	Kildare	Hosp. Y	Kildare	13-Jun	n	B	a	18-Aug	Home premise (other)	Dublin	28-Aug	c	2-Sep	e
20	Horse 16	t	g	a <sup>k</sup>	Other	Meath	Hosp. Y	Kildare	13-Jun	n <sup>l</sup>	B	i	-	Home premise (other)	Dublin	28-Aug	c	2-Sep	e
21	Foal 8	t	c	f	Other	Wexford	Hosp. Y	Kildare	13-Jun	n <sup>l</sup>	B	a	31-Aug	Home premise (other)	Wexford	5-Sep	c	7-Sep	d
22	Horse 17	s	g	a	Farm D	Meath	Farm D	Meath	-	v	A	a	29-Aug	Home premise (Farm D)	Dublin	5-Sep	c	6-Sep	e
23	Horse 18	s	g	a	Farm D	Meath	Clinic X	Meath	25-Apr	i	A	i	-	Home premise (Farm D)	Dublin	8-Sep	c	10-Sep	e
24	Horse 19	s	m	a	Farm E	Meath, Louth	Farm E	Louth	-	cc	A	i	-	Home premise (Farm E)	Louth	18-Sep	c	22-Sep	e
25	Horse 20	t	m	a	Other	Wicklow	Hosp. Y	Kildare	13-Jun	n	B	a	21-Sep	Home premise (other)	Wicklow	21-Sep	c	24-Sep	e
26	Foal 9	t	f	f	Farm F	Meath	Farm F	Meath	20-Jul	i	A	a	20-Sep	Home premise (Farm F)	Meath	27-Sep	c	29-Sep	e
27	Foal 10	t	f	f	Farm G	Meath	Farm G	Meath	4-Apr	i	A	i	-	Home premise (Farm G)	Meath	26-Oct	c	28-Oct	e
28	Horse 21	t	m	a	Other	Monaghan	Hosp. Y	Kildare	13-Jun	n	B	i	-	Home premise (other)	Monaghan	17-Nov	c	21-Nov	e
29	Horse 22	t	g	a	Farm H	Meath	Farm H	Meath	-	i <sup>j</sup>	A	i	-	Home premise (Farm H)	Meath	5-Dec	c	11-Dec	e

*Continued*

Case number	Coding (Cullinane <i>et al.</i> , 2007) <sup>a</sup>	Breed <sup>b</sup>	Sex <sup>c</sup>	Age <sup>d</sup>	Home premise	Infection			Clinical signs			Diagnosis		Death				
						Infection premise	Most-likely infection date	Probable mode of infection <sup>e</sup>	Infection cluster	Clinical presentation <sup>f</sup>	Date of initial signs	Diagnosis premise	Diagnosis date <sup>g</sup>	Confirmed/ unconfirmed <sup>h</sup>	Date	Method		
U1	Foal 2	t	f	f	Farm A	Farm A	Meath	1-Mar	i	A	a	21-Apr	Home premise (Farm A)	Meath	11-May	u	10-May	d
U2	Foal 1	t	f	f	Farm A	Farm A	Meath	1-Mar	i	A	a	3-May	Home premise (Farm A)	Meath	5-May	u	3-May	d
U3	-	t	c	f	Farm A	Farm A	Meath	1-Mar	i	A	a	21-Apr	Home premise (Farm A)	Meath	-	u	30-May	d
U4	-	t	c	f	Farm A	Farm A	Meath	4-May	i	A	a	12-Jun	Home premise (Farm A)	Meath	14-Jun	u	14-Jun	d
U5	Foal 4	t	f	f	Farm A	Farm A	Meath	3-May	i	A	a	4-Jun	Hospital B	Kildare	12-Jun	u	10-Jun	d
U6	-	t	g	a	Other	Wicklow	Kildare	13-Jun	n	B	a	10-Jul	Home premise (other)	Wicklow	11-Jul	u	13-Jul	e
U7	Horse 7	s	s	a	Other	Kildare	Kildare	13-Jun	n	B	a	21-Jul	Home premise (other)	Kildare	21-Jul	u	25-Jul	e
U8	-	s	f	f	Farm E	Meath, Louth	Clinic X	25-Apr	i	A	i	-	Home premise (Farm E)	Louth	-	u	13-May	e
U9	-	t	f	f	Farm A	Meath	Clinic X	25-Apr	i	A	g <sup>a</sup>	-	Home premise (Farm A)	Meath	-	u	23-May	e

a Cullinane *et al.* (2007)  
b Breed: t, thoroughbred; s, sport horse  
c Sex: m, mare; f, filly; s, stallion; g, gelding  
d Age: a, adult; f, foal  
e Probable mode of infection: cc, close contact between a mare and foal; i, iatrogenic; n, nosocomial; v, vector  
f Clinical presentation: a, acute; i, inapparent carrier; ?, clinical presentation confused by pre-existing condition  
g Diagnosis date: date of sample collection leading to a diagnosis of EIA. Case 2 was confirmed during retrospective testing in mid-June; case 17 was held at the Central Veterinary Research Laboratory for several months following confirmation; and cases U1, U2 and U5 were diagnosed based on samples collected at post-mortem  
h Confirmed/unconfirmed: c, confirmed; u, unconfirmed  
i Method: d, death from natural causes; e, euthanasia  
j These three horses may have been infected after leaving Veterinary Hospital Y, and have been classified as possible tertiary cases. Further detail is available in Chapter 4  
k A, yearling  
l Suspected; supporting evidence is lacking  
m The clinical presentation was confused by an underlying condition

determined the *infection window* which included the full period during which infection may have occurred;

- *Diagnosis date*: the date of sample collection leading to a diagnosis of EIA, either using the Coggins test, for confirmed cases, or other methods such as ELISA, immunoblot or PCR, for unconfirmed cases; and
- *Date of first clinical signs*: the date when clinical signs, consistent with EIA, were first reported.

The following spatial data were collected from each case:

- *The home premise*: the farm where the case was normally resident;
- *The infection premise*: the location where each case most-likely became infected; and
- *The diagnosis premise*: the location of each case when disease status was clarified (either as a confirmed or an unconfirmed case).

We developed detailed timelines, maps and cluster diagrams to evaluate temporal, spatial and spatio-temporal relationships, and to critically appraise alternative hypotheses concerning introduction and transmission. These were constructed for each case, for each cluster, and for the overall outbreak. For each case, a range of modes of infection were evaluated, including:

- *Iatrogenic*: the mechanical transfer of virus from an infected horse through the use of contaminated needles, instruments, blood or blood products
- *Close contact*: the mechanical transfer of the virus from a foal to a mare, or vice-versa, through contact with infected secretions and abrasions, and
- *Vector-borne*: the mechanical transfer of virus by insects, typically tabanids.

For the purposes of the investigation, cases of hospital acquired infection, but without evidence of any of the three above-mentioned modes of infection, were considered the result of *nosocomial* transmission (Smith 2004). The World Health Organization defines nosocomial infection as an infection acquired in hospital which is not present or incubating at admission (Ducel *et al.* 2002).

The data were collated in Microsoft Excel (Microsoft Corporation, Redmond, WA, USA), and analysed using descriptive methods. Mapping was conducted using ArcGIS (version 9.0, ESRI, Redlands, CA, USA). We discussed aspects of this outbreak with a range of people with international expertise in the field.

### 2.3 The legal investigation

The Special Investigation Unit (SIU) of DAFF commenced an investigation on 5 July 2006 into the circumstances surrounding the importation of hyperimmune plasma, without licence, from Italy and its subsequent administration. With assistance from An Garda Síochána (Ireland's national police force) throughout this

investigation, a number of Irish premises were searched under warrant, and a number of people were interviewed, with statements taken under caution. Assistance was also sought on a number of aspects of the investigation from the Italian authorities, following a formal request from the Irish Department of Justice. Officers from the SIU and Gardai (police) travelled to Italy to progress this mutual assistance request.

## 3. RESULTS

### 3.1 The outbreak, in time and space

A total of 38 EIA cases were identified during the 2006 outbreak, including 29 confirmed and 9 unconfirmed cases (Table 1). The number of new EIA cases during 2006, by date of diagnosis, is presented in Figure 1. Unconfirmed cases U3, U8 and U9 are not included in this Figure, as no diagnostic testing was conducted. Cases were linked within 2 clusters, X and Y, which were centred in counties Meath and Kildare, respectively (Figure 2). A total of 21 cases were associated with cluster X, including 14 confirmed (1-5, 15-17, 22-24, 26-27, 29) and 7 unconfirmed (U1-U5, U8-U9) cases, and 17 cases with cluster Y, including 15 confirmed (6-14, 18-21, 25, 28) and 2 unconfirmed (U6-U7) cases.

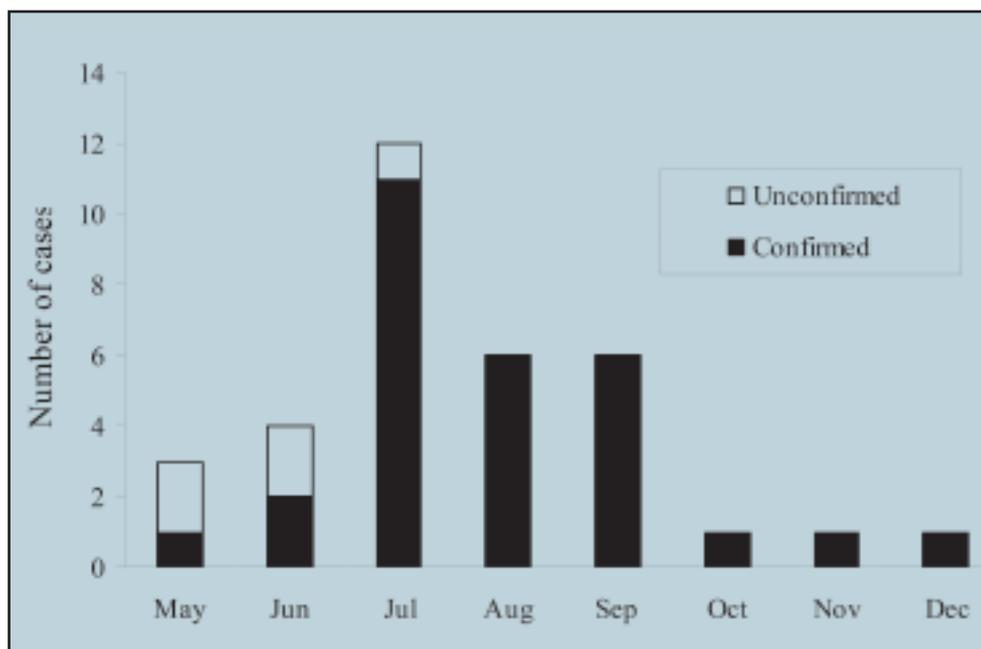


Figure 1. The number of new EIA cases during 2006, by date of diagnosis. Unconfirmed cases U3, U8 and U9 are not included, as no diagnostic testing was conducted

### 3.2 Source of introduction

Case 3, U1, U2 and U3 can each be considered index cases. Each involved a young foal, born on Farm A. On 01 March 2006, each foal had been administered hyperimmune plasma by a veterinarian from Veterinary Practice X. This plasma was believed to have been imported from Italy. By the time of this investigation, from mid-June 2006, this plasma was no longer available for further analysis.

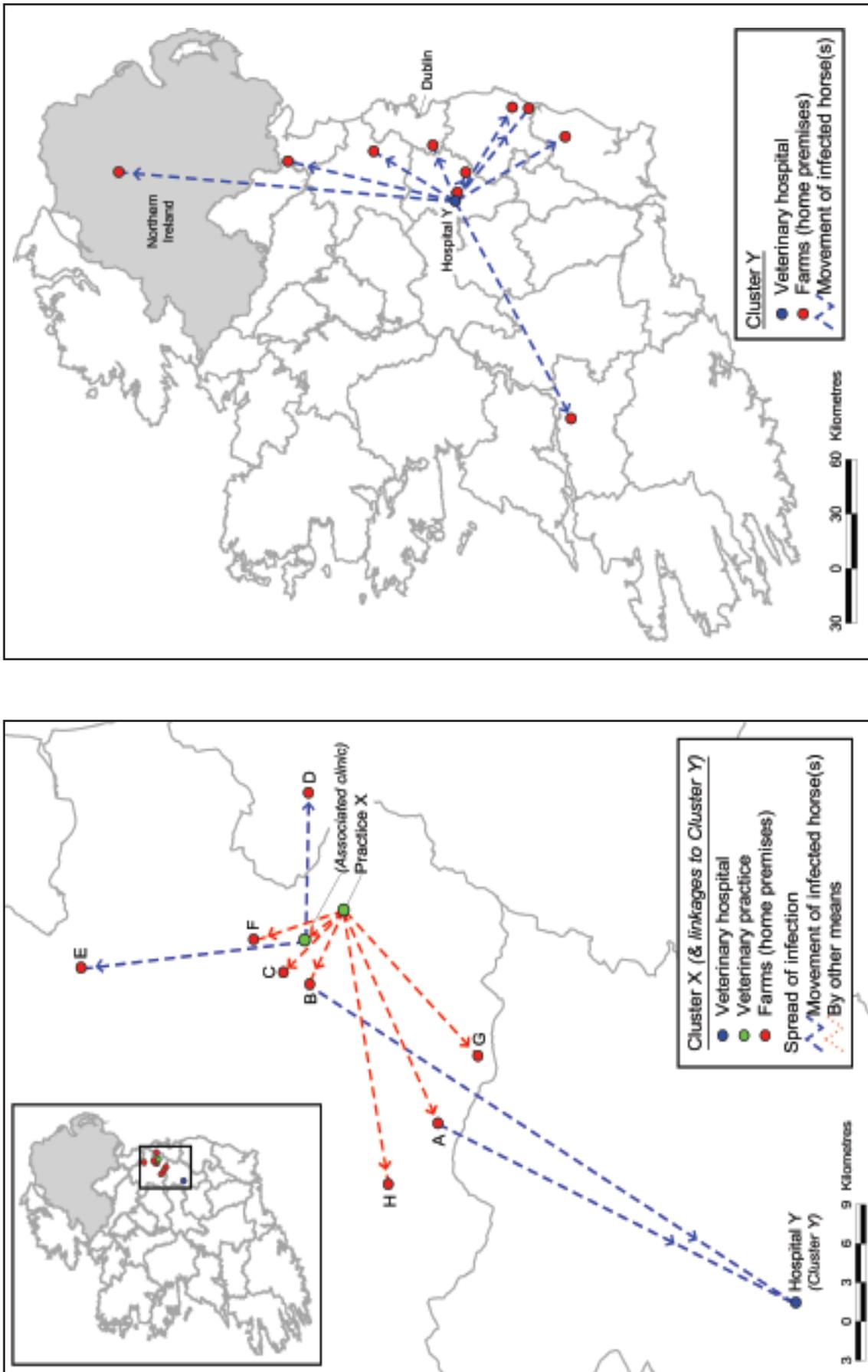


Figure 2. Location of the 38 EIA cases during the 2006 outbreak in Ireland, including EIA cases associated with clusters X (left) and Y (right). In cluster X (left), which spanned counties Dublin, Kildare and Meath, the home premises are shown as red dots, the main premise and associated clinic of Veterinary Practice X as green dots and Veterinary Hospital Y as a blue dot. The spread of infection between premises occurred following the movement of infected horses (dotted blue lines) or by other means (dotted red lines). In cluster Y (right), Veterinary Hospital Y is shown as a blue dot, and linkages with home premises (red dots) as blue dotted lines

### 3.3 Modes of transmission and spread

The probable modes of transmission and spread are presented in Table 1.

In cluster X:

- *Iatrogenic transmission* was likely in 13 cases (6 confirmed [2, 3, 16, 23, 26, 27] and 7 unconfirmed [U1-U5, U8, U9]), and possible in 1 confirmed case [29] where supporting evidence was lacking.
- *Close contact* was likely in 4 confirmed cases (1, 4, 5 and 24).
- *Vector-borne transmission* was likely in 3 confirmed cases (15, 17 and 22).

The infection linkages between cases in cluster X is presented in Figure 3.

In cluster Y:

- *Nosocomial transmission* was likely in 14 confirmed (6-14, 19-21, 25, 28) and 2 unconfirmed (U6, U7) cases. These sixteen cases, and Veterinary Hospital Y, are considered in greater detail

by More *et al.* (submitted). Briefly, nosocomial transmission is probable with ten of these cases, which were each confirmed either prior to discharge (7-9) or after returning, without any other cases, to their home premise (10, 12, 14, 25, 28, U6, U7). The remaining 6 horses left Hospital Y as three separate pairs (in-patient foal 11, accompanying mare 6; cases 19 and 20, a mare and yearling gelding, respectively; in-patient foal 21, accompanying mare 13) to other farms, and the potential for subsequent transmission can not be discounted, as a result of iatrogenic transmission (all pairs), close contact (the 1<sup>st</sup> and 3<sup>rd</sup> pairs) or vector-borne transmission (the 1<sup>st</sup> and 3<sup>rd</sup> pairs). Cases 11, 20, 21 were confirmed later than their respective pair.

- *Vector-borne transmission* was likely in 1 confirmed case (18).

The daily temperature and relative humidity in Kildare Town at noon during March to December 2006 is presented in Figure 4. Veterinary Practice X and Veterinary Hospital Y are located approximately 49 and 2 km of the centre of Kildare Town, respectively.

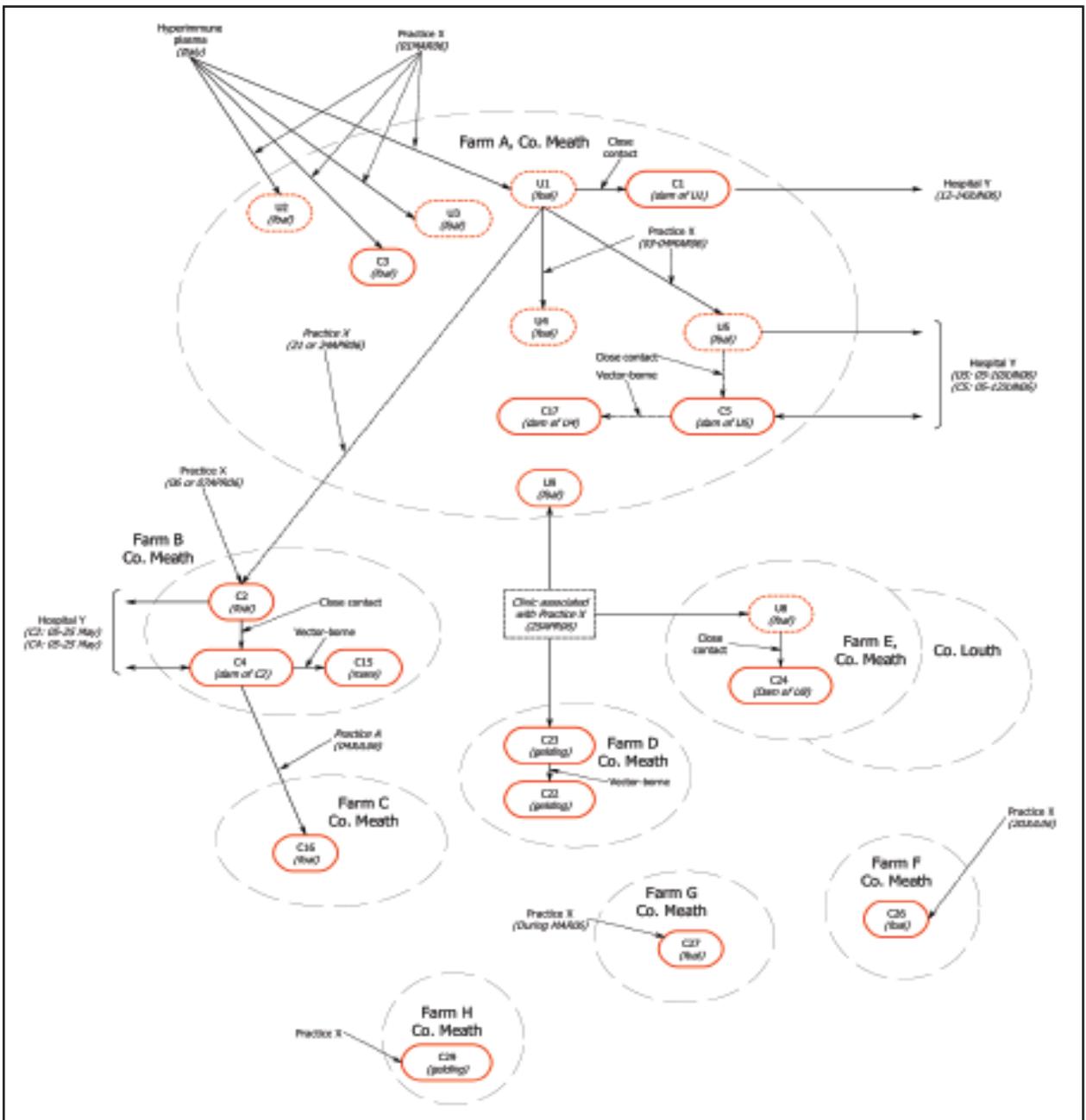


Figure 3. Probable infection linkages between cases in cluster X

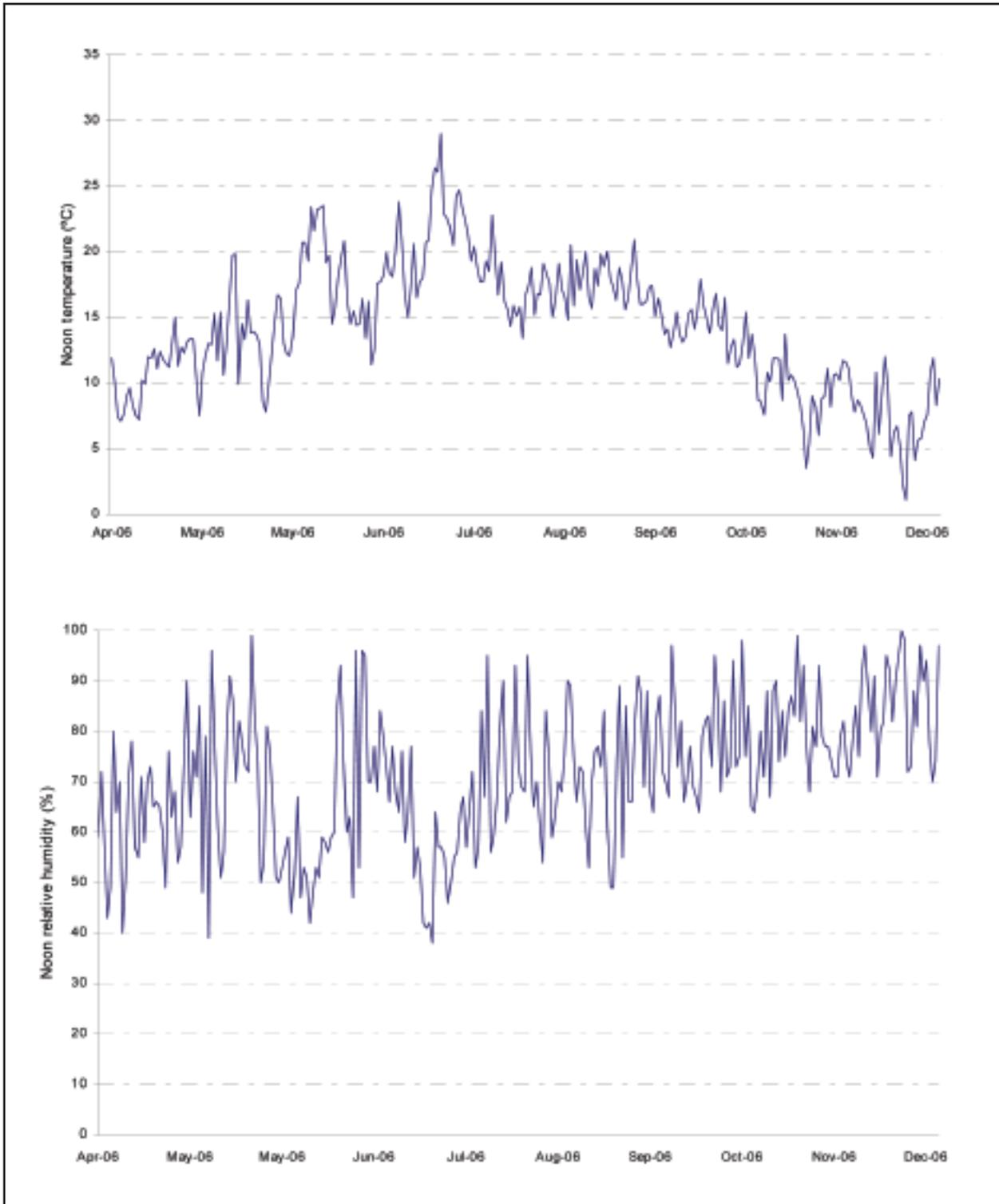


Figure 4. Noon temperature (top) and relative humidity (bottom) in Kildare Town, Co. Kildare during March to December 2006

## 4. DISCUSSION

### 4.1 Introduction of the EIA agent

In the five years prior to 2006, EIA was reported in a number of EU member states (France, Germany, Greece, Italy, Latvia, Lithuania, Romania) and near neighbours (Bosnia and Herzegovina, Croatia, Serbia and Montenegro, Turkey, Ukraine) (OIE 2006a). In Italy, sporadic outbreaks of EIA have occurred for many years (Guarini *et al.* 1957; Coddassa 1975; OIE 2007), linked to the importation of live horses for slaughter from a number of countries, including Romania where EIA is endemic (Anon. 2007a). In mid-2006, there was a significant outbreak of EIA in Italy, which has been associated with the distribution of plasma (licensed for use *in vitro*, but not *in vivo*) from a production facility in Tuscany, and an infected donor horse was subsequently identified (Passamonti 2007). The infectious agent was probably introduced into Ireland with the importation, without license, of plasma from this facility in Italy. To our knowledge, only four animals (case 3 and unconfirmed cases U1, U2 & U3) received this plasma; in each case, the plasma was believed to have been administered by the attending veterinary practice (Veterinary Practice X) on 01 March 2006. In Ireland, hyperimmune plasma is widely used as a prophylactic measure against *Rhodococcus equi* infection in foals, even though published results on its efficacy are conflicting (e.g. Giguère *et al.* 2002; Caston *et al.* 2006). Hyperimmune plasma is classified as an animal remedy, as defined in the Animal Remedies Act 1993, and must be authorised by the Irish Medicines Board (IMB) if it is to be supplied, possessed, administered etc. There is not currently, nor has there ever been, any hyperimmune plasma authorised by the IMB in this country. However, the European Communities (Animal Remedies) Regulations (No. 2) 2007 (and formerly the Animal Remedies Regulations 2005) allow for the import, possession and use etc under a licence granted by the Minister for Agriculture, Fisheries and Food, of an animal remedy authorised in another member state. In recent years, such licences have been granted in respect of the import of hyperimmune plasma from the United Kingdom.

### 4.2 Transmission and spread

With respect to transmission, the outbreak can be considered as two distinct, but linked, components, including cluster X with 21 (including 14 confirmed and 7 unconfirmed) EIA cases, and cluster Y with 17 (15 confirmed, 2 unconfirmed) cases. In the following discussion, we have solely focused on transmission and spread for 22 of these cases: each of the 21 cases from cluster X and the single case from cluster Y (case 18) where nosocomial transmission was not suspected. The remaining 16 cases from cluster Y (6-14, 19-21, 25, 28, U6, U7, each linked to nosocomial transmission in Veterinary Hospital Y), are examined in detail by More *et al.* (submitted).

A total of 14 cases (7 confirmed and 7 unconfirmed, all in cluster X) were probably infected as a result of iatrogenic transmission, linked to the activities of a single veterinary practice (Veterinary Practice X and its associated clinic). Transmission occurred both between and within farms, and was generally linked to the administration of plasma and fluids. It is believed that four foals (case 3, U1-U3) became infected on 1 March 2006, following the administration of hyperimmune plasma imported from Italy. In three cases (case 16, U4, U5), it is likely that transmission was associated with the use of contaminated equipment; these animals received fluids directly after fluids had been given to an infected animal. A further three cases (case 23, U8, U9) were treated in the clinic associated with Veterinary Practice X on the same day with a common treatment (draining and flushing of a wound or sinus). Although most cases of iatrogenic transmission were believed to have occurred before the disease was known to be in the country;

two (case 16 on 4 July 2006; case 26 on 20 July 2006) may have been infected after the outbreak had been confirmed. These 2 cases are linked to the treatments of clinically ill EIA cases.

It is likely that 4 cases (15, 17, 18 and 22) became infected following vector-borne transmission. Three of these horses were adults, whereas case 18 was a foal. In each situation, each of these horses had been co-grazing (in the same field) with a clinically ill horse during periods of high risk for vector activity. Vector-borne transmission was confined to three cases (case 17 on Farm A, case 15 on Farm B, case 22 on Farm D) in County Meath in the Republic of Ireland and one (case 18) in County Derry in Northern Ireland, on farms that varied greatly in size, from Farm A (approximately 180 acres and 200 horses) to Farm D (approx. 22 acres and 9 horses). Although there were differences in farm management (according to farm size), we observed no difference in vector control strategies between large and small studs. In this outbreak, we are confident that vector-borne transmission was not associated with between-farm spread. The minimum distance between infected premises was 1 mile (1.61 km; Farm B to Farm C); based in the available literature 200 yards (182.9 m) (Anon. 2001) or 200 m (Barros and Foil 2007) is the recommended distance to avoid vector-borne transmission. Further, a total of 14 contiguous farms (with 290 horses) associated to cluster X were restricted and tested on three occasions over a 90 days period, however, no positive animals were detected. There has been little to no work on tabanid species in Ireland. However, based on international reports, tabanid activity is increased with increasing temperature (greater than 20°C, optimally 25-29°C) and substantially reduced with cloud, rain and wind (Khan 1953). Tabanids appear to favour periods of high relative humidity (Dia *et al.* 1998). In Kildare Town, noon temperatures exceeded 20°C for several periods between 3 June and 5 August 2006. The noon temperature exceeded 25°C for only 3 days in mid-July. Humidity generally exceeded 60% throughout the outbreak (Figure 4).

Other transmission methods apart from iatrogenic and vector-borne transmission have been reported, including transplacental, colostrum, lacteal and venereal transmission (Sponseller 2003). In the current outbreak, infection was detected in four mare-foal pairs, with the mare becoming infected subsequent to her foal. These pairs were found on Farm A (mare case 1 and foal U1; mare case 5 and foal U5), Farm B (mare case 4 and foal case 2) and Farm E (mare case 24 and foal U8). In each case, transmission occurred during a low-risk period for vector activity, and there was no evidence of iatrogenic transmission. At post-mortem of foal U1, a cut was observed in the mucous membrane of the mouth, which may suggest some form of blood exchange from foal to mare. In this investigation, transmission to these 4 mares is ascribed to 'close contact'.

The potential role of people in the spread of such equine infection is well-recognised. As one example, in the late 1970s and 1980s, people played a role in the rapid international spread of contagious equine metritis, a highly contagious venereal infection of equids caused by *Taylorella equigenitalis* (Timoney 1996; Matsuda and Moore 2003). The infection can be transmitted indirectly by contaminated equipment, such as vaginal specula, examination sleeves, insemination equipment, etc., or by personnel who fail to observe adequate hygienic precautions in handling mares and stallions at the time of breeding (Timoney 1996). Similarly, infection control has become a key issue in veterinary teaching hospitals (Smith *et al.* 2004; Traub-Dargatz *et al.* 2004), particularly with respect to enteric and respiratory pathogens (Smith 2004). Codes of practice, providing guidelines for veterinarians, horse owners and breeders, now play a key role in control programmes, both nationally (Anon. 2007b) and within equine hospitals (Weese 2004). The existing industry voluntary code of practice has been modified to include EIA guidelines (Anon. 2007b). Relevant

chapters in the Code of Professional Conduct of the Veterinary Council of Ireland are also under review.

## 5. CONCLUSIONS

EIA was probably introduced into Ireland with the importation from Italy, without license, of contaminated hyperimmune plasma. Subsequently, the initial administration of this plasma, and much of the subsequent transmission and spread of the agent in cluster X, was probably related to iatrogenic causes. Most cases of iatrogenic transmission occurred before the disease was known to be in the country. These results highlight the need for high standards of hygiene in the administration of medicines, and the danger of using non-registered products. In contrast to previous reports, principally from the US, vector-borne transmission was of lesser importance, and could only be attributed to within-farm transmission over very short distances. This study highlights the importance of epidemiological investigations, concurrent with ongoing control efforts, during exotic disease incursions. Results from the current investigation provided 'real-time' information about the behaviour of the infection in Ireland, which contributed to continual fine-tuning of both national and local control strategies, as warranted. At times, the behaviour of this infection during the Irish outbreak was not as classically described, predominantly based on experiences from the US.

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# A REVIEW OF IRELAND'S WATERBIRDS, WITH EMPHASIS ON WINTERING MIGRANTS AND REFERENCE TO H5N1 AVIAN INFLUENZA

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## ABSTRACT

Ireland is characterised by its diversity and large abundance of wetlands, making it attractive to a wide variety of waterbirds throughout the year. Some 86 waterbird species are regularly recorded in Ireland, including 34 species that occur year round. This paper presents an overview of Ireland's waterbirds, including ecological factors relevant to the potential introduction, maintenance, transmission and spread of infectious agents, including the H5N1 avian influenza virus, in Ireland. Particular emphasis is placed on five groups of wintering migrants (dabbling and sieving wildfowl, grazing wildfowl, diving wildfowl, waders and gulls), noting that the H5N1 avian influenza virus has mainly been isolated from this subset of waterbirds. Ireland's wetlands are visited during the spring and summer months by hundreds of thousands of waterbirds which come to breed, predominantly from southern latitudes, and during the autumn and winter by waterbirds which come from a variety of origins (predominantly northern latitudes), and which are widely distributed and often congregate in mixed-species flocks. The distribution, feeding habits and social interactions of the five groups of wintering migrants are considered in detail. There is very substantial mixing of waterbird populations, in Ireland, throughout Europe and internationally. Throughout Ireland, there is interaction between different waterbird populations (breeding migrants, the wintering migrants and resident waterbird populations). There is also a regular and complex pattern of movement between feeding and roosting areas, and between wetlands and farmland, which will each also increase the mixing of waterbird species and populations. These interactions are likely to facilitate the rapid transmission and spread of the H5N1 avian influenza virus, if it were present in Ireland.

## 1. INTRODUCTION

The wetlands of northwest Europe are extremely important for millions of waterbirds, both resident and migratory. During summer months, waterbirds migrate to these wetlands to breed, whereas in winter, northern and boreal-nesting species migrate to these wetlands, either to overwinter or on passage to wintering grounds further south. Ireland plays a critical role in the ecology of these waterbirds, given its location (along a major flyway), mild (generally ice-free) climate and abundance of wetlands (Crowe, 2005).

An understanding of waterbird ecology is important to disease epidemiology, noting the role of these birds in the maintenance and spread of low pathogenic avian influenza (LPAI). As yet, however, the role of waterbirds in the epidemiology of H5N1 avian influenza (a highly pathogenic, HPAI, strain) remains uncertain. The current outbreak of H5N1 avian influenza was first detected in China in 1996 (Webster *et al.*, 2007a), and has subsequently appeared in many countries throughout Asia, Europe and Africa (Kilpatrick *et al.*, 2006). Ongoing studies are highlighting substantial differences in the behaviour of H5N1 and previous AI viruses, suggesting that the H5N1 virus is in rapid evolution (Webster *et al.*, 2007b). These differences include direct transmission of H5N1 viruses from wild birds to humans, transmission predominantly via the respiratory route, increased thermal stability and varying pathogenicity in waterfowl.

Within the European Union, coordinated measures have been developed to prevent and control avian influenza. Influenza surveillance has been increased, and import bans are placed on susceptible imports from third countries with H5N1 outbreaks (Anon., 2007a). Ireland has developed a range of relevant measures, including a contingency plan and ongoing risk assessments (Anon., 2007b).

Detailed information has recently been prepared on Ireland's waterbirds (Crowe, 2005). As yet, however, a review of this material has not been prepared, nor is information readily available of ecological factors that might be relevant to the introduction,

maintenance, transmission and spread of infectious agents, such as the H5N1 avian influenza virus, between and within waterbird populations in Ireland. This paper seeks to address this issue. Particular emphasis is placed on five groups of wintering migrants (dabbling and sieving wildfowl, grazing wildfowl, diving wildfowl, waders and gulls), noting that the H5N1 avian influenza virus has mainly been isolated from this subset of the broader waterbird population.

## 2. IRELAND'S WATERBIRDS

### 2.1 Overview

Ireland is characterised by a diversity and large abundance of wetlands (Figure 1), making it attractive to a wide variety of waterbirds throughout the year. Wetlands are defined by the Ramsar Convention as areas of water, marsh, fen or peatland, whether natural or artificial, permanent or temporary, with water that is static or flowing, fresh, brackish or salt, including marine waters, the depth of which at low tide does not exceed six metres (Ramsar Convention, 2000).

Waterbirds are defined as all species which are dependent on such wetlands, and some 86 species are regularly recorded (Table 1) in Ireland, many of which (34 species) occur year round. However, very few of these are entirely resident. Few remain in Ireland throughout the year with no immigration or emigration. Mute Swan is one example. Rather, the majority of the waterbirds which occur in Ireland are migratory, and are part of the East Atlantic Flyway (Figure 2), delimited by long-term studies of marked (ringed) birds (Wernham *et al.*, 2002). This is a generalised picture of the distribution and movements of migratory waterbirds.

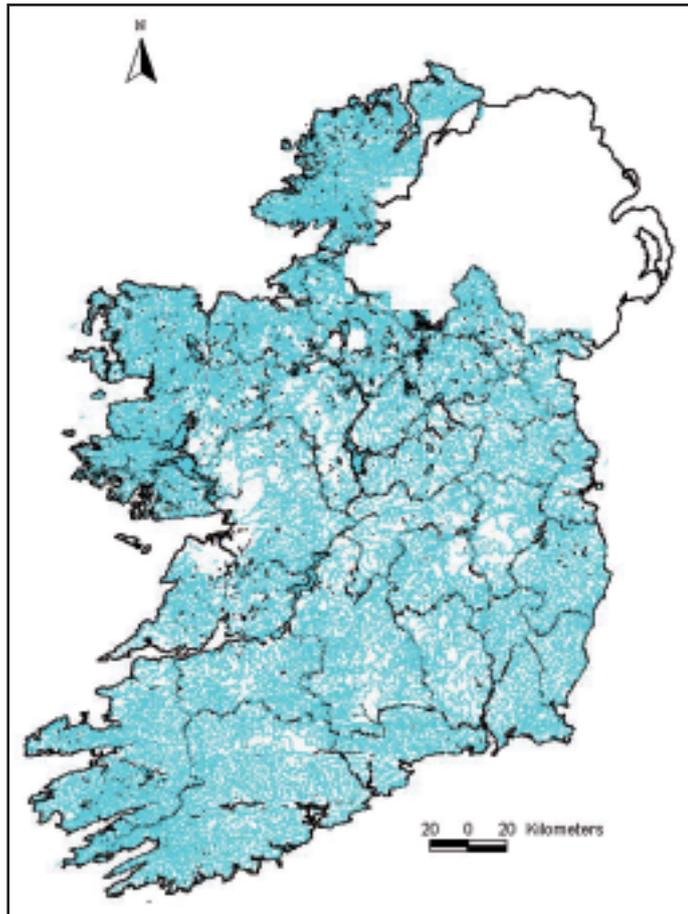


Figure 1. Ireland's wetlands, including rivers streams, reservoirs, ponds, lakes and canals

Table 1. Waterbird species occurring in Ireland

SPECIES		OCCURRENCE IN IRELAND
<b>Divers &amp; Grebes</b>		
Red-throated Diver	<i>Gavia stellata</i>	wintering-September to April, small numbers (< 10 pr) breed in Donegal
Black-throated Diver	<i>Gavia arctica</i>	wintering-September to April (Scarce)
Great Northern Diver	<i>Gavia immer</i>	wintering-September to April
Little Grebe	<i>Tachybaptus ruficollis</i>	year round
Great Crested Grebe	<i>Podiceps cristatus</i>	year round, numbers increase during the winter due to immigrating birds
<b>Shearwaters &amp; Petrels</b>		
Manx Shearwater	<i>Puffinus puffinus</i>	breeding-March to August
European Storm-petrel	<i>Hydrobates pelagicus</i>	breeding-March to August
Leach's Storm-petrel	<i>Oceanodroma leucorhoa</i>	breeding-March to August and passage September to October
Fulmar	<i>Fulmarus glacialis</i>	year round
<b>Gannet</b>		
Gannet	<i>Morus bassana</i>	year round
<b>Cormorants</b>		
European Shag	<i>Phalacrocorax aristotelis</i>	year round, few seen inshore outside the breeding season
Cormorant	<i>Phalacrocorax carbo</i>	year round, some immigration during the winter
<b>Hérons</b>		
Grey Heron	<i>Ardea cinerea</i>	year round
Little Egret	<i>Egretta garzetta</i>	year round
<b>Wildfowl (Swans Geese &amp; Ducks)</b>		
Mute Swan	<i>Cygnus olor</i>	year round
Bewick's Swan	<i>Cygnus columbianus</i>	wintering-October to April
Whooper Swan	<i>Cygnus cygnus</i>	wintering-October to April
Greenland White-fronted Goose	<i>Anser anser flavirostris</i>	wintering-October to April
Greylag Goose	<i>Anser anser</i>	year round (feral birds), augmented by wintering birds-October to April
Canada Goose	<i>Branta canadensis</i>	year round (feral birds)
Barnacle Goose	<i>Branta leucopsis</i>	wintering-October to April
Light-bellied Brent Goose	<i>Branta branta hrota</i>	wintering-October to April
Shelduck	<i>Tadorna tadorna</i>	wintering-September to April
Wigeon	<i>Anas penelope</i>	wintering-September to April

Gadwall	<i>Anas strepera</i>	year round, augmented by wintering birds-October to April (scarce)
Teal	<i>Anas crecca</i>	year round, augmented by wintering birds-September to April
Mallard	<i>Anas platyrhynchos</i>	year round, augmented by wintering birds-September to April
Pintail	<i>Anas acuta</i>	wintering-September to April
Shoveler	<i>Anas clypeata</i>	wintering-September to April
Pochard	<i>Aythya ferina</i>	predominantly wintering-September to April, small numbers breed
Tufted Duck	<i>Aythya fuligula</i>	predominantly wintering-September to April, small numbers breed
Scaup	<i>Anas marila</i>	wintering-September to April
Eider	<i>Somateria mollissima</i>	wintering-September to April
Long-tailed Duck	<i>Clangula hyemalis</i>	wintering-September to April
Common Scoter	<i>Melanitta nigra</i>	predominantly wintering-September to April, small numbers breed
Goldeneye	<i>Bucephala clangula</i>	wintering-September to April
Red-breasted Merganser	<i>Mergus serrator</i>	wintering-September to April, small numbers breed in West
Goosander	<i>Mergus merganser</i>	year round, small numbers breed (scarce)
Ruddy Duck	<i>Oxyura jamaicensis</i>	year round (feral birds)
<b>Rail &amp; Coots</b>		
Water Rail	<i>Rallus aquaticus</i>	year round
Moorhen	<i>Gallinula chloropus</i>	year round, augmented by wintering birds-September to April
Coot	<i>Fulica atra</i>	year round, augmented by wintering birds-September to April
<b>Waders</b>		
Oystercatcher	<i>Haematopus ostralegus</i>	year round, augmented by wintering birds-September to April
Ringed Plover	<i>Charadrius hiaticula</i>	year round, augmented by wintering birds-September to April
Golden Plover	<i>Pluvialis apricaria</i>	wintering birds-September to April, breeding birds-April to September, some overlap in populations
Grey Plover	<i>Pluvialis squatarola</i>	wintering birds-September to April
Lapwing	<i>Vanellus vanellus</i>	wintering birds-September to April, breeding birds-April to September, some overlap in populations
Knot	<i>Calidris canutus</i>	wintering birds-September to April
Sanderling	<i>Calidris alba</i>	wintering birds-September to April
Little Stint	<i>Calidris minuta</i>	passage birds-August to October (scarce)
Curlew Sandpiper	<i>Calidris ferruginea</i>	passage birds-August to October (scarce)
Purple Sandpiper	<i>Calidris maritima</i>	wintering birds-September to April
Dunlin	<i>Calidris alpina</i>	wintering birds-September to April, small numbers breed in west
Ruff	<i>Philomachus pugnax</i>	spring & autumn passage (scarce)
Jack Snipe	<i>Lymnocyptes minimus</i>	wintering birds-September to April
Snipe	<i>Gallinago gallinago</i>	year round, augmented by wintering birds-September to April
Woodcock	<i>Scolopax rusticola</i>	year round, augmented by wintering birds-September to April
Black-tailed Godwit	<i>Limosa limosa</i>	wintering birds-August to April
Bar-tailed Godwit	<i>Limosa lapponica</i>	wintering birds-September to April
Whimbrel	<i>Numenius phaeopus</i>	passage birds-April to September
Curlew	<i>Numenius arquata</i>	year round, augmented by wintering birds-September to April
Redshank	<i>Tringa totanus</i>	year round, augmented by wintering birds-September to April
Greenshank	<i>Tringa nebularia</i>	wintering birds-September to April
Common Sandpiper	<i>Actitis hypoleucos</i>	summer visitor-breeding birds present April to September
Turnstone	<i>Arenaria interpres</i>	wintering birds-September to April
<b>Skuas, Gulls &amp; Terns</b>		
Great Skua	<i>Stercorarius skua</i>	passage birds-April to October
Arctic Skua	<i>S. parasiticus</i>	passage birds-April to October
Mediterranean Gull	<i>Larus melanocephalus</i>	year round, very small breeding numbers (scarce)
Black-headed Gull	<i>Larus ridibundus</i>	year round, some local migration to/from breeding areas
Common Gull	<i>Larus canus</i>	year round, some local migration to/from breeding areas in west.
Lesser Black-backed Gull	<i>Larus fuscus</i>	occur during the breeding season, March/April to August/September
Herring Gull	<i>Larus argentatus</i>	year round, some local migration
Great Black-backed Gull	<i>Larus marinus</i>	year round, some local migration
Little Gull	<i>Larus minutus</i>	wintering birds-September to April (scarce)
Black-legged Kittiwake	<i>Rissa tridactyla</i>	year round
Iceland Gull	<i>Larus glaucooides</i>	wintering birds-September to April (scarce)
Glaucous Gull	<i>Larus hyperboreus</i>	wintering birds-September to April (scarce)
Sandwich Tern	<i>Sterna sandvicensis</i>	occur during the breeding season, March/April to August/September
Roseate Tern	<i>Sterna dougallii</i>	occur during the breeding season, March/April to August/September (very local)
Common Tern	<i>Sterna hirundo</i>	occur during the breeding season, March/April to August/September
Arctic Tern	<i>Sterna paradisaea</i>	occur during the breeding season, March/April to August/September
Little Tern	<i>Sterna albifrons</i>	occur during the breeding season, March/April to August/September (scarce)
<b>Auks</b>		
Common Guillemot	<i>Uria aalge</i>	year round, though occur inshore/ land during the breeding season, March/April to August/September
Razorbill	<i>Alca torda</i>	year round, though occur inshore/ land during the breeding season, March/April to August/September
Black Guillemot	<i>Cepphus grylle</i>	year round, though occur inshore/ land during the breeding season, March/April to August/September
Puffin	<i>Fratercula arctica</i>	occur during the breeding season, March/April to August/September (scarce)

Table 2. Flyway origins of species occurring in Ireland outside the breeding season

Species	Breeding	Wintering	Flyway estimate <sup>1</sup>	All-Ireland estimate	
Red-throated Diver	<i>Gavia stellata</i>	Arctic/ boreal W Eurasia, Greenland	Europe, Greenland	300,000	1,025+
Black-throated Diver	<i>Gavia arctica</i>	N Europe & W Siberia	NW Europe, Mediterranean, Black & Caspian Seas	375,000	<1,000
Great Northern Diver	<i>Gavia immer</i>	N America, Greenland, Iceland	NW Europe	5,000	<1,000
Little Grebe	<i>Tachybaptus ruficollis</i>	Europe, NW Africa	Europe, NW Africa	340,000	2,345+
Great Crested Grebe	<i>Podiceps cristatus</i>	NW Europe	NW Europe	475,000	5,385+
Great Cormorant	<i>Phalacrocorax carbo</i>	NW Europe	NW Europe	120,000	13,710+
Grey Heron	<i>Ardea cinerea</i>	W Europe, NW Africa	W Europe, NW Africa	274,500	2,960+
Little Egret	<i>Egretta garzetta</i>	Ireland, UK, Continent, N Africa	Ireland, UK, Continent, N Africa	134,000	<1,000
Mute Swan	<i>Cygnus olor</i>	Ireland <sup>a</sup>	Ireland <sup>a</sup>	11,440 <sup>a</sup>	11,440
Bewick's Swan	<i>Cygnus columbianus bewickii</i>	Arctic N Russia	NW Europe	29,000	380
Whooper Swan	<i>Cygnus cygnus</i>	Iceland	Ireland, UK, Iceland	20,900	12,730
Greenland White-fronted Goose	<i>Anser albifrons flavirostris</i>	W Greenland	Scotland, Ireland	33,000	11,340
Greylag Goose	<i>Anser anser</i>	Iceland	UK, Ireland	89,100	5,030 <sup>b</sup>
Canada Goose	<i>Branta canadensis</i>	Ireland	Ireland	1,050	1,050
Barnacle Goose	<i>Branta leucopsis</i>	Greenland	Scotland, Ireland	54,100	9,035
Light-bellied Brent Goose	<i>Branta bernicla hrota</i>	Canada, Greenland	Ireland	21,750	30,000
Common Shelduck	<i>Tadorna tadorna</i>	NW Europe	NW Europe	300,000	14,610
Eurasian Wigeon	<i>Anas penelope</i>	W Siberia, NW & NE Europe	NW Europe	1,500,000	82,370+
Gadwall	<i>Anas strepera</i>	NW Europe	W Europe	60,000	630
Eurasian Teal	<i>Anas crecca</i>	N & NW Europe	NW Europe	400,000	45,010+
Mallard	<i>Anas platyrhynchos</i>	N Europe	NW Europe	4,500,000	38,250+
Northern Pintail	<i>Anas acuta</i>	N Europe, W Siberia	NW Europe	60,000	1,235
Northern Shoveler	<i>Anas clypeata</i>	N, NW, Central Europe	NW, Central Europe	40,000	2,545
Common Pochard	<i>Aythya ferina</i>	Russia, NE & NW Europe	NE & NW Europe	350,000	37,780
Tufted Duck	<i>Aythya fuligula</i>	N & NW Europe	NW Europe	1,200,000	36,610
Greater Scaup	<i>Aythya marila</i>	W Siberia, N Europe	W Europe	310,000	4,430
Common Eider	<i>Somateria mollissima</i>	See <sup>c</sup> below	See <sup>c</sup> below	1,548,000 <sup>c</sup>	2,890
Long-tailed Duck	<i>Clangula hyemalis</i>	Iceland & Greenland	N Atlantic	125,000	<1,000
Common Scoter	<i>Melanitta nigra</i>	N & NW Europe, W Siberia	Baltic, E Atlantic	1,600,000	23,190
Common Goldeneye	<i>Bucephala clangula</i>	N, NW & Central Europe	NW & Central Europe	400,000	9,665
Red-breasted Merganser	<i>Mergus serrator</i>	NW & Central Europe, Iceland, E Greenland	NW & Central Europe, Iceland	170,000	3,390
Water Rail	<i>Rallus aquaticus</i>	Iceland	Faeroes, Scotland, Ireland	Unknown	Unknown
Common Moorhen	<i>Gallinula chloropus</i>	Europe & N Africa	Europe & N Africa	3,550,000	Unknown
Common Coot	<i>Fulica atra</i>	E, N, W Europe	NW Europe	1,750,000	33,160
Eurasian Oystercatcher	<i>Haematopus ostralegus</i>	N, C, W Europe	Europe, NW Africa	1,020,000	67,620
Ringed Plover	<i>Charadrius hiaticula</i>	Iceland, N & NW Europe	W Europe, N Africa, Mediterranean	73,000	14,580
European Golden Plover	<i>Pluvialis apricaria</i>	Iceland, the Faeroes, Greenland	Ireland, W Britain, Continent, NW Africa	930,000	166,700+
Grey Plover	<i>Pluvialis squatarola</i>	Arctic Russia, NE Canada	Wadden Sea, Ireland, UK, S & W Africa	247,000	6,315
Northern Lapwing	<i>Vanellus vanellus</i>	Europe	Europe, N Africa	6,750,000	207,700+
Red Knot	<i>Calidris canutus</i>	Canada, Greenland	W Europe	450,000	18,970
Sanderling	<i>Calidris alba</i>	NE Canada, Greenland, Svalbard	E Atlantic, W & S Africa	123,000	6,680
Purple Sandpiper	<i>Calidris maritima</i>	E Atlantic	E Atlantic	75,000	3,330
Dunlin	<i>Calidris alpina</i>	N Scandinavia, Russia, NW Siberia	W Europe, Mediterranean, N Africa	1,330,000	88,480
Jack Snipe	<i>Lymnocyptes minimus</i>	N Russia, S Sweden, N Poland, N Belarus, Baltic	W & S Europe, N & W Africa	>1,000,000	Unknown
Snipe	<i>Gallinago gallinago</i>	N Europe	S & W Europe, W Africa	>2,500,000	Unknown
Woodcock	<i>Scolopax rusticola</i>	Europe	W & S Europe, N Africa	17,500,000	Unknown
Black-tailed Godwit	<i>Limosa limosa</i>	Iceland, the Faeroes	Britain, Ireland, Continent, N Africa	47,000	13,880
Bar-tailed Godwit	<i>Limosa lapponica</i>	N Europe, N Russia	W Europe, NW Africa	120,000	16,280
Whimbrel	<i>Numenius phaeopus</i>	Iceland, the Faeroes, Scotland	W Africa	675,000	Unknown

Species		Breeding	Wintering	Flyway estimate <sup>1</sup>	All-Ireland estimate
Eurasian Curlew	<i>Numenius arquata</i>	W, N & Central Europe	W Europe, Mediterranean, NW Africa	850,000	54,650+
Common Redshank	<i>Tringa totanus</i>	See <sup>d</sup> below	See <sup>d</sup> below	400,000 <sup>d</sup>	31,090
Common Greenshank	<i>Tringa nebularia</i>	Scotland, Scandinavia	W & SW Europe, NW, W & S Africa	420,000	1,265
Ruddy Turnstone	<i>Arenaria interpres</i>	NE Canada, Greenland	W Europe, NW Africa	150,000	11,810
Mediterranean Gull	<i>Larus melanocephalus</i>	Black Sea, C, S, W Europe	Black Sea, Mediterranean, NW Europe, NW Africa	660,000	<200
Black-headed Gull	<i>Larus ridibundus</i>	Greenland, N & W Europe	S & W Europe	4,250,000	Unknown
Common Gull	<i>Larus canus</i>	Iceland, Ireland, Britain	Europe, N Africa	1,725,000	Unknown
Lesser Black-backed Gull	<i>Larus fuscus</i>	Greenland, Iceland, Ireland, UK, Belgium, France	W Europe, W France	550,000	Unknown
Herring Gull	<i>Larus argentatus</i>	Iceland, Ireland, Britain, NW France, Germany	NW Europe	590,000	Unknown
Great Black-backed Gull	<i>Larus marinus</i>	NW France, Britain, Ireland, Iceland, N Europe	E Atlantic S to Iberia	440,000	unknown

<sup>1</sup> From Wetlands International (2002).

<sup>2</sup> From Hutchinson (1979).

<sup>3</sup> From Sheppard (1993).

<sup>a</sup> The Irish Mute Swan population has been elevated to biogeographic population (Wetlands International, 2002), and the threshold is thus the same as that for all-Ireland.

<sup>b</sup> Additional birds from feral population – c. 2,000 individuals.

<sup>c</sup> The relevant population on which to base the 1% threshold for Common Eider has been taken as the NW European total which comprises the four populations in this region (Britain/Ireland 73,000, Baltic/Wadden Sea 850,000 – 1,200,000, Norway/NW Russia 300,000 – 550,000 and White Sea 20,000 – 30,000).

<sup>d</sup> The relevant populations for Common Redshank include two populations, *robusta* (breed in Iceland & the Faeroes, winter Britain, Ireland, NW France) & *britannica* (breed in Britain & Ireland, winter Britain, Ireland, NW France).

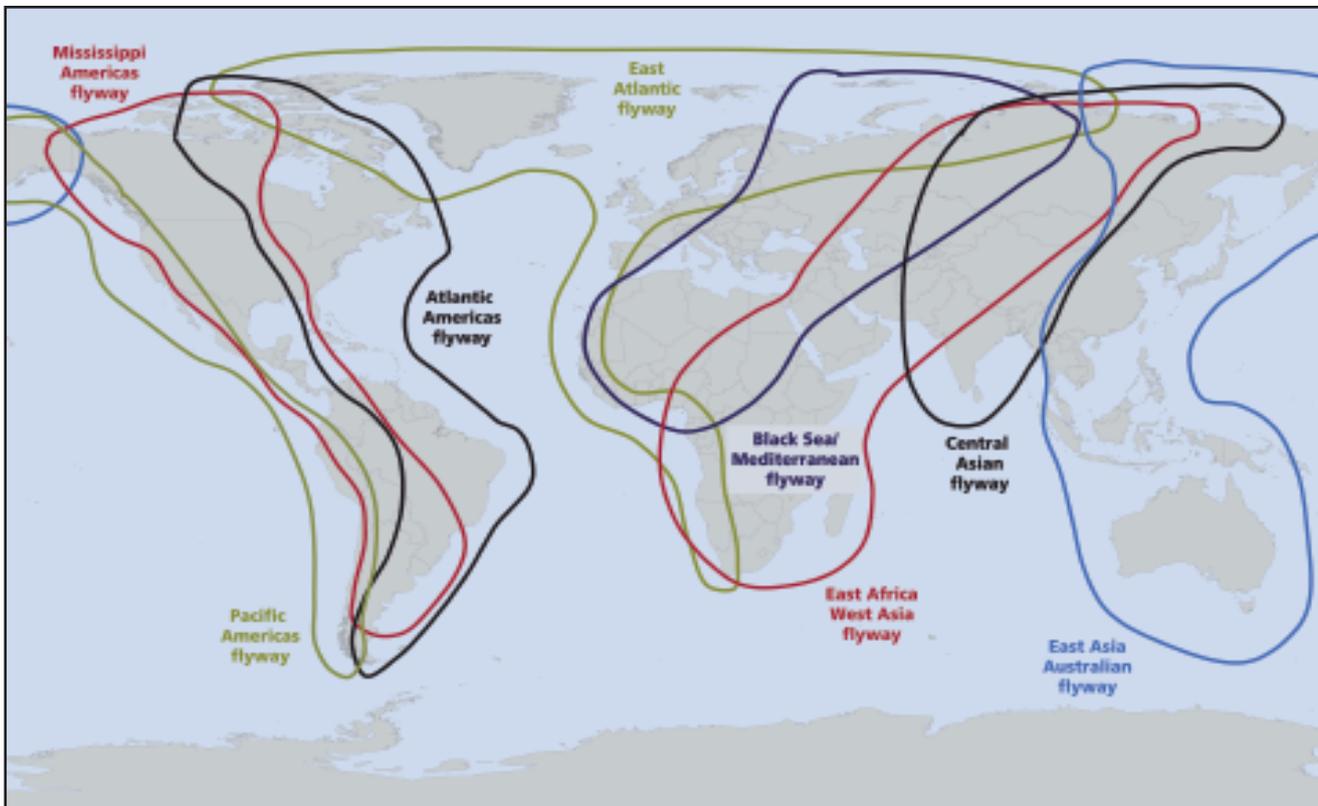


Figure 2. Global flyways. "Flyways: Wetlands International. Compiled by FAO AGAH, EMPRES Programme. FAO 2005. All right reserved"

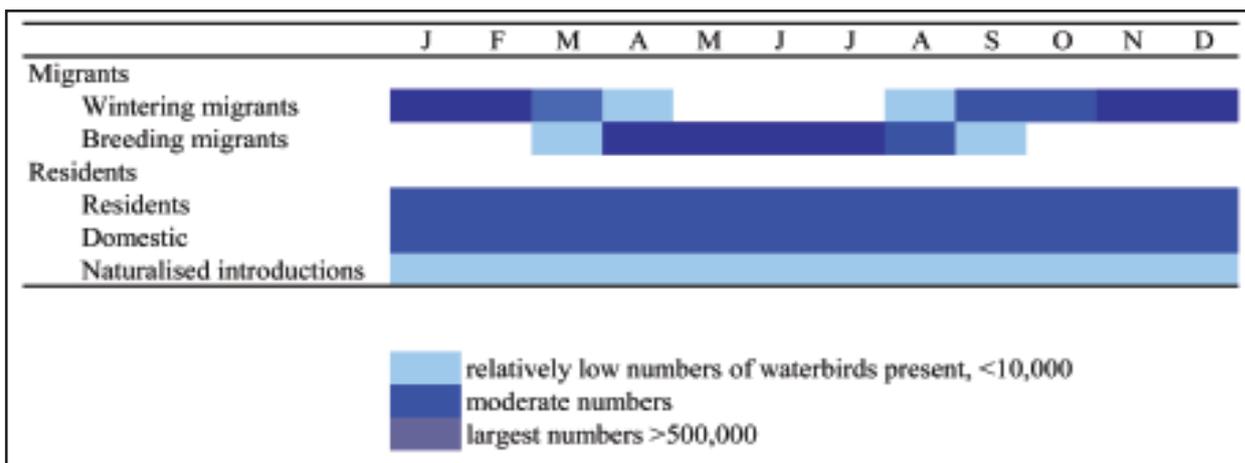


Figure 3. The number of migrant and resident waterbird present in Ireland throughout the year

## 2.2 Migratory flyways

The concept of a flyway is based on the migratory behaviour of birds. Flyways are typically north-south in orientation, with migratory birds moving to warmer climes during the autumn, and then returning during the spring to more northerly breeding areas. Many species migrate along well-defined routes, and consistently use the same sites as stop-over and/or wintering sites.

Some eight general migratory flyways have been defined (Davidson & Pienkowski 1987). The East Atlantic Flyway (Figure 2) extends from east Canada, across northern Europe to west Siberia in the north, and also south along the east Atlantic shores of northwest Europe and west Africa. Most migratory waterbird species which occur in Ireland during the winter have originated from one or more of the following areas:

- *North/northwest*: Canada, Greenland and Iceland.
- *Northeast*: the Netherlands, Denmark, Germany, Fennoscandia, the Baltic, western Russia (west of the Ural Mountains).
- *Far-eastern*: Russia east of the Ural Mountains and Siberia.
- *Central/east Europe*: Europe east of and including Poland, Czech Republic and Austria.

The breeding origins of waterbird species occurring in Ireland during the winter are summarised in Table 2. Most migratory waterbird species which breed in Ireland winter further south, in continental Europe or west Africa (i.e., they belong to the same principal flyway).

## 2.3 Migrants

### a. Breeding migrants

During the spring and summer months, hundreds of thousands of waterbirds come to Ireland to breed, predominantly from southern latitudes. These breeding migrants begin to arrive in Ireland in March, and are present in highest numbers between April and August, with some individuals remaining into early October. These waterbirds breed predominantly around Ireland's coastline, colonising the cliffs and islands. Some also nest inland, on lake islands and along the shorelines of lakes, rivers and streams. The breeding migrants include seabirds (petrels and shearwaters, Gannet *Morus bassana*, cormorants, gulls, terns and auks), as well as a number of other species/groups such as Red-throated Diver *Gavia stellata*, grebes, herons, swans, feral geese, ducks, rails, coots, waders, Great Skua, gulls, terns and auks.

### b. Wintering migrants

During the autumn and winter, Ireland's mild winter climate relative to most other European countries, together with its

diversity of wetlands, make it attractive over a million northern and boreal-nesting migrant waterbirds. Therefore, most of the wintering, or non-breeding, migrants come from northern latitudes. These birds begin to arrive from as early as July, with most occurring in Ireland between September and February, and some individuals remaining into early May. They occur in largest numbers of coastal estuaries, and on a selection of inland lakes, such as Lough Neagh in Northern Ireland and Lough Corrib in Co. Galway. Wintering waterbirds include fewer bird groups (divers, grebes, herons, swans, geese, ducks, rails, coots, waders and gulls), but a much broader diversity of species within these groups compared with breeding.

## 2.4 Residents

Many waterbirds remain in Ireland year-round. These include grebes, cormorants, herons, Mute Swan, some duck species and some gulls. However, as mentioned above, Mute Swan is one of very few examples of an entirely resident species, remaining in Ireland throughout the year with no immigration or emigration. Most other species are joined by additional birds during the autumn and winter months migrating from arctic and boreal-nesting areas.

Ireland also supports a number of introduced waterbirds, which remain relatively local throughout the year. These include:

- *Naturalised introductions*: Some wildfowl species have escaped from collections, and are free-living (e.g. Greylag Goose *Anser anser* and Canada Goose *Branta canadensis*). While these birds are sedentary, and do not generally move large distances, they cannot be easily distinguished from their wild counterparts.
- *Wildfowl bred for hunting*: Large numbers of Mallard *Anas platyrhynchos* are farmed, and released during the autumn for hunting.
- *Domestic wildfowl*: This group includes farmyard geese and ducks, and birds from wildfowl collections. Some of the farmyard geese and ducks have interbred with naturalised Greylag geese and Mallard respectively, and are part of the feral populations described above.

## 2.5 Interactions between populations

Most waterbirds occurring in Ireland come from more than one population. For example, small numbers of Coot (almost 4,000 pairs) breed in Ireland (Gibbons *et al.*, 1993), while wintering numbers exceed 33,000 individuals (Crowe *et al.*, in press). It is believed that the breeding birds are resident, and that during the winter, Britain and Ireland receive large numbers of immigrating birds from northern Europe, Scandinavia and the Baltic (Wernham *et al.*, 2002).

There are many other similar examples where resident breeding birds are augmented by winter migrants, e.g. Great Crested Grebe, Teal, Moorhen and Oystercatcher (Table 1). Some breeding seabird species, such as Kittiwake, become oceanic in nature outside the breeding season, when they are seldom recorded in inshore waters. Other species are entirely migratory; the five tern species and Common Sandpiper occur during the breeding period only, while most of the other wader species occur on passage and/or during the winter. For some species, many distinct groups have been recognised, and discrete populations have been defined, some of which have been split taxonomically into subspecies. For example, there are three populations of Dunlin *Calidris alpina* which occur in Ireland. *Calidris alpina schinzii* breeds in Ireland and winters further south in southwest Europe and northwest Africa, *C. a. arctica* breeds in Greenland and occurs in Ireland during spring and autumn on passage, while *C. a. alpina* breeds in Scandinavia and Siberia and winters in Ireland. Other species, such as Golden Plover, breed and winter in Ireland, although the origins of the respective populations differ; Irish-breeding birds move south to winter, while the non-breeding birds come from the population breeding in Iceland and the Faeroes. Further details on the status of all waterbirds occurring in Ireland are presented in Table 1.

Furthermore, there are periods (between March and early May and later between July and October) when there is considerable mixing of breeding and wintering (non-breeding) migrants (Figure 3). Waterbirds of varying origins regularly occur together. Examples include:

- Close to 10,000 post-breeding terns congregate in Dublin Bay in August and September prior to their southward migration, and mix with thousands of migrant geese, waders and gulls arriving from faraway arctic breeding grounds.
- Large numbers of Icelandic-breeding Greylag Geese (roughly 2,000 birds) mix with a resident flock of 800 feral Greylag Geese at Lough Swilly each winter.

## 2.6 Interactions between species

Outside the breeding season, most waterbirds are highly gregarious, and generally assemble in large, and often mixed-species flocks. By doing so, they reduce their risk to predation, as a flock of birds is more likely to detect a predator than a single bird. Flocks of swans and geese often include family parties which tend to remain intact for most of the first year. Although preferred wetlands among different waterbird groups (dabbling ducks, swans etc; see below) is to some extent exclusive, some of the larger wetland complexes include a variety of habitat types, and may support many different groups. For example, Lough Derg in counties Tipperary, Galway and Clare supports significant concentrations of a range of both dabbling and diving wildfowl, as well as waders and gulls. Further, waterbird species tend to gather together in mixed flocks where their favoured food is available.

During the breeding period itself, most species tend to nest either solitary, with many pairs holding and defending territories (e.g. Lapwing), or in dense colonies, where birds nest in close proximity, usually on cliffs and/or on islands, where they afford greater protection from predation and disturbance. It is not unusual for colonial species to nest in mixed-species colonies.

## 3. IRELAND'S WINTERING WATERBIRDS

### 3.1 Wintering waterbird surveys

Wintering waterbirds in the Republic of Ireland have been monitored for almost 40 years as part of three main surveys, the *Wetlands Enquiry* (1971/72-1973/74) (Hutchinson, 1979), the *Winter Wetlands Survey* (1984/85-1986/87) (Sheppard, 1993) and the *Irish Wetland Bird Survey* (I-WeBS, 1994/95-present) (Crowe, 2005). In most cases, parallel surveys have been carried out in Northern Ireland, with the most recent, the *Wetland Bird Survey* (WeBS), in operation since 1993/94. An example of information generated from I-WeBS (specifically, the distribution and abundance of Mallard, *Anas platyrhynchos*) is presented in Figure 4. These surveys have served to highlight the importance of wetlands in Ireland for wintering waterbirds, and have defined a suite of wetlands of significance, many of which have since been designated as Special Protection Areas (SPAs) under the EU Birds Directive (EEC/79/409) (Anon., 2006). To this end, waterbird populations, and the wetlands upon which they rely, continue to be monitored in Ireland through I-WeBS and WeBS.

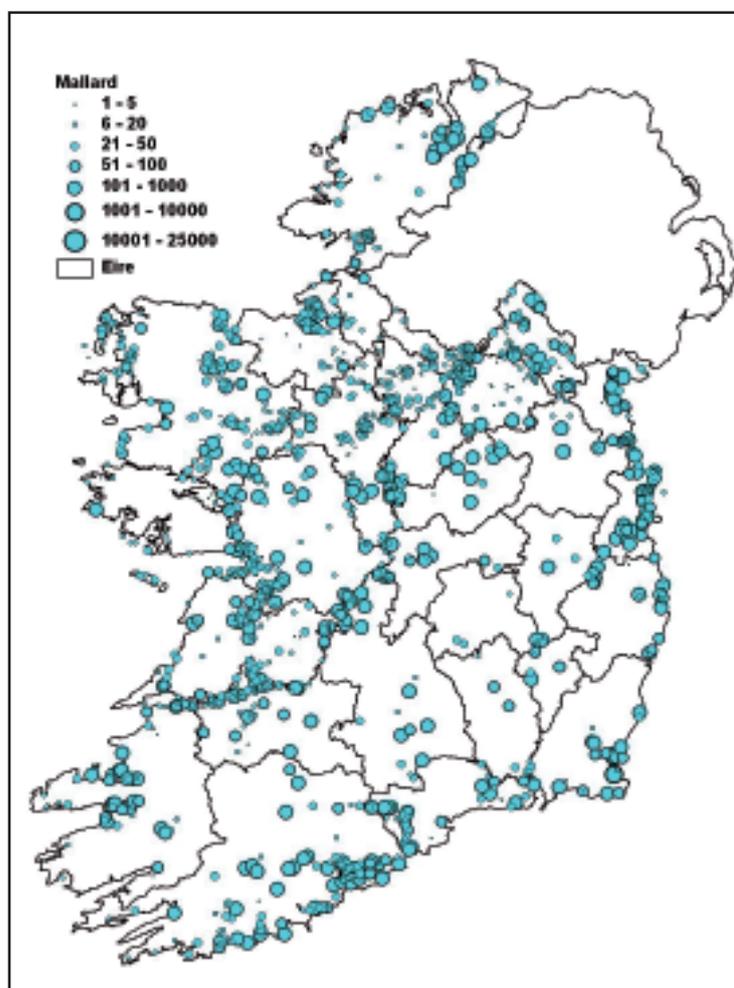


Figure 4. Distribution and abundance of Mallard (*Anas platyrhynchos*) in Ireland. These data were collected by BirdWatch Ireland during the Irish Wetland Bird Survey. The counts were conducted over the last 10 years, mainly from September to March. At each sampling site, the circle represents the maximum number of Mallard supported, based on the maximum number observed at each of the recording sites on a single occasion during the last 10 years



Figure 5. (Eurasian) Wigeon (*Anas penelope*).  
Photographer: Ronnie Martin



Figure 8. Mallard (*Anas platyrhynchos*).  
Photographer: John Carey



Figure 6. Gadwell (*Anas strepera*).  
Photographer: Eddie Dunne



Figure 9. (Northern) Pintail (*Anas acuta*).  
Photographer: Michael Finn



Figure 7. Teal (*Anas crecca*).  
Photographer: John Carey

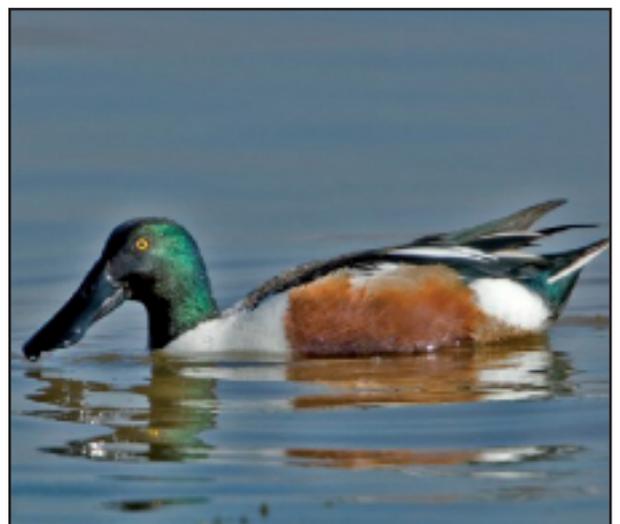


Figure 10. (Northern) Shoveler (*Anas clypeata*).  
Photographer: Ken Kinsella



Figure 11. Pochard (*Aythya ferina*).  
Photographer: Billy Clarke



Figure 14. Black-headed Gull (*Larus ridibundus*).  
Photographer: John Carey

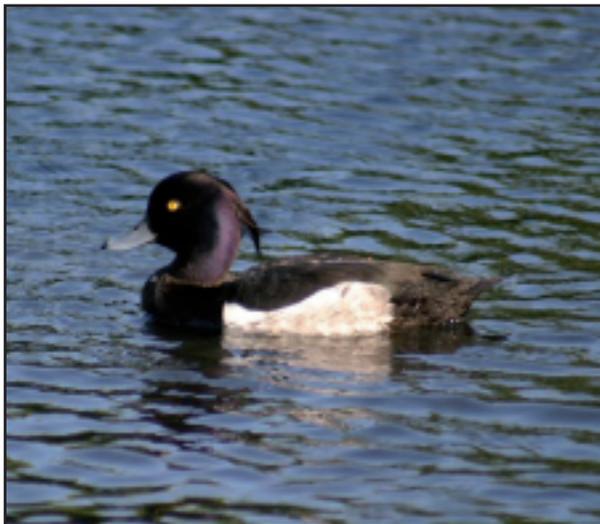


Figure 12. Tufted Duck (*Aythya fuligula*).  
Photographer: Ronnie Martin



Figure 15. Common Gull (*Larus canus*).  
Photographer: Billy Clarke



Figure 13. (Northern) Lapwing (*Vanellus vanellus*).  
Photographer: Billy Clarke

### 3.2 Within-winter movements

Many waterbird species are highly site-faithful, returning to the same wintering areas each year. While most species are entirely dependent on wetland habitat, others can be found considerable distances from wetland sites. Swans, geese, and some wader species are regularly seen feeding on grassland and/or stubble, and use wetland habitats only for roosting.

During the course of the winter, there is regular temporal and spatial movement of waterbird species. Along the coast, roosting and feeding is largely dictated by tide. Many swan and goose species feed by day, and often flight large distances (occasionally in excess of 20 km) to their wetland roosts at night. Many duck and wader species feed by night as well as by day. The roosting and feeding locations and patterns of movements of these waterbird species are less defined.

Large-scale movements of waterbirds between wetland sites have been directly related to weather conditions. There is a noticeable decline in some waterbirds during early autumn, particularly resident species such as Little Grebe, Cormorant and Mallard. It is

thought that this reflects a shift in range of these species as they begin to disperse from coastal sites to exploit small inland wetlands that are replenished by increasing rainfall levels. In contrast, during cold weather periods, when such small wetlands are more likely to become frozen over, there is reversal of this movement, as species are forced to move at times large distances to larger waterbodies, riverine sites or to coastal sites, all which are less likely to become frozen.

During particularly cold weather periods in Europe, a number of species from northern Europe, and even Britain, are known to move west into Ireland, with its milder climate. It is known that Lapwing and Golden Plover are particularly sensitive to such cold weather periods, when numbers in Ireland have been seen to increase dramatically. In extreme situations, Wigeon and Teal in Britain and Ireland move further south into France and Iberia. Here, it is known that there is some mixing with other populations breeding on the Black and Mediterranean Seas.

### 3.3 Waterbird species

Waterbirds are highly variable in size and shape, and have adopted a wide range of techniques that enable them to successfully exploit the variety of food types provided by wetland habitats. In general, wildfowl species feed by dabbling, sieving, diving (for example, to obtain benthic food items, or to prey on fish) and/or grazing, waders by probing or surface pecking, and gulls by surface pecking. Many species exhibit more than one method of feeding. For example, most dabbling ducks are also capable of diving, but do so for much shorter periods of time.

The wintering waterbirds can be divided into three main groups:

- *Wildfowl* include swans, geese and ducks, and are also often accompanied by their 'allies', the divers, grebes, rails, as well as Cormorant, Little Egret and Grey Heron.
- *Waders* include the long-legged wading birds that frequent intertidal flats and shallow water, especially along coastal sites. This group comprises Oystercatcher, plovers, lapwings, sandpipers, curlews, woodcocks.
- *Gulls* include the large family of seabirds that occupy a wide variety of wetland and non-wetland habitats. Some gull species have learned to co-exist successfully with man and have thrived in human habitats.

*Terns* are summer migrants, and mostly occur on passage during the autumn and spring months only, and very seldom are terns recorded during the mid-winter period.

Almost 140 waterbird species have been recorded during I-WeBS and WeBS. However, this total includes many vagrant species, which for a variety of reasons have strayed away from their usual flyways. More regularly, some 58 species occur in significant numbers at a variety of sites in Ireland, including 33 wildfowl, 20 wader and 5 gull species.

#### a. Dabbling and sieving wildfowl

##### *Distribution and feeding habits*

Dabbling is the preferred technique which has given a large group of duck species their collective name. Dabbling ducks in Ireland include Shelduck, Wigeon, Gadwall, Teal, Mallard, Pintail and Shoveler (see Figures 5-10). This technique is also employed by other species, particularly swans.

Dabbling species feed mostly on seeds or invertebrate prey present on the surface of the water. They access food at slightly greater depths by dipping their heads and necks below the water. The long necks of swans allow them to access deeper food items than the

ducks. These species can all extend their reach by up-ending into a vertical position, with their tails pointed in the air. Virtually all species which dabble feed by pecking at individual items. However, the dabbling ducks can also feed by sieving dense concentrations of smaller food, where they suck in water through a slightly open bill, and filter out the food items as the water is then expelled out at the sides.

With the exception of Shelduck, which is exclusively coastally distributed, most dabbling species occur on a variety of relatively shallow wetlands, both inland and coastal. Dabbling species are often recorded on the lee shore, where the wind has blown seeds and invertebrates into a relatively narrow band. Temporary flooded fields are particularly attractive, where abundant food items surface from the soil or pasture. Wigeon, Gadwall, Teal and Mallard in particular are regularly seen taking advantage of such food resources. They are widely distributed throughout the country.

##### *Social interactions*

Dabbling species are regularly recorded feeding together in large, and usually mixed, flocks, each species exploiting different feeding niches. Some species gain added benefit by feeding communally. Shoveler are often recorded feeding closely to the tail of the bird in front. The combined action of paddling feet is particularly effective in stirring up the water and increasing the amount of food brought to the surface. Wigeon regularly feed alongside swans and Coot, and parasitise them as they return to the surface with food. Gadwall have also been recorded feeding on aquatic plants brought to the surface by diving Coot and Goldeneye.

#### b. Grazing wildfowl

##### *Distribution and feeding habits*

Whooper and Bewick's Swans, Greenland White-fronted, Greylag, Barnacle and Light-bellied Brent Geese and Wigeon (Figure 5) are all grazing species. The swans and first two species of goose listed also feed on stubble. Light-bellied Brent Goose and Wigeon spend the autumn and early part of the winter grazing coastal vegetation (particularly *Zostera* spp. (eelgrass), *Enteromorpha* spp. and *Ulvae* sp. (green algae)), and move to feed on grasslands once these coastal supplies have become depleted. Most swans and Wigeon, tend to remain close to water at all times, while the remaining species listed above may be found considerable distances from wetlands. All of these species return to roost by night on wetlands.

Whooper Swan and Wigeon are the most widely distributed species of this group, found grazing next to wetlands in almost all counties. Greenland White-fronted Geese are largely concentrated in Wexford Harbour, in particular on the Slobs, though small numbers also occur at approximately 30 locations elsewhere in the country. The range of migratory (Icelandic) Greylag Geese is also quite restricted, and just six flocks are recognised in the Republic. However, the introduced population of this species is much more widespread, and small numbers occur throughout the country, and throughout the year. Barnacle and Light-bellied Brent Geese remain along the coast throughout the winter period. The former species is distributed mostly on the islands along the west and northwest coast of Ireland, where it feeds predominantly on grasslands. Light-bellied Brent Geese occur on estuaries along the east, south and southwest coasts, and increasingly use coastal grasslands as the winter progresses. Wigeon also feed on grassland, but are restricted to those adjoining wetlands, for security.

##### *Social interactions*

While these species tend to mix while in wetlands (as described in

'Dabbling species' above), the majority tend to assemble in single-species flocks while grazing. This is most likely due to differences in range, and also preferred feeding times during the day. However, mixed-species flocks do occur. For example, Wigeon and Light-bellied Brent Goose associate at some sites, though mostly when feeding on coastal vegetation. The diets of Light-bellied Brent Geese and Black-tailed Godwits (see 'Waders' below) are markedly different, though they are often seen feeding together.

### c. Diving wildfowl

#### *Distribution and feeding habits*

Diving species forage by diving in an area, and seek food either visually, or by touch. They feed on submerged aquatic vegetation, or on animal prey, particularly molluscs and crustaceans and/or fish. The list of diving species in Ireland is quite extensive, and includes the divers, grebes, Cormorant, Pochard, Tufted Duck, Scaup, Eider, Long-tailed Duck, Common Scoter, Goldeneye, and Red-breasted Merganser, Moorhen and Coot. Some of the species listed above are largely marine, and are seldom seen close to shore during the winter. These include the divers, Eider, Long-tailed Duck, Common Scoter and Red-breasted Merganser. All remaining species, with the exception of Scaup which occurs predominantly along the coast and on a few select inland sites, are widely distributed, especially on large deep wetlands; Great-crested Grebe, Little Grebe, Cormorant and Goldeneye are found on a variety of both inland and coastal wetlands, while Pochard, Tufted Duck and Coot are mostly distributed on inland waterbodies (Figures 11 and 12).

#### *Social interactions*

The marine species listed above are usually found in discrete groups, and seldom interact with other species present inshore, or on inland wetlands. Inland, Little Grebe, Pochard, Tufted Duck and/or Coot are regularly seen feeding together, despite their different feeding habits. Pochard and Coot are primarily vegetarian, while Little Grebes and Tufted Ducks prey on animal material. Tufted Ducks in particular also occasionally feed in shallow waters, often alongside dabbling ducks, particularly on spilt grain.

### d. Waders

#### *Distribution and feeding habits*

The majority of wader species wintering in Ireland are exclusively coastal throughout the winter period. Here, they prey largely on marine invertebrates present in sandy and muddy substrates of estuaries, open coast and along rocky shoreline.

A number of wader species, namely Oystercatcher, Golden Plover, Lapwing, Jack Snipe, Snipe, Woodcock, Black-tailed Godwit and Curlew, also forage on a variety of soil and surface-feeding invertebrates present in farmland. Oystercatchers and Black-tailed Godwits use mostly coastal grasslands, while Golden Plover, Lapwing, Jack Snipe, Snipe, Woodcock and Curlew are much more widely distributed on a variety of both coastal and inland sites. Both Golden Plover and Lapwing (Figure 13) are also known to forage on grassland sites at night, possibly to avoid Black-headed and Common Gulls (see below).

#### *Social interactions*

Waders are highly gregarious, and large numbers occur on coastal sites in Ireland. Inland, Lapwing and Golden Plover flocks often mix, and occasionally include other species, such as Black-headed Gull. Curlew are often also present, but in general tend to form more

discrete flocks. Jack Snipe, Snipe and Woodcock are skulking species, and are highly elusive, and are less likely to interact with the above species.

### e. Gulls

#### *Distribution and feeding habits*

Gull species occurring in Ireland are predominantly coastal. Most tend to feed at sea, on fish and on offal discarded from fishing trawlers. Some, such as Herring Gull, scavenge close to human habitation, particularly on rubbish tips. Black-headed and Common Gulls (Figures 14 and 15) also occur on a variety of coastal and inland farmland sites throughout the country, where they forage for earthworms and other soil invertebrates.

#### *Social interactions*

The feeding and roosting habits of most gull species wintering in Ireland are broadly similar, and large numbers regularly assemble, particularly on coastal sites throughout the Irish coastline. Additionally, Black-headed Gull and Common Gull occur, often together, on a variety of inland sites. Here, they are associated with wetlands, but also regularly occur on pasture. They are often recorded feeding alongside Golden Plover and Lapwing. Both gull species are known to parasitise Golden Plover and Lapwing.

## 4. CONCLUSION

Ireland is attractive to a wide variety of waterbirds, due to the variety and abundance of wetlands. Over one million waterbirds, comprising mostly migrants from arctic and boreal breeding areas, spend the winter in Ireland, congregating predominantly on wetland sites, and occurring alongside resident waterbirds, often in large mixed-species flocks. There is very substantial mixing of waterbird populations, in Ireland, throughout Europe and internationally. Throughout Ireland, there is interaction between different waterbird populations (breeding migrants, the wintering migrants and resident waterbird populations) and species. There is also a regular and complex pattern of movement between feeding and roosting areas, and between wetlands and farmland, which will each also increase the mixing of waterbird species and populations. These interactions are likely to facilitate the rapid transmission and spread of the H5N1 avian influenza virus, if it were present in Ireland.

## 5. REFERENCES

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## MODELLING THE DEMOGRAPHICS OF THE IRISH CATTLE POPULATION

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### ABSTRACT

In recent years, competent authorities have committed very substantial resources to the creation and maintenance of databases capable of recording important animal event data, such as births, deaths and movements. This has primarily been driven by the need to insure the quality and safety of animal products. However, it can also be used to assist policy makers in decision making. Despite the abundance of animal event data, as yet there is little published information about the use of these data to better understand the demography of cattle populations. This study reports the development of, and outputs from, a demographic model of the Irish cattle population. The demographic model was based on a series of life tables detailing age specific probabilities of survival up to a maximum of 17 years. These outputs were used to determine characteristics of the Irish cattle population, including estimated mortality rates, life expectancies and age profiles, and estimated cattle numbers by age and date. Separate life tables were developed for each of the 204 monthly birth cohorts born between January 1989 and December 2005. Within the Irish cattle population, the peak estimated mortality rate occurs at 29-33 months. The estimated life expectancy at birth of cattle in Ireland was 42 months. When the survival rates for all the cohorts within a population are calculated, then it is possible to use these rates as a model for determining future population size and answering cohort specific queries.

### 1. INTRODUCTION

In recent years, the competent authorities of both EU and non-EU states have committed very substantial resources to the creation and maintenance of databases capable of recording important animal event data, such as births, deaths and movements. The recent trend in data collection has been driven by the need to reassure consumers about the quality and safety of animal products and to ensure the origin and traceability of beef prompted by BSE concerns in the 1990s (for example, Golan et al., 2004, Scanga et al., 2007). Policy makers need access to key information to aid decision making with regard to animal health, animal welfare, resource allocation and planning (Baldock et al., 2003). However, despite the abundance of animal event data, as yet there is little published information about the use of these data to better understand the demography of cattle populations.

Actuarial life tables are a standard method used to calculate survivorship rates from cohorts with known birth and exit data (Chiang, 1984). These rates may then be used to estimate the survival experience of cohorts with unknown exit data. Cohort life tables provide a longitudinal perspective on the exit experience of a particular cohort from birth through consecutive ages until no further cohort members remain (Carey, 1993). If the survival rates for all the cohorts within a population are calculated, then it is possible to use these rates as a model for determining future population size and answering cohort specific queries. The cohort life table gives a comprehensive description of survivorship, and, as such, is fundamental to the study of populations (Chi and Yang, 2003). The theory and methodology of life tables is discussed in detail in ecology textbooks (e.g. Price 1984, Ricklefs and Miller 1999), although only survivorship is considered further here.

This study reports the development of, and outputs from, a demographic model of the Irish cattle population.

### 2. MATERIALS AND METHODS

#### 2.1 The data

##### 2.1.1 The Cattle Movement Monitoring System

The Cattle Movement Monitoring System (CMMS) is the traceability database for all Irish cattle with records on greater than 20 million cattle (Anon., 2003). The primary purpose of the CMMS database is to provide a comprehensive record of the origin, identity and life history of Irish cattle before they enter the food chain. Data are collated from farmers, marts, local authority abattoirs, meat export premises, live export licensed locations and knackery premises. For each animal, data are recorded about birth, movements and exit (death on-farm, slaughtered in Ireland, export). Birth data is complete from January 1996 onwards and exit data from January 2000 onwards. Data were extracted from CMMS using queries run on Microsoft SQL Server 2005 (Microsoft Corporation, Redmond, WA, USA) and downloaded to Microsoft Excel 2003 for further analysis.

##### 2.1.2 The Central Statistics Office livestock survey

In Ireland, a livestock survey is conducted twice yearly (June and December) by the Central Statistics Office (CSO) to provide estimates of the livestock numbers (Anon., undated). The December survey is conducted on 30,000 farms, and the results provide trends between the reference and preceding years, based on returns from the same matched sample of farms. We used the results from the December surveys in this study to estimate total annual birth numbers for the years when birth data were not recorded by the Department of Agriculture, Fisheries and Food (DAFF) (i.e. 1989 to 1996).

## 2.2 Model development

### 2.2.1 Overview

We developed a demographic model of the Irish cattle population based on a series of life tables (one for each monthly birth cohort), detailing age specific probabilities of survival up to a maximum of 17 years. These outputs were used to determine characteristics of the Irish cattle population, including estimated mortality rates, life expectancies and age profiles, and estimated cattle numbers by age and date (Figure 1).

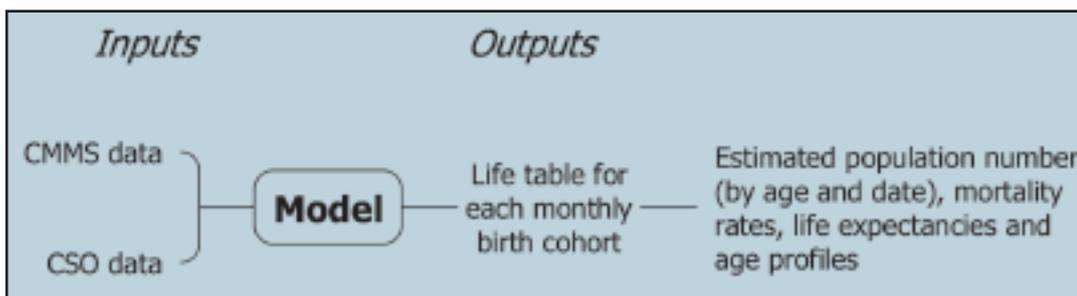


Figure 1. Inputs and outputs of the demographic model of the Irish cattle population

### Life table notation

Standard life table notation was used (Figure 2), as follows:

- $x$ , age (months);
- $l_x$ , number of cattle alive at age ( $x$ );
- $d_x$ , the number of cattle exiting between age ( $x$ ) and age ( $x+1$ );
- $q_x$ , the exit rate at age  $x$  [also, the probability of exiting between age ( $x$ ) and age ( $x+1$ )];
- $p_x$ , the probability of surviving to age ( $x+1$ ), given survival to age ( $x$ );
- ${}_0p_x$ , the probability of surviving from age (0) (that is, birth) to age ( $x$ );
- $q_x^*$ , the estimated proportion of cattle that exited at age  $x$  from those born in the cohort; and
- ${}_0q_x^*$ , the estimated proportion of cattle of any birth cohort exiting before age  $x$ .

### 2.2.2 Model calculations

Based on CMMS data availability (see Table 1), birth cohorts were managed as one of three cohort groups, as follows:

- Birth and exit data were available for all birth cohorts born from January 2000 to December 2005 (*Group A*);
- For all birth cohorts born between January 1996 and December 1999, birth data were available but exit data were only available for those animals exiting after December 1999 (*Group B*); and
- Neither birth nor exit data were available for birth cohorts born between January 1989 and December 1995 (*Group C*).

#### Group A monthly birth cohorts

As  $l_x$  and  $d_x$  were available,  $q_x$  and  $p_x$  could be calculated directly, using standard methods (Figure 2, Ebert, 1999):

$$q_x = \frac{d_x}{l_x} \tag{1}$$

$$p_x = 1 - q_x \tag{2}$$

#### Group B monthly birth cohorts

Within this group,  $q_x$  could not be calculated. Data were missing for both the numerator ( $d_x$  was only available for some animals) and denominator ( $l_x$  were not available, apart from  $l_0$ ).

For animals alive at (and following) 01 January 2000,  $d_x$  were available. For example, for animals in the January 1996 birth cohort,  $d_{48}$  was known, whereas  $l_{48}$  was not. Using exit data ( $d_x$ ) available from 01 January 2000, we calculated a surrogate statistic,  $q_x^*$ :

$$q_x^* = \frac{d_x}{l_0} \tag{3}$$

For animals that died prior to 01 January 2000,  $d_x$  was not available. Therefore,  $q_x$  was estimated indirectly, again using a surrogate statistic  $q_x^*$ , after calculating the mean exit rate of animals born in the same month from relevant Group A monthly birth cohorts. For example,  $q_0^*$  for animals in the January 1996 birth cohort was equal to the mean  $q_0^*$  for animals born in January 2000, January 2001, ..., January 2005.

These methods were used to calculate  $q_x^*$  for all animals in the Group B monthly birth cohorts. Therefore,  $q_{719}^*$  was available for those animals in the January 1996 birth cohort that survived to December 2005.

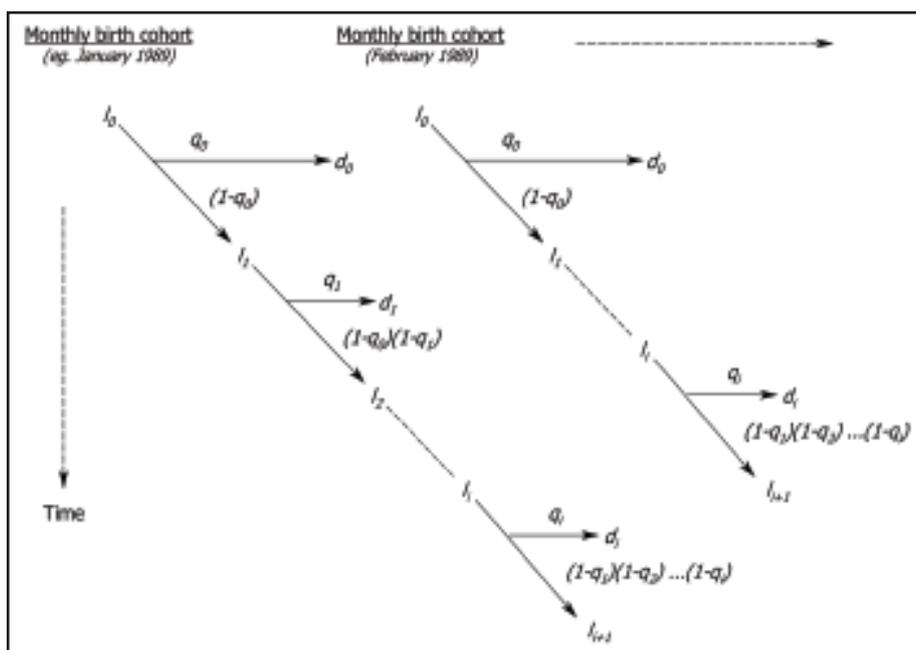


Figure 2. Standard life table notation, noting  $x$  is age (months),  $l_x$  is the number of cattle alive at age ( $x$ ),  $d_x$  is the number of cattle exiting between age ( $x$ ) and age ( $x+1$ ), and  $q_x$  is the exit rate at age  $x$

Table 1. Availability of birth and exit data from the Cattle Movement Monitoring System database for monthly birth cohorts within the Irish cattle population during 1989 to 2006

Group A monthly birth cohorts							
	2000	2001	2002	2003	2004	2005	
Births known <sup>a</sup>	+	+	+	+	+	+	
Exits known <sup>a</sup>	+	+	+	+	+	+	
a. Birth and exit data available on CMMS							
Group B monthly birth cohorts							
	1996	1997	1998	1999			
Births known <sup>b</sup>	+	+	+	+			
Exits known <sup>c</sup>	-	-	-	-			
b. Birth data available on CMMS c. Exits for cohorts born from 1996-2000 are not known, but exits for those cohorts are known from 2000 onwards, however it is not known how many survived up to that point							
Group C monthly birth cohorts							
	1989	1990	1991	1992	1993	1994	1995
Births known <sup>d</sup>	-	-	-	-	-	-	-
Exits known <sup>e</sup>	-	-	-	-	-	-	-
d. Birth data was estimated based on CSO data e. Exit data was estimated using exit rates from the Groups A and B monthly birth cohorts							

Then,  $q_x^*$  was converted to  $q_x$ , to enable standard life table methods. Firstly,  ${}_0q_x^*$  was calculated using the following formula:

$${}_0q_x^* = \sum_{n=0}^{n=x-1} q_n^* \tag{4}$$

For example,  ${}_0q_5^* = q_0^* + q_1^* + q_2^* + q_3^* + q_4^*$

${}_0p_x$  can be calculated as:

$${}_0p_x = 1 - {}_0q_x \tag{5}$$

And  $p_x$  and  $q_x$  as:

$$p_x = \frac{{}_0p_{x+1}}{{}_0p_x} \tag{6}$$

$$q_x = 1 - p_x \tag{7}$$

### Group C monthly birth cohorts

The CSO livestock surveys include annual estimates of cattle births. Similar estimates are available from the CMMS database during 1996 to 2005. During this period, the CSO estimates were less than the CMMS estimates by an average multiplicative discrepancy of 1.27 (Figure 3). Therefore, the total number of animals born each

year between 1989 and 1996 was estimated from the CSO livestock survey, using an inflation of 1.27. The total number of animals in each Group C monthly birth cohort was determined after calculating the mean percentage of cattle born in equivalent months during 1996 to 2005. For example, the size of the January 1990 birth cohort was calculated as the estimated number of animals born in 1990 multiplied by the mean January-born percentage (number of cattle born in January one year divided by the total number of cattle born in that year) during 1996 to 2005.

Exit data were not available from the CMMS database for cattle in the Group C month birth cohorts. Therefore, we made two assumptions to enable mortality rates to be calculated:

- The 15 year survival rate ( ${}_0p_{180}$ ) was 0.005; and
- Beyond 10 years, mortality rates increased exponentially.

Therefore, within the Group B monthly birth cohort  $q_{119}$  was estimated and  $q_{180}$  was assumed. The slope of the regression line for log mortality rate was calculated using:

$$Slope = \frac{y_2 - y_1}{x_2 - x_1} \tag{8}$$

where  $y$  is log mortality rate, and  $x$  is age (in months).

The log rates at each age were then calculated using:

$$\log(q_x) = \log(q_{119}) + (x - 119) * slope \tag{9}$$

$q_x$  could then be calculated for each age  $x$ . Through a process of trial and error, a value for  $q_{180}$  of 0.115 enabled us to create a life-table with  ${}_0p_{180} = 0.005$ . Using this life-table, we calculated the life expectancy of cattle during each month of life.

### 2.3 Model validation

The model was developed using data to 2005. Once 2006 data became available on CMMS, we compared the predicted and actual number of exits ( $d_x$ ) during 2006, and the actual rates of exit ( $q_x$ ) for 2006 compared to the average actual rates during 1996-2005 by age.

### 3. RESULTS

#### 3.1 Model outputs

We developed separate life tables for each of the 204 monthly birth cohorts born between January 1989 and December 2005. An extract of the life table for the September 1989 birth cohort, using a hypothetical initial population of 100,000 animals and an observation period of 195 months, is presented in Table 2.

Within the Irish cattle population, the peak estimated mortality rate occurs at 29-33 months (Figure 4). The estimated life expectancy at birth of cattle in Ireland was 42 months. Estimated life expectancy increases above 3 years of age, peaking at 46 months, and dropping to zero at 216 months of age (Figure 5). The age profile of the Irish cattle population on 31 December 2005 is presented in Figure 6. The estimated number of cattle present in the national herd on 31 December 2005, by age, is presented in Table 3.

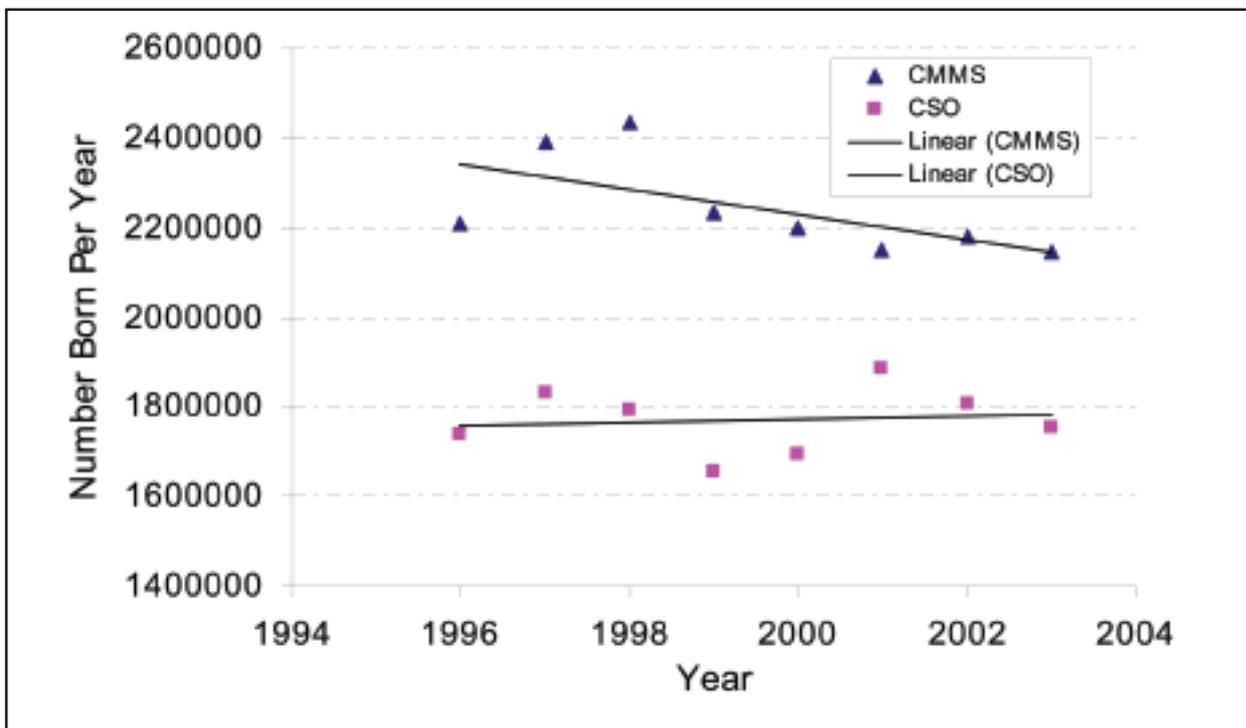


Figure 3. Number of cattle in Ireland during 1996 to 2003 with trend line, based on CMMS and CSO birth data

Table 2: Extract of the life table for the September 1989 birth cohort of the Irish cattle population, using a hypothetical initial population of 100,000 animals and an observation period of 195 months

Date	Exact age (months)	Of 100,000 cattle born		Probability that an animal reaching this age:			For an animal reaching this age, expected number of months of life remaining
		Number alive at exact age	Number dying during the following month	Lives another month	Exits within a month	Survives from birth to age X	
	$x$	$l_x$	$d_x$	$p_x$	$q_x$	$oP_x$	$e_x$
Sep 89	0	100,000	1,337	0.9866	0.0133	0.9856	41.83
Oct 89	1	98,663	1,133	0.9885	0.0114	0.9672	41.39
Nov 89	2	97,529	629	0.9935	0.0064	0.9594	40.86
-	-	-	-	-	-	-	-
Jul 90	10	93,665	823	0.9912	0.0087	0.9136	34.39
-	-	-	-	-	-	-	-
Mar 92	30	42,505	3,427	0.9193	0.0806	0.3644	3.3
Nov 93	50	21,750	346	0.9840	0.0158	0.1881	4.4
-	-	-	-	-	-	-	-
Jan 98	100	10,908	129	0.9881	0.0118	0.1186	2.6
-	-	-	-	-	-	-	-
Mar 02	150	2,186	121	0.9445	0.0554	0.0440	1.1
-	-	-	-	-	-	-	-
Jul 05	190	41	6	0.8483	0.1516	0.000	5.3
Dec 05	195	17	3	0.8280	0.1719	0.000	4.7

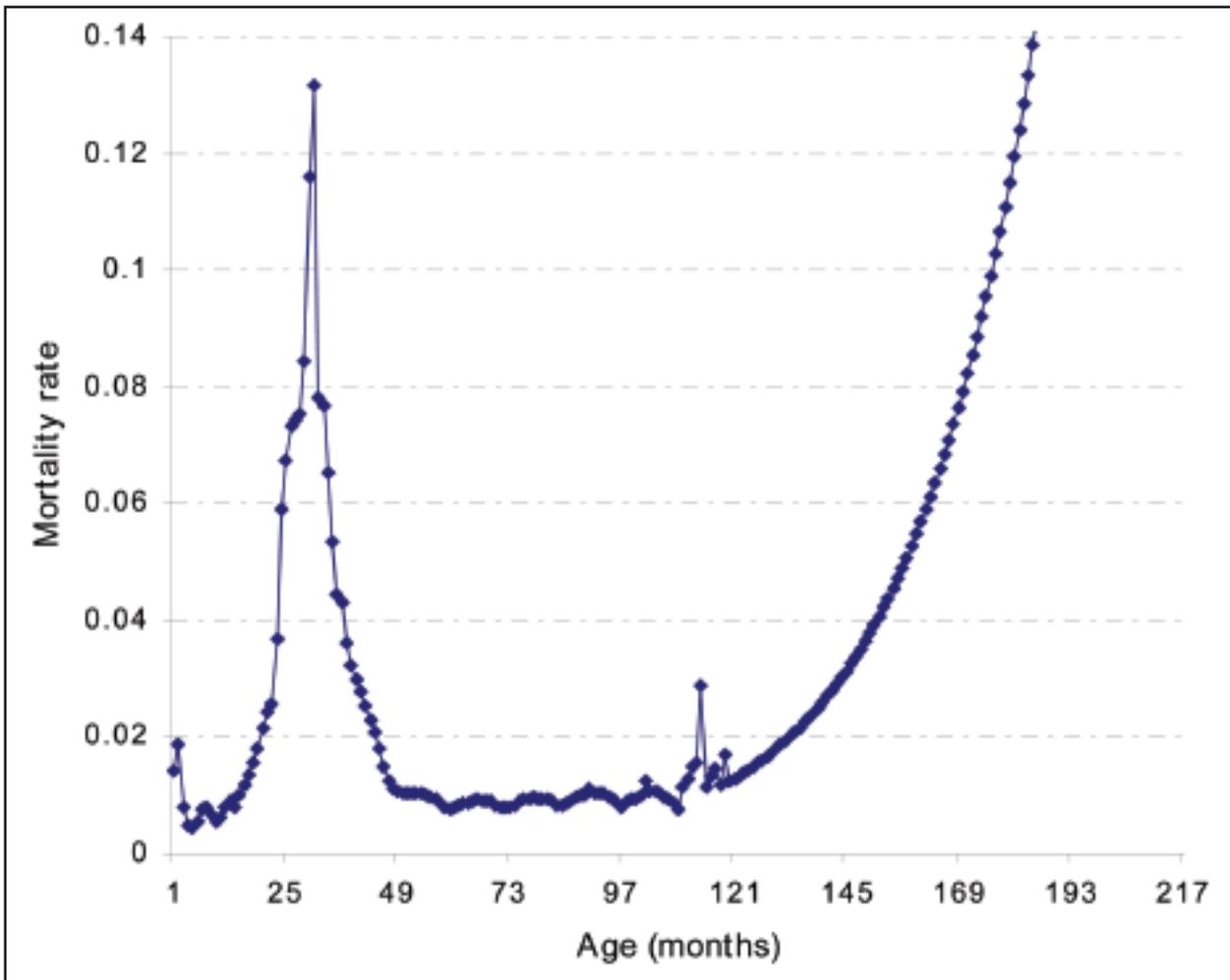


Figure 4. The estimated mortality rate of the Irish cattle population, by age

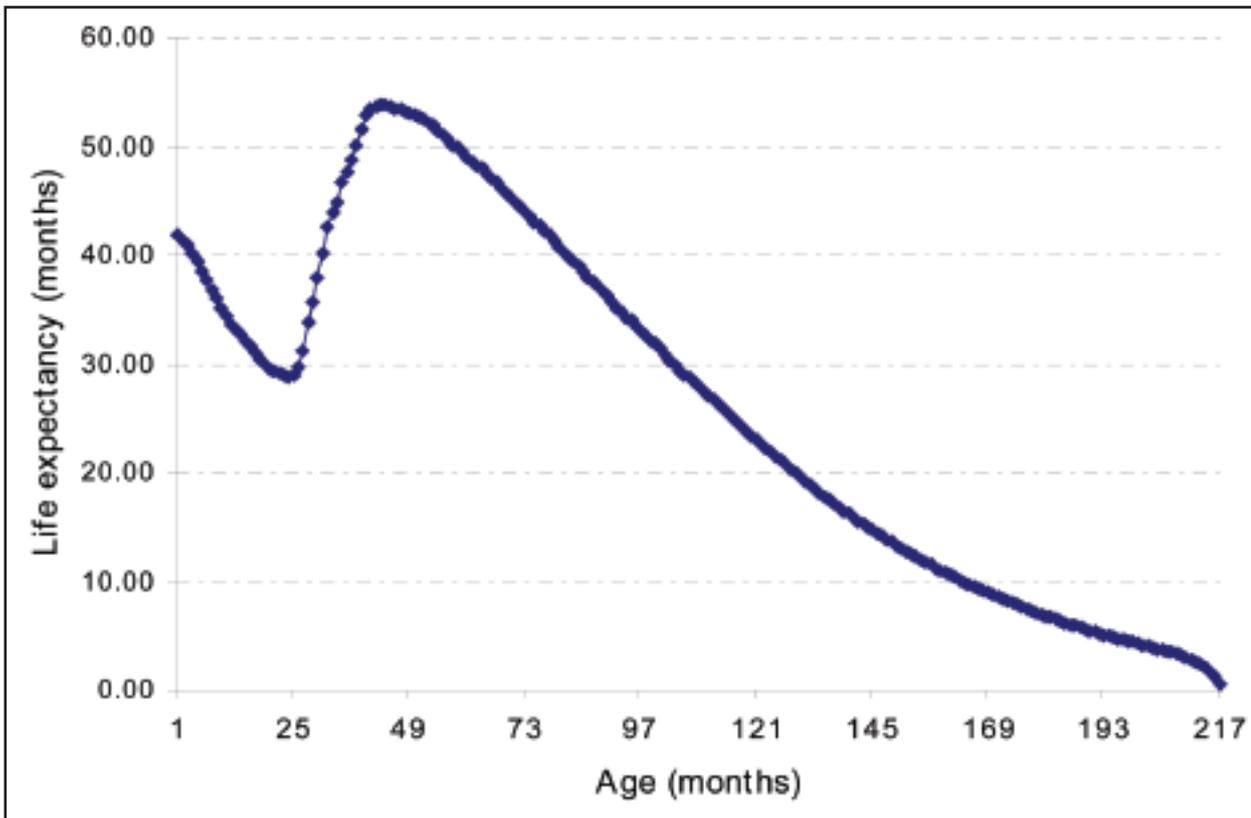


Figure 5. The estimated life expectancy of the Irish cattle population, by age

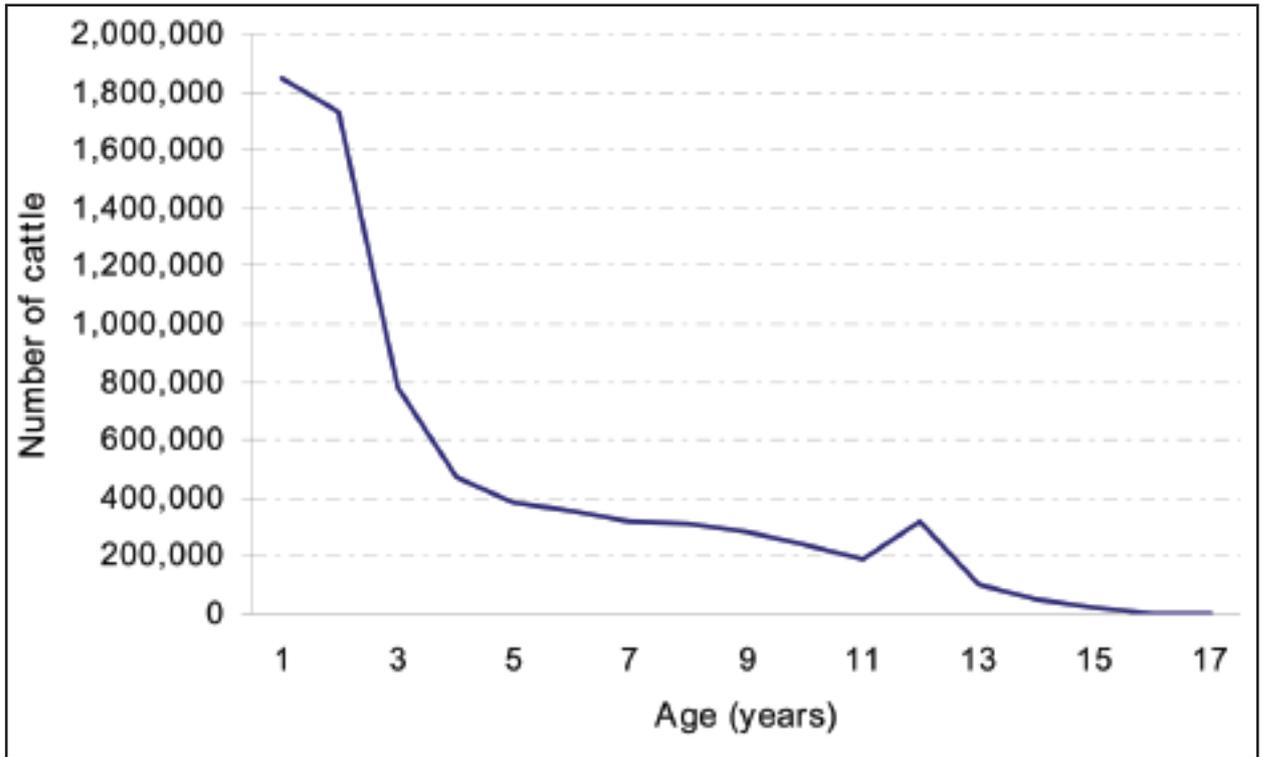


Figure 6. Estimated age profile of the Irish cattle population on 31 December 2005

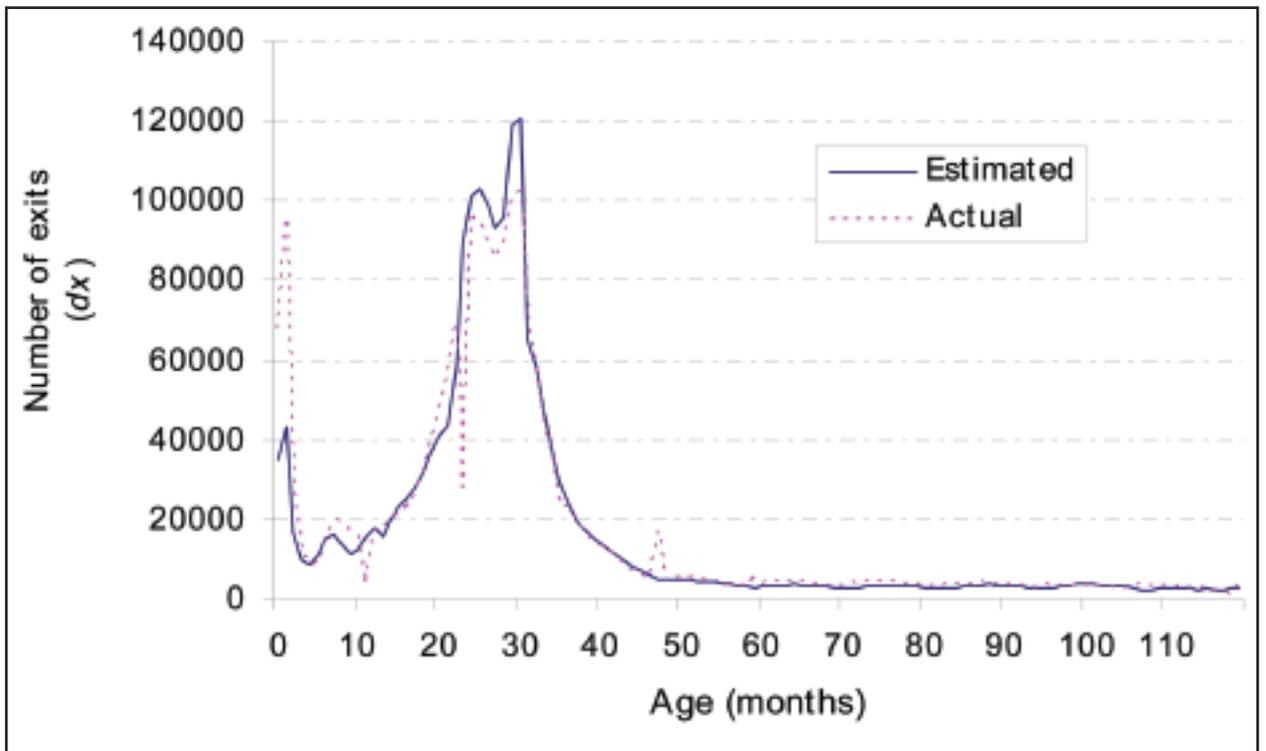


Figure 7. Comparison of predicted and actual number of exits ( $d_x$ ) during 2006, by age

### 3.2 Model validation

The predicted and actual number of age-related exits ( $d_x$ ) during 2006 (Figure 7), and the age-related exit rates ( $q_x$ ) during 2006 in comparison to the average rates during 1996-2005 (Figure 8), were similar, apart from the initial weeks of life.

Table 3. Estimated size of the Irish cattle population on 31 December 2005, by age group

Age group (years)	Number of cattle
0-1	1,847,588
1-2	1,733,015
2-3	780,268
3-4	469,499
4-5	383,468
5-6	356,709
6-7	319,562
7-8	313,010
8-9	283,761
9-10	241,004
10-11	190,127
11-12	319,562
12-13	100,844
13-14	52,275
14-15	18,938
15-16	3,442
16-17	228
Total	7,238,584

### 4. DISCUSSION

Life table methodology is widely used in ecological population studies such as primates (Bronikowski 2002) and pets (Nasser 1991). This model is the first published account of similar methodology to determine aspects of the demography of a national cattle population. Using this model, it has been possible to estimate a range of potentially valuable demographic measures about the Irish cattle population, including mortality rates, life expectancies and age profiles, and estimated cattle numbers by age and date.

As expected, the estimated peak mortality rates are in synchrony with the optimal age for the harvesting of beef (Figure 4). Animals between 3 and 5 years of age have an increased life expectancy, in comparison to younger cattle, reflecting the high mortality rate among those younger animals that are destined for slaughter (rather than breeding) (Figure 5). In Ireland, meat producing animals are generally culled between 2 and 3 years of age. A further, much smaller, mortality peak occurs at approximately 110 months (Figure 4), which is probably coincident with the end-of production cow cull in both dairy and beef animals. The model suggests that there are few animals greater than 18 years of age in the national herd. While only a small number of individuals may live to this age or above, it is most likely that the survival rate is effectively zero sooner than this.

This study highlights the difficulties that can arise, in the absence of formal centralised data collection systems, when seeking to answer apparently simple demographical questions. For example, complete data were available which enabled us to rapidly determine the age profile of Group A birth cohorts up to 72 months of age. However, data beyond this age were not complete. Further, among the Group C birth cohorts, neither birth nor exit data were available. In these circumstances, demographic information could only be estimated following the completion of a series of relatively complex tasks. When competent authorities have appropriate data

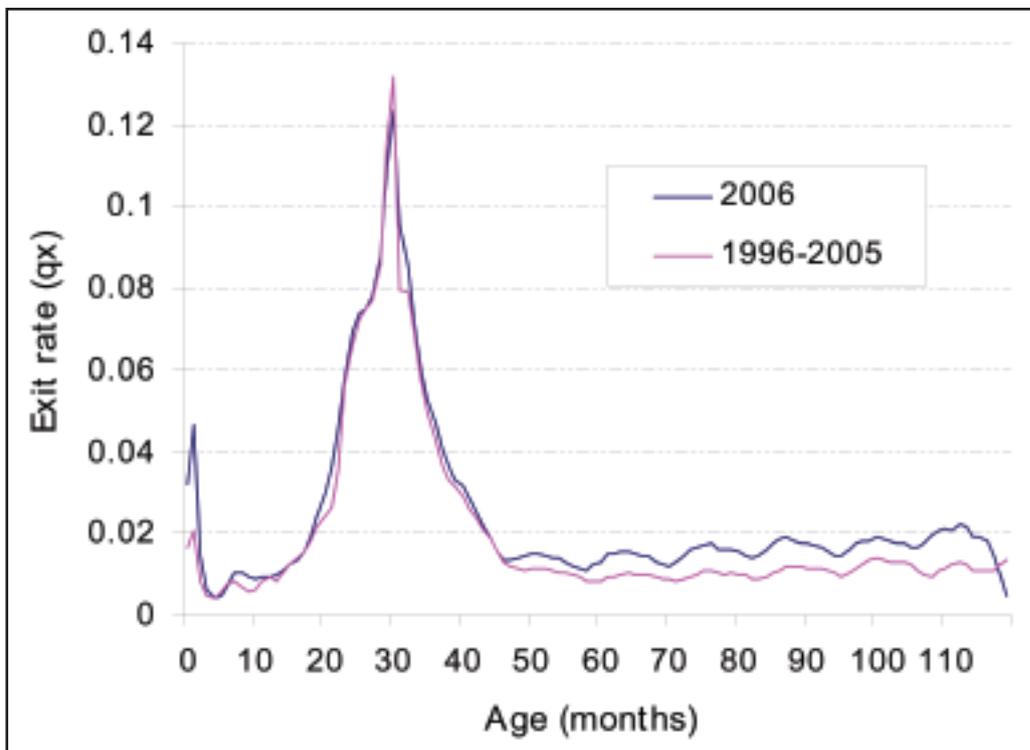


Figure 8. Comparison of actual rates of exit ( $q_x$ ) from the Irish cattle population for 2006 with the average rates recorded during 1996-2005, by age

capture systems in place, it is possible to rapidly generate a range of potentially useful demographic information, for use in the face of animal disease emergencies, such as FMD, and to help decision makers in formulating policy formulation.

A number of assumptions were made during model development. Firstly, it was assumed that the exit rates from the Group A monthly birth cohorts were applicable to the monthly birth cohorts in Groups B and C. This presupposes no major temporal change in the pattern of exits from the cattle population from pre-existing Groups B and C to Group A. However, cattle exits are strongly influenced by the economic environment such as changes in markets for beef or live exports. There have also been government schemes, such as the purchase for destruction scheme, which may have altered the exit rates during this time. However, this assumption is only of concern with regard to historical data, as in the future, exit rates will be based on real exit data without underlying assumptions. As future data becomes available, the accuracy of exit rates will improve. The reform of the Common Agricultural Policy and the related Single Farm Payment, it is postulated, will have significant effects on exit rates in the future as the agricultural environment is altered (Anon., 2007). Secondly, it is assumed that the relationship between the CSO and CMMS birth figures, as established between 1996 and 2003, are accurately applicable to Group C cohorts. The animal birth data from CSO was consistently less than that from the CMMS. CSO data is based on a sample of farms, reflecting the accuracy of data supplied by participating farmers. Further, the CSO data reflect the number of animals, less than 1 year of age, present on surveyed farms at the start of each December. Unlike the CSO data, the CMMS data (which records all births) takes account of animals born during a particular year, but have died or otherwise exited prior to December. Thirdly, it is assumed that the survival rate to 180 months is 0.005. This is a conservative estimate. It is also assumed that mortality rates beyond age 120 months have an exponential rate of mortality. A similar approach is used in human demographic studies, providing a mathematical explanation for the aging process, which eventually leads to death (Lee and Ryan, 2001). At ages greater than 180 m, it is very unlikely that animals were exported or slaughtered for beef.

Substantial data are available about the Irish cattle population, including detailed records to enable individual animals to be traced from birth to exit. Using these data, this model provides demographic information to assist national policy-makers. Although the current study has focused on the overall cattle population, specific questions about individual cohorts stratified by sex or breed could be addressed in the future. An analysis of exits is particularly pertinent to national culling decisions, noting that the accurate information is needed when considering alternative culling strategies (for example, in relation to bovine spongiform encephalopathy). Scenario analysis can be performed to plan for future population changes especially with the predicted decline in cattle numbers that may follow recent changes in the Common Agricultural Policy, such as the Single Farm Payment Scheme (Anon., 2004). This modelling approach could be duplicated for other species and in other settings, if suitable raw data were available.

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## TRENDS IN THE IRISH COW POPULATION AND THE RATE AT WHICH THEY WERE CULLED DURING 2003 TO 2006

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### ABSTRACT

Cows are the main economic production units of Ireland's cattle industry. Therefore, demographic information, including overall numbers and survival rates, are relevant to the Irish agricultural industry. However, few data are available on the demographics of cows within a national population, either in Ireland or elsewhere, despite the recent development of comprehensive national cattle databases in many EU Member States. This study has sought to determine the rate of cow culling from the national herd; to determine the rate of culling by type (dairy, beef), age, method of exit, date of exit and interval between last calving and exit; to calculate the national cow on-farm mortality rate; and to compare the Irish rates with published data from other countries. This work was conducted using data recorded in the national Cattle Movement Monitoring System (CMMS). Culling refers to the exit of cows from the national herd, as a result of death but regardless of reason, and cow-culling rate was calculated as the number of cow exits (as defined above) each year divided by the number of calf births in the same year. Culling rate was determined by type (dairy or beef), date of birth, method of exit (slaughter or on-farm death), month of exit, and interval between last calving and exit. The average cow-culling rate during 2003 to 2006 was 19.6% (21.3% for dairy, 18% for beef). While comparisons must be treated with caution, it concluded that the overall rates of culling in Ireland fell within published internationally accepted norms. The on-farm mortality rate of 3.2-4.1% was similar to that reported in comparable studies.

### 1. INTRODUCTION

Cows are the main economic production units of Ireland's cattle industry. Therefore, demographic information, including overall numbers and survival rates, are relevant to the Irish agricultural industry. However, few data are available on the demographics of cows within a national population, either in Ireland or elsewhere, despite the recent development of comprehensive national cattle databases in many EU Member States. Previous studies of culling in Ireland have focused on small numbers of animals in well-managed herds with good on-farm records. Studies by Crosse and O'Donovan (1998) and Crosse *et al.* (undated) were directed more at the 'reasons' for culling in well managed dairy herds. A similar approach has generally been described in published studies from other countries.

The policy environment throughout the European Union may affect culling decisions. In 2003, reforms to the Common Agricultural Policy (CAP) led to the introduction of direct payments and the principle of decoupled support (Anon., 2003). Decoupled payments are typically based on the historical use of an input like land so benefits are capitalized into the value of the asset, benefiting the owner of the land and in Ireland the vast majority of 'owners' are the actual farmers of the land. It is widely anticipated that decoupling will decrease cattle numbers over time.

The national movement database (the Cattle Movement Monitoring System, CMMS), proves an opportunity to investigate the demographics of cows within the national herd. Summary information from this database have been prepared annually (CMMS 2003, 2004, 2005 and 2006), including figures for slaughtering and on-farm deaths. However, to this point, these relate to the full population but not separately for cows. Using CMMS, this study has sought to determine the rate of cow culling from the national herd; to determine the rate of culling by type (dairy, beef), age, method of exit, date of exit and interval between last calving and exit; to calculate the national cow on-farm mortality rate; and to compare the Irish rates with published data from other countries. In addition, this study provides the basis for preliminary assessment of the impact of CAP reforms on cow numbers in Ireland.

### 2. MATERIALS AND METHODS

#### 2.1 The national database

In response to the BSE crisis during the 1990s, the European Commission legislated for the establishment of a National Movement Database by means of Council Regulation (EC) 820/97 (Anon., 1997), which was in turn replaced by Regulation (EC) 1760/2000 (Anon., 2000). The Department of Agriculture, Fisheries and Food (DAFF) over a 3-year period introduced a comprehensive system of movement notifications, which included the recording on the database of all bovine births, imports, movements, slaughtering, exports and deaths. As required under the Regulation, the database was fully operational by 01 January 2000. Data is collected from a variety of sources including keepers, marts, abattoirs, export locations and knackeries and only data that has fulfilled relevant validation criteria is accepted onto the CMMS database.

Bovine population activity and trading patterns varied over the four years of this study and during this time the CMMS database recorded, approximately, the following transactions annually:

- i) 1.7 million movements to slaughter at 45 export approved abattoirs;
- ii) 90,000 movements to slaughter at 400 Local Authority abattoirs;
- iii) 220,000 on-farm deaths, the vast majority of which had their carcasses collected and disposed of in approximately 30 category 2 intermediate plants (knackeries);
- iv) 1.6 million movements through 100 marts (cattle markets);
- v) 180,000 animals exported through 3 ports and 15 assembly centres;
- vi) 800,000 direct farm-to-farm movements, between 125,000 registered holdings and keepers; and
- vii) 2.2 million calf birth registrations, with data collected on date of birth, breed, sex, birth holding, breed of sire and dam and tag number of dam. The dam is only eligible if recorded as a cow that was present on the birthing holding on the relevant date of birth.

In addition, prior to de-coupling, the database also recorded all

premiums paid to farmers and in respect of individual animals.

### 2.2 Data extraction

This work was conducted using the annual CMMS extracts, compiled by DAFF's Information Systems Division shortly after each year-end, that were used as the basis of the CMMS Annual Statistics Report for 2003, 2004, 2005 and 2006 (DAFF, 2003-2006). Each extract included records of all movements to slaughter at export-approved abattoirs (i. in the above-mentioned list), all movements to slaughter at Local Authority abattoirs (ii) and knacker collection and disposal of on-farm deaths (iii.). Subsequently, we only retained those records that related to cows. In this study, a cow was defined as a female animal to which at least one calf had been registered; therefore, eligible records were identified after determining the 'last calving date', if present. In each yearly extract, heifers (a subset of cows) were identified based on the date of first recorded calving.

### 2.3 Data analysis

In this study, culling refers to the exit of cows from the national herd, as a result of death but regardless of reason. Therefore, culling encompasses slaughter (whatever the reason, including disease control) and on-farm death, but not disposal of surplus stock from an individual herd, by export or otherwise, where the removed animal continued to give further production and/or economic return for a new keeper. The cow culling rate was calculated as the number of cow exits (as defined above) each year divided by the number of calf births in the same year. The cow mortality rate was calculated as the number of on-farm deaths each year divided by the number of births in the same year. In each case, the number of births was used as a proxy for the number of 'productive' cows. Further, each numerator was calculated from the extracted CMMS datafiles, and each denominator from the relevant published CMMS Annual Statistics report. Further, data from these reports was used to determine the number of cattle in the national herd.

Data management and extraction was conducted using FoxPro® Database (Microsoft Corporation, Redmond, WA, USA), and data analysis using Microsoft Excel® (Microsoft Corporation, Redmond, WA, USA). Culling rate was determined by type (dairy or beef; see Table 1), date of birth (not recorded prior to 1996), method of exit (slaughter or on-farm death), month of exit, and interval between last calving and exit.

Table 1. Animal type (dairy, beef), by breed (code, percentage based on Irish cow population in 2005<sup>a</sup>) as recorded in the Irish Cattle Movement Monitoring System (CMMS) database

Dairy breeds (48.2%), any animal recorded on the database as one of the following breeds:	Beef breeds (50.4%), any other breeds including:
FR (Friesian/Holstein)- 47.1%	AA (Angus) – 6.3 %
AY (Ayrshire)	BB (Belgian Blue) – 2.6 %
BS (Brown Swiss)	CH (Charolais) – 12.1 %
RD (Danish Red)	HE (Herford) – 7.7 %
GU (Guernsey)	LM (Limousin) – 12.1 %
JE (Jersey)	SI (Simmental) – 7.8 %
KE (Kerry)	SH (Shorthorn) – 1.8 % <sup>b</sup>
MO (Montbelliarde) – 1.1 %	SA (Salers)
MY (MRI/MRY) Meuse Rhine (Y) Issel	SD (South Devon)
NO (Normande)	
NR (Norwegian)	
SR (Swedish Red)	
<p>a. Breed percentages are presented for 98.6% of the 2005 cow population. The shortfall (1.4%) includes all other breeds (that is, those without a supplied percentage)</p> <p>b. Although some Shorthorn cows may be milked in dairies, in this study all were regarded as beef animals</p>	

## 3. RESULTS

### 3.1 The national herd

The number of cattle in the national herd at year's end remained relatively constant during 2003 to 2006 (Table 2). Cattle numbers in 2006 were noticeably lower than in earlier years (Figure 2). During this period, there was substantial, but relatively consistent, within-year fluctuation, from a low of approximately 6.5 million at the end of each year to a high of approximately 7.1 million at the end of May following the spring calving season (Figure 1). The number of calf birth registrations was relatively constant during 2003 to 2006, both for dairy and beef breeds (Table 3).

Table 2. The total number of animals in the Irish cattle population at the end of years 2003 to 2006, as reported previously (CMMS, 2003, 2004, 2005, 2006)

	End of year:				
	2003	2004	2005	2006	Average
Total number of cattle	6,589,974	6,501,788	6,532,706	6,321,823	6,486,573

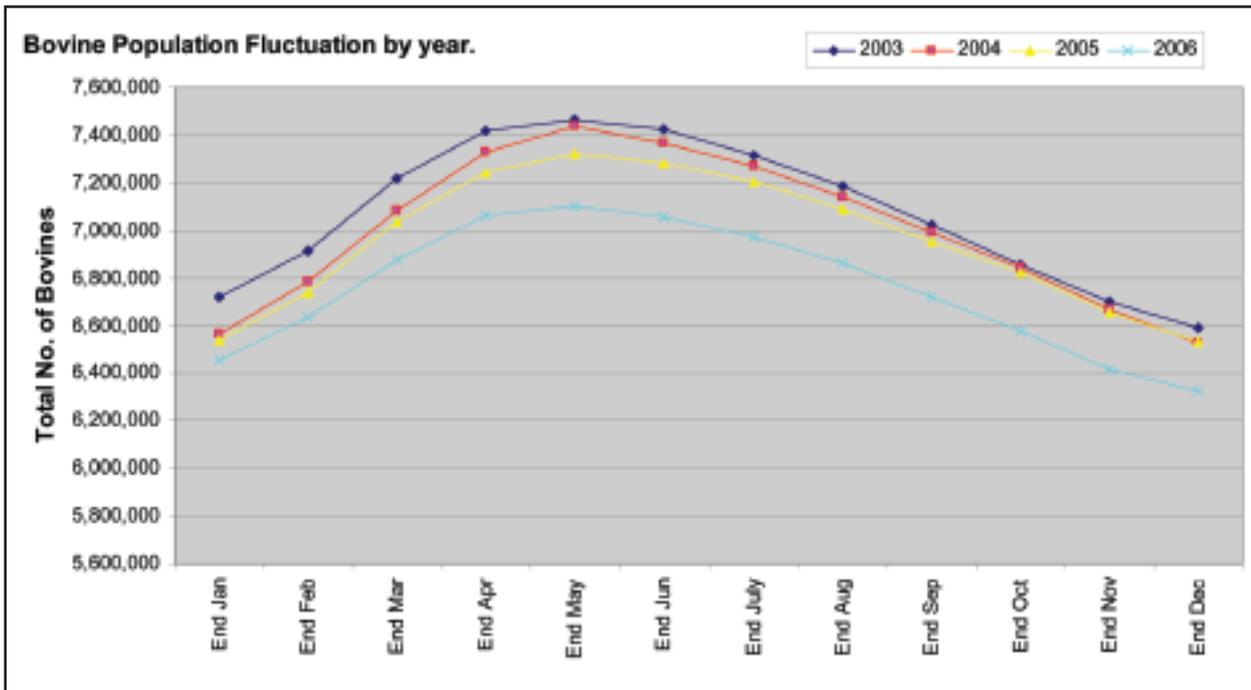


Figure 1. Annual fluctuations in the total number of cattle in the Irish national cattle herd, by year, between 2003 and 2006

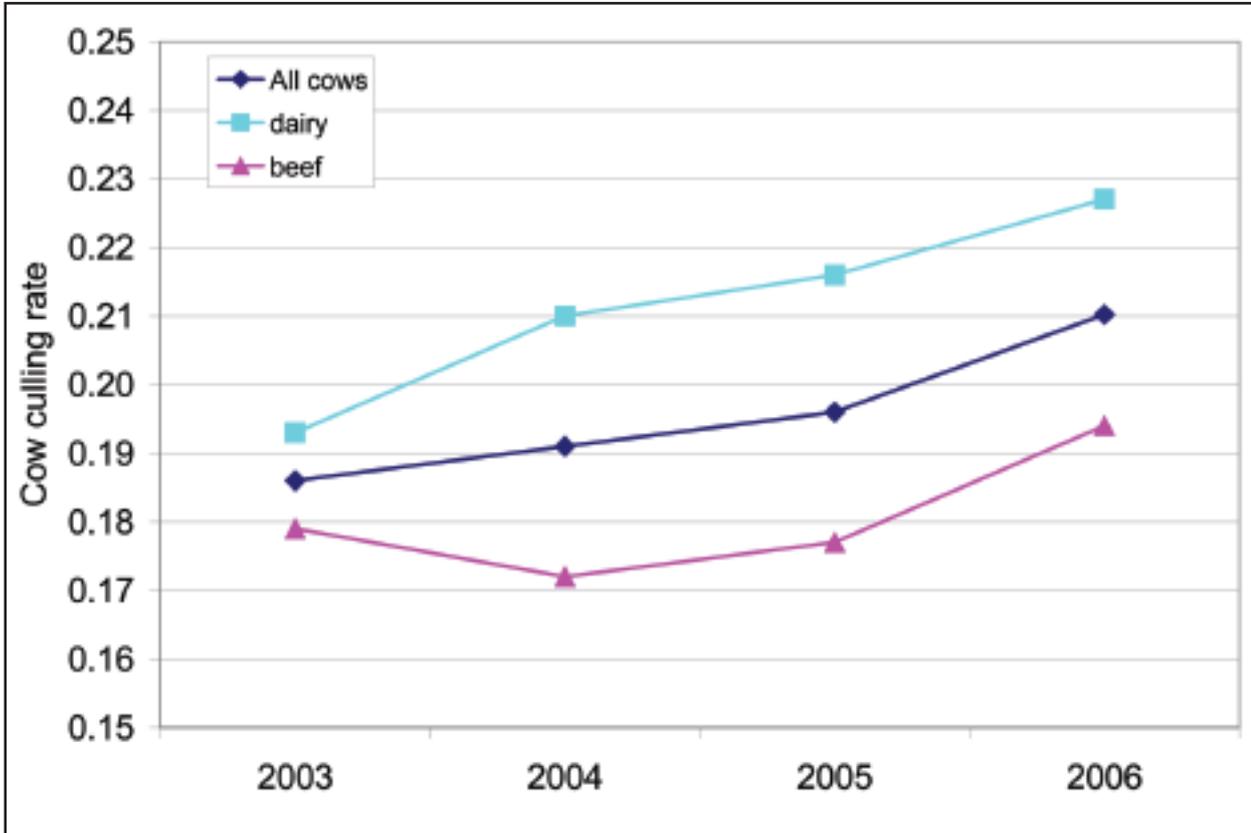


Figure 2. Changes in the cow-culling rate in the national Irish cattle herd, by year and type, during 2003 to 2006

### 3.2 Cows culled

The recorded number of calves entering (by year, type and age of cull-cow replacement), and cows exiting (by year, type and method of exit) the national Irish cattle herd, during 2003 to 2006 is presented in Table 3. The overall culling rate, by year and type, is presented in Figure 2. There was an increase in the recorded number of calf birth registrations in 2004 compared with 2003, both for dairy and beef (Table 3). During 2005 and 2006, there was also an increase in the recorded number of cows culled, both for dairy and beef, but a drop in the number of calves registered, particularly in dairy (Table 3). The cow culling rate was higher in dairy than beef, and the ratio of the culling rates for dairy to beef increasing progressively over time (Table 3).

The age at which cows were culled, by year, by type and by method of exit, during 2003 to 2006 is presented in Table 4. Table 5 provides details of the interval from the last recorded calving date to culling by year, by type and by means of exit thus giving information as to when during the subsequent lactation and during the productive cycle of the cow she was culled. Table 6 shows the numbers of cows culled by year, by calendar month and by means of exit.

Table 3. Recorded number of calves entering (by year, type and dam age), and cows exiting (by year, type and method of exit) the national Irish cattle herd, during 2003 to 2006

	2003	2004	2005	2006
<b>1. Recorded calf entries</b>				
<b>1a. All dams</b>				
Dairy	1,064,861	1,066,342	1,049,014	1,038,520
Beef	1,079,819	1,104,834	1,101,051	1,092,742
Total	2,144,680	2,171,176	2,150,065	2,131,262
<b>1b. Heifer dams only</b>				
Dairy	220,114	223,974	235,477	235,395
(Average dam calving age [months])	[29.3]	[28.8]	[28.6]	[28.8]
Beef	187,167	190,517	187,504	190,528
(Average dam calving age [months])	[31.3]	[31.2]	[31]	[31]
Total	407,281	414,491	422,981	425,923
(Average dam calving age [months])	[30.2]	[29.9]	[29.7]	[29.8]
<b>2. Recorded cow exits</b>				
<b>2a. Slaughter</b>				
Dairy	170,216	189,150	189,020	192,653
(%)	(16.0%)	(17.7%)	(18.0%)	(18.6%)
Beef	158,946	154,922	157,281	170,522
(%)	(14.7%)	(14.0%)	(14.3%)	(15.6%)
Total	329,162	344,072	346,301	363,175
(%)	(15.3%)	(15.8%)	(16.1%)	(17.0%)
<b>2b. On-farm deaths</b>				
Dairy	34,949	36,676	40,092	45,548
(%)	(3.3%)	(3.4%)	(3.8%)	(4.4%)
Beef	34,342	33,684	36,234	40,973
(%)	(3.2%)	(3.0%)	(3.3%)	(3.7%)
Total	69,291	70,360	76,326	86,521
(On-farm mortality rate, %)	(3.2%)	(3.2%)	(3.5%)	(4.1%)
<b>2c. Slaughter and on-farm deaths</b>				
Dairy	205,165	225,826	229,112	238,201
(Cow culling rate, %)	(19.3%)	(21.2%)	(21.8%)	(22.9%)
[Difference between cow exits and heifer entries]	14,949	-1,852	6,365	-2,806
Beef	193,288	188,606	193,515	211,495
(Cow culling rate, %)	(17.9%)	(17.1%)	(17.6%)	(19.4%)
[Difference between total cow exits and heifer entries]	-6,121	1,911	-6,011	-20,967
Total	398,453	414,432	422,627	449,696
(Cow culling rate, %)	(18.6%)	(19.1%)	(19.7%)	(21.1%)
[Difference between total cow exits and heifer entries]	8,828	59	354	-23,773

Table 4. The number (percentage) of cows culled, by year, by age, by type and by means of exit (either slaughter or on-farm death [O.F.D.])

Years	< 3Yrs	3-4 Yrs	4-5 Yrs	5-6 Yrs	6-7 Yrs	> 7 Yrs	Total			
2003										
Beef O.F.D.	1,855	2,942	2,765	2,677	2,341	21,762	34,342			
Beef Slaughter.	7,768	13,730	14,381	12,717	11,657	98,693	158,946			
Dairy O.F.D.	2,780	3,393	3,324	3,588	3,666	18,198	34,949			
Dairy Slaughter.	6,416	13,158	15,691	18,468	18,723	97,760	170,216			
O.F.D. Total	4,635	6,335	6,089	6,265	6,007	39,960	69,291			
Slaughter Total	14,184	26,888	30,072	31,185	30,380	196,453	329,162			
Years	< 3Yrs	3-4 Yrs	4-5 Yrs	5-6 Yrs	6-7 Yrs	7-8 Yrs	>8 Yrs	Total		
2004										
Beef O.F.D.	1,829	2,824	2,640	2,834	2,796	2,536	18,225	33,684		
Beef Slaughter.	6,379	12,330	13,644	12,831	11,848	11,378	86,512	154,922		
Dairy O.F.D.	3,082	4,033	3,464	3,515	3,911	3,618	15,053	36,676		
Dairy Slaughter.	6,570	15,248	17,710	18,810	20,622	20,870	89,320	189,150		
O.F.D. Total	4,911	6,857	6,104	6,349	6,707	6,154	33,278	70,360		
Slaughter Total	12,949	27,578	31,354	31,641	32,470	32,248	175,832	344,072		
Years	< 3Yrs	3-4 Yrs	4-5 Yrs	5-6 Yrs	6-7 Yrs	7-8 Yrs	8-9 Yrs	>9 Yrs	Total	
2005										
Beef O.F.D.	2,105	2,896	2,899	2,879	3,086	3,216	2,952	16,201	36,234	
Beef Slaughter.	5,713	10,972	13,396	13,642	13,176	12,746	12,275	75,361	157,281	
Dairy O.F.D.	3,437	4,228	4,176	3,724	3,740	4,149	3,896	12,742	40,092	
Dairy Slaughter.	6,054	15,336	19,426	19,334	20,020	20,802	20,479	67,569	189,020	
O.F.D. Total	5,542	7,124	7,075	6,603	6,826	7,365	6,848	28,943	76,326	
Slaughter Total	11,767	26,308	32,822	32,976	33,196	33,548	32,754	142,930	346,301	
Years	< 3Yrs	3-4 Yrs	4-5 Yrs	5-6 Yrs	6-7 Yrs	7-8 Yrs	8-9 Yrs	9-10 Yrs	>10 Yrs	Total
2006										
Beef O.F.D.	2,332	3,132	3,074	3,037	3,405	3,568	3,456	3,076	15,893	40,973
Beef Slaughter.	7,286	12,752	14,443	14,097	14,359	13,923	13,719	12,677	67,266	170,522
Dairy O.F.D.	4,022	5,271	4,784	4,653	4,307	4,155	4,067	3,671	10,618	45,548
Dairy Slaughter.	6,170	17,283	20,325	21,257	19,939	19,578	19,575	18,584	49,942	192,653
O.F.D. Total	6,354	8,403	7,858	7,690	7,712	7,723	7,523	6,747	26,511	86,521
Slaughter Total	13,456	30,035	34,768	35,354	34,298	33,501	33,294	31,261	117,208	363,175

Table 5. The number of cows culled, by year, by interval since most-recent calving, by type and by means of exit (either slaughter or on-farm death [O.F.D.] )

Interval from Last calving - 2003									
Months	0-1 Mth	2-3 Mths	3-6 Mths	6-9 Mths	9-12 Mths	12-15 Mths	15-18 Mths	>18 Mths	Total
Beef O.F.D.s	6,918	3,945	4,159	4,354	7,420	3,771	1,105	2,670	34,342
Beef Slaughtings	4,692	9,027	24,784	35,052	25,645	20,721	17,072	21,953	158,946
Dairy O.F.D.s	10,902	5,033	3,391	3,080	5,619	3,526	941	2,457	34,949
Dairy Slaughtings	8,084	12,012	23,019	30,852	31,074	26,126	17,191	21,858	170,216
Total O.F.D.s	17,820	8,978	7,550	7,434	13,039	7,297	2,046	5,127	69,291
Total Slaughtings	12,776	21,039	47,803	65,904	56,719	46,847	34,263	43,811	329,162
Interval from Last calving - 2004									
Months	0-1 Mth	2-3 Mths	3-6 Mths	6-9 Mths	9-12 Mths	12-15 Mths	15-18 Mths	>18 Mths	Total
Beef O.F.D.s	6,670	4,050	4,673	5,033	6,104	3,243	1,145	2,766	33,684
Beef Slaughtings	4,196	8,159	23,649	36,360	23,960	18,731	16,975	22,892	154,922
Dairy O.F.D.s	10,624	5,408	4,095	3,884	5,454	3,541	1,100	2,570	36,676
Dairy Slaughtings	8,307	11,074	23,453	34,563	34,191	30,391	22,044	25,127	189,150
Total O.F.D.s	17,294	9,458	8,768	8,917	11,558	6,784	2,245	5,336	70,360
Total Slaughtings	12,503	19,233	47,102	70,923	58,151	49,122	39,019	48,019	344,072
Interval from Last calving - 2005									
Months	0-1 Mth	2-3 Mths	3-6 Mths	6-9 Mths	9-12 Mths	12-15 Mths	15-18 Mths	>18 Mths	Total
Beef O.F.D.s	7,493	4,608	4,984	4,723	6,331	3,735	1,208	3,152	36,234
Beef Slaughtings	4,394	9,047	24,080	31,922	22,292	21,509	19,190	24,847	157,281
Dairy O.F.D.s	10,755	6,114	4,474	4,052	5,913	4,299	1,359	3,126	40,092
Dairy Slaughtings	7,945	10,652	21,981	29,266	30,314	34,733	25,987	28,142	189,020
Total O.F.D.s	18,248	10,722	9,458	8,775	12,244	8,034	2,567	6,278	76,326
Total Slaughtings	12,339	19,699	46,061	61,188	52,606	56,242	45,177	52,989	346,301
Interval from Last calving - 2006									
Months	0-1 Mth	2-3 Mths	3-6 Mths	6-9 Mths	9-12 Mths	12-15 Mths	15-18 Mths	>18 Mths	Total
Beef O.F.D.s	8,092	4,726	5,658	5,967	7,904	4,091	1,265	3,270	40,973
Beef Slaughtings	5,424	9,862	25,241	35,932	27,157	23,923	18,920	24,063	170,522
Dairy O.F.D.s	12,601	6,611	4,907	4,633	6,985	4,954	1,301	3,556	45,548
Dairy Slaughtings	7,682	10,060	20,870	29,527	34,843	36,667	25,379	27,625	192,653
Total O.F.D.s	20,693	11,337	10,565	10,600	14,889	9,045	2,566	6,826	86,521
Total Slaughtings	13,106	19,922	46,111	65,459	62,000	60,590	44,299	51,688	363,175

Table 6. Number of cows culled by year, by month of exit and by means of exit (either slaughter or on-farm death [O.F.D.] )

	2003		2004		2005		2006		Average	
	Slaughter (O.F.D.)									
Jan	27,455	5,647	22,953	4,705	14,437	5,344	25,737	6,340	22,646	5,509
Feb	23,207	7,812	21,509	6,819	21,361	7,150	25,324	8,387	22,850	7,542
Mar	18,326	12,590	23,358	11,149	21,682	11,200	27,321	14,325	22,672	12,316
Apr	19,773	11,402	20,671	10,759	22,609	11,491	23,310	13,747	21,591	11,850
May	25,475	7,942	20,736	7,352	29,180	8,614	30,611	10,701	26,501	8,652
Jun	27,173	4,380	28,081	4,326	32,208	5,487	35,589	5,201	30,763	4,849
July	33,769	3,223	30,314	3,117	30,381	3,722	32,557	3,748	31,755	3,453
Aug	25,358	2,811	31,446	3,424	33,536	3,731	31,481	3,457	30,455	3,356
Sep	30,767	2,822	31,440	3,778	35,490	3,783	32,393	3,796	32,523	3,545
Oct	34,429	3,033	36,454	4,889	34,166	4,766	33,593	6,001	34,661	4,672
Nov	36,456	3,499	41,183	4,808	41,544	5,897	39,220	5,844	39,601	5,012
Dec	26,974	4,130	35,927	5,234	29,707	5,141	26,039	4,974	29,662	4,870
Total	329,162	69,291	344,072	70,360	346,301	76,326	363,175	86,521	345,678	75,625

## 4. DISCUSSION

### 4.1 Calculating culling rates

In this study, culling refers to the removal of cows from the national herd as a result of slaughter rate and on-farm death. With the exception of a small number of high genetic merit animals, few cows are exported live from Ireland. Our definition is in contrast to the use of 'culling' in many farm-based studies, where culling would encompass the disposal of surplus stock from an individual herd on the open market, by export or otherwise, where the removed animal will continue to give further production and/or economic return for a new keeper. Further, some studies refer to involuntary culling as the removal of for instance 'infertile cows' and voluntary culling as the removal of low yielding cows (Crosse and O'Donovan, 1998). Our use of cull is equivalent to the 'herd turnover rate' as proposed by Hadley *et al.* (2006), and covers the removal of the cow from the national herd either 'voluntarily' or 'involuntarily' through her disposal in a slaughter plant or 'involuntarily' as an on-farm death. These, together with exports constitute an 'exit' from the Irish database of live animals. Herd turnover rate is recommended as the term to represent the magnitude of removals from the herd (Fetrow *et al.*, 2006).

In this study, the cow-culling rate was calculated using calf births as an estimate for cow numbers in any particular year. We acknowledge that there is the potential for both underestimation (cow infertility, pregnancy loss) and overestimation (multiple births) of the true number of cows, using this approach. This approach was taken, based on CMMS data available. While this has provided a valuable insight into culling in the Irish national cattle herd, comparison with other studies (which are generally based on intensive studies in a relatively small number of herds) needs to be conducted with care.

### 4.2 The Irish cow population

The whole bovine population fluctuates from a low of 6,464,038 million animals at the start of January to a high of 7,103,634 million animals at the start of June (CMMS statistics report, 2006) and in same manner the number of 'cows' in the population also varies from day to day over the entire year as some 400,000 cows are slaughtered or die on-farm and are replaced by pregnant heifers calving. It is therefore difficult to determine with precision the total productive cow population for a given year. To illustrate, a cow and her replacement may both be present in the cow population simultaneously if a heifer has already calved and the cow being culled has not yet been slaughtered. Similarly, both are present during the same calendar year if a cow were culled in the early part of the year and her replacement (heifer) calves later in the same year.

The consistency in recorded births per year (Table 3) and the balance in the numbers of heifers entering and cows being culled reflect stability in the cow population year on year. In 2003, 407,281 heifers were recorded as calving for the first time and so entering the cow population, this is only slightly above (8,828) the total number, 398,453 of cows culled in the same year. In other words, the number of entries was roughly equivalent to the number of exits. However, in 2006 despite a rise in the number of heifers calving compared to 2003, there was a net loss of 23,773 cows from the national herd (equivalent to a fall of 1.1%).

These data give some indication of a fall in total cow numbers, and therefore in the total cattle population in 2006 (Figure 1). This was widely predicted as a result of the recent decoupling of EU support payments in Ireland. There was constant increase year on year of 0.4 – 0.6% in the overall cull rate, increasing from 18.6% in 2003

to 21.1% in 2006 (Table 3); within this increase however, the proportion of dairy cows slaughtered in 2004 was higher and the proportion of beef cows slaughtered in 2004 was lower (Figure 2). So for 2004 the cull rate increased but this was due to an increase in dairy cow culling. Table 3 also demonstrates that there is a difference in the proportion of dairy and beef cows slaughtered each year, e.g. in 2003, 16.0% of dairy cows were slaughtered compared to 14.7% of beef cows slaughtered. Thus the absolute numbers of dairy cows has fallen (Table 3) while the number of beef cows has risen (Table 3), however the increase in beef cow slaughtering in 2006 (Table 3) may be the beginning of this trend in beef cows also. Table 3 gives the cow numbers and cull rate for dairy and beef cows. Any trends appearing will require ongoing monitoring over the next number of years as other market forces will influence farmer decisions in this regard.

The most surprising figure to emerge from these data (Table 4) is the consistency of the annual percentage loss rate from the cohort population once the animals are older than 4 years. The birth date of animals born prior to 1996 is not recorded on the database; it is not possible to further calculate the age breakdown of this 32.3% (2006) of the abattoir culls over 10 years old. Of the cull cows, some 8.6% to 9.7% per year belong to each known age cohort population. Assuming the same proportion of losses in each age cohort as in the 4 to 10 year old cohorts then it is probable that only about 5% of the cow population is over 13 years old.

The total number of beef cows in the cow population in 2005 is higher than the numbers of dairy cows (Table 1). The total numbers of on farm deaths and animals slaughtered (Table 4) for each age cohort to age 10 is also less for beef cows; confirming that there is a higher proportion (~54%) of beef cows over 9 years of age in the cow population. In Ireland, beef cows survive longer than dairy cows.

### 4.3 Number of on-farm deaths

There are peaks in the number of on-farm deaths within one month and 9-12 months following the last recorded calving (Table 5). The former highlights the significance of a calving event in the life cycle of a cow. On average, 24.5% of all cows that die on-farm, die within one month of their last reported calving date. The latter accounts for 17.1% of on-farm deaths. We speculate that this may also be related to a calving or pre-calving event, but from which no live birth is recorded on the database. This accords with data from the study conducted by Sol *et al.* (1984) who also found a culling peak shortly after calving attributed to calving difficulties, mastitis, teat injuries and other health problems. In Ireland, because the majority of cows calve in the spring, on-farm deaths in cows peaks in March and April (Table 6).

### 4.4 Number of cows slaughtered

Cows are slaughtered at varying times post-calving with a peak between 6 and 9 months after the last recorded calving date (Table 5). Since the majority of cows calve in the early part of the year, most cows are slaughtered in the autumn (Table 6). Sol *et al.* (1984), who also found a slaughter peak commencing some 6-months post calving, suggest that culling at the end of lactation is mainly a reflection of reproductive failure coupled with high prices. In general, farmers would prefer to cull a cow at the end of peak lactation and off pasture. Once an animal is housed, direct feeding costs become more expensive. Cows, however, are sent to the factory at various times during the year (Table 6). The data reflects that while an individual farmer may wish to remove a cow from the herd at the end of the grazing season, many such cows are then finished for slaughter by specialised cow finishers and thus slaughtered at any time and the distinction is not provided in this study. The higher numbers appear in the autumn as the grazing

season finishes.

#### 4.5 Age and lactation number when culled

Analysis of the data for the four years of this study shows that heifers in Ireland on average first calve aged between 29.7 and 30.2 months (dairy, 28.6-29.3 months; beef, 31.0-31.3 months) (Table 3). This data, in combination with Table 4 enabled us to determine in which lactation a cow was culled. Esslemont and Kossaibati (1997) found that cumulatively 41.3% of dairy cows sent for slaughter were removed by their 3<sup>rd</sup> lactation. Sol *et al.* (1984) also reported an average age of culling of 5.7 years (3<sup>rd</sup> lactation) in their study population. In Ireland, the age of the dairy herd is likely to be somewhat older than this. During 2003-2005 and in 2006, 32% and 35% cows were culled at less than 6 years of age, respectively (Table 4). Therefore, some 65-68% of dairy cows were retained in the national herd into their 4<sup>th</sup> lactation and beyond.

#### 4.6 Comparing culling rates

Crosse and O'Donovan (1998) found an average annual cull figure of 17.6% (range 15.2 to 22.6%) for the period 1980 to 1985 in 22 well managed large Irish dairy herds. Further, Crosse *et al.* (undated) found the average annual cull figure to be 15.2% for the period 1990 to 1994. However, in each case, the sample size was small. These rates and studies related to culling only in dairy herds in Ireland and while they represent all age cohorts, the rates include both voluntary and non-voluntary reasons for culling but do not include on-farm deaths. Reports published from the UK (Esslemont and Kossaibati, 1997) and Australia (Stevenson and Lean, 1998) describe average annual involuntary culling rates of 22% and 24% respectively, in dairy herds. Involuntary culling in these reports consists of all cow disposals, apart from disposals due to cows being surplus to requirements or old age. Further, comparable studies from the U.K. (Whitaker *et al.*, 2000; Whitaker *et al.*, 2004) report culling rates of 22.1%, and 22.6%, and from the Netherlands (Sol *et al.*, 1984) culling rates in dairy herds of 18.8% in 1951, and between 23.1 and 33% during 1968-1983. Hadley *et al.* (2006) analysed culling statistics over a 7-year period 1993-1999 across 10 US states, and found an average culling rate (slaughter and death) of 31.6%, which was marginally above the stated optimal figure of 19-29%. These studies appear to have been conducted in closely managed herds, many with computerised records. In the current study, the reported annual average national herd-culling rate was 19.6% (dairy average 21.3%; beef average 18%), which covers all types of management in all types of herds (Table 3).

#### 4.7 Comparing on-farm mortality rates

Thomsen and Houe (2006) have studied dairy cow mortality or on-farm death rates and state that there is "no overview over what might be considered 'natural' or 'normal' level of mortality in dairy cow production". In the current study, the calculated mortality rate of 3.2-4.1% (Table 3) is not dissimilar to comparable studies detailed by these authors. They reviewed 13 studies of dairy cow mortality and in the study of Nørgaard *et al.* (1999) a crude death rate of between 3 and 4%, in Denmark for the period 1974-1993, or Stephenson and Lean (1998) 4.3%, in Australia, are similar to the rate in the Irish Republic. In Denmark, the mortality rate amongst cows has risen from 2% in 1990 to 4% in 2001 (Thomsen *et al.*, 2007). Fetrow *et al.* (2006) put forward the proposition that cows reported as on-farm deaths will increase following the FDA 2004 rules prohibiting non-ambulatory cattle entering the food chain and the updating in 2005 of recommendations regarding humane transport. The mortality rate in Ireland increased from 3.2% (2003) to 4.1% (2006) as shown in Table 3. It is likely that the reported mortality rates have risen in Ireland for similar reasons consequential to revised rules for slaughter of casualty cattle post

BSE, and also fitness to transport regulations.

#### 4.8 Why are animals culled?

In most culling studies, determining reason(s) for culling is the primary objective of the study. For this reason, well-managed dairy herds are often chosen because of the high level of record keeping. In general, however, farmers do not record reasons for culling. Further, cows are frequently sold in open markets, without further detail as to whether they then move to slaughter or to other herds where they will continue to give economic return to their new keepers in the short or longer term.

This study covers the whole population, and provides an overview of culling in the broad spectrum of management on Irish cattle herds. To illustrate the potential variation, in cow fattening herds every cow is destined for culling in as short an interval as possible giving a culling rate of 100%. In milk-recorded dairy herds, a cow's economic breeding index (EBI) will be taken into account and this also may result in higher than normal culling rates. In a pedigree herd, a cow with high genetic merit may survive an infertile year and/or continue to be used for the harvesting of ova.

Many studies give detailed account as to the reasons for culling and often an animal is culled for a number of reasons. Crosse *et al.* (undated) found that the primary reasons for culling are:

- Infertility/reproduction 23.5%
- Mastitis 12.1%
- Low production and old age 13.4%
- Other reasons 36.7%
- Surplus 14.3%

Secondary considerations, such as the age of a cow, will also be taken into account when deciding to cull for infertility problems. Bascom and Young (1988) also found that the most common primary reason for culling was infertility followed by mastitis and production, but that the decision to cull was a multi-factored decision influenced by factors such as age, breed and temperament.

There is some information, which may be gleaned from this study that may give assistance in helping the reader surmise a possible reason for the culling. The database records the interval between the last calving date and the date of the exit (Table 5). It would be reasonable to deduce that the longer the interval between the last calving date and the date of exit, the more likely that one of the reasons for culling is infertility. It could also mean the cow was a poor producer, did not thrive, was hard to fatten or was particularly thin. If that were the case, a farmer is likely to cut his/her losses and not persist with trying to fatten the animal. Similarly, the shorter the interval the more likely the reason is for disease/production difficulties.

## 5. CONCLUSIONS

The study found the average culling rate in Ireland over the 4-year period was 19.6% for all cows; 21.3% for dairy type cows and 18% for beef type cows and while the comparison with other published studies must be guarded because the base data is not fully compatible the conclusion is that the overall rates of culling in Ireland fall within published internationally accepted norms. As a component of the culling rate the on-farm mortality rate of 3.2-4.1% found in this study is likewise not outside rates found in comparable studies. In Ireland 65-68% of dairy cows survive past their third lactation, which indicates a longer milking life than reported elsewhere. The study also found that average age of heifers calving and replacing culled cows was between 29.7 and 30.2 months.

There is only limited evidence as yet of the widely anticipated decrease in cattle numbers as a consequence of the change to decoupled payments following the 2003 reforms of the Common Agricultural Policy (CAP).

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## AN INTRODUCTION TO IMPORT RISK ANALYSIS FOR AQUATIC ANIMALS

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### ABSTRACT

With increasing international trade, there are increasing risks to countries that unwanted aquatic animal pathogens will enter and spread. Import risk analyses (IRAs) provide an objective, transparent and defensible method of assessing disease risks associated with imports. The International Aquatic Animal Health Code provides internationally recognised guidelines for import risk analyses. This paper describes and illustrates the main elements of IRAs for aquatic animals and their products, including hazard identification, risk assessment, risk management and risk communication. Sources of additional information are listed, both on concepts and methodology, and also the application of import risk analysis in aquatic animal health management.

### 1. INTRODUCTION

The potential impact of infectious diseases has led many countries to undertake import risk analyses (IRA). These analyses seek to support the development of policies to prevent the entry and spread of unwanted pathogens as trade in animal products increases under the various multilateral agreements administered by the World Trade Organization (WTO). For example, in the mid 1990s, farmed shrimp production was severely affected by several international waves of infectious diseases. As an immediate response, Australia placed a ban on the import of shrimp products not for human consumption, noting that these products were being used as bait for fishing, which will come in direct contact with populations of both wild and cultured shrimp. An import risk analysis was then conducted to systematically evaluate the risk of introduction of these infectious diseases, through this and other pathways. As a result of the IRA, importation of cooked shrimp was permitted. Importation of green (uncooked) shrimp was only permitted following the removal of the cephalothorax in an approved facility (Anon., 2000).

The importation of animals and animal products involves a degree of disease risk to the importing country. This risk may be represented by one or more diseases or infections. The principal aim of import risk analysis is to provide importing countries with an objective and defensible method of assessing the disease risks associated with the importation of animals, animal products, animal genetic material, feedstuffs, biological products and pathological material. It forces a thorough and logical approach to be adopted in considering the likelihood of undesirable events, and identifies gaps in our current knowledge. The analysis should be transparent. This is necessary so that the exporting country is provided with clear reasons for the imposition of import conditions or refusal to import. Transparency is also essential because data are often uncertain or incomplete and, without full documentation, the distinction between facts and the analyst's value judgements may blur. This paper describes and illustrates the main elements of IRAs for aquatic animals and their products.

*IRA provides an objective, transparent and defensible method of assessing disease risks associated with imports.*

### 2. THE INTERNATIONAL AQUATIC ANIMAL HEALTH CODE

In undertaking an import risk analysis, a country must be guided by the International Aquatic Animal Health Code of the Office International des Epizooties (OIE; World Organization of Animal Health, 2007). The OIE Code provides guidelines for national authorities to assist them in addressing the principles laid out in the WTO's Agreement on the Application of Sanitary and Phytosanitary Measures (the so-called SPS Agreement). In addition to the more formal WTO mechanisms, the OIE has voluntary in-house mechanisms for assisting Member Countries to resolve differences, which may arise from the outcomes of IRAs.

The SPS Agreement recognises the OIE as the relevant international organisation responsible for the development and promotion of international animal health standards, guidelines, and recommendations affecting trade in live animals and animal products. WTO Members may choose to adopt a higher level of protection than that provided by international agreements, if there

is a scientific justification that the level of protection provided by the relevant international agreements is inappropriate. However, in such circumstances, under the terms of the SPS Agreement, WTO Members must justify the level of protection with an IRA, and apply a consistent approach to risk management.

The section in the OIE Code on risk analysis contains new concepts to be embraced by animal disease control authorities. The OIE Code consists of four chapters:

- General Considerations,
- Guidelines for Risk Assessment,
- Evaluation of Competent Authorities, and
- Zoning and compartmentalisation.

Both qualitative and quantitative approaches to import risk analyses are recognised by OIE.

Decisions based on an IRA, as described in the OIE Code, is preferable to a zero-risk approach because it should lead to more objective decisions on imports and provides a sound basis for competent authorities to discuss any differences which may arise concerning potential risks.

*The International Aquatic Animal Health Code of the OIE provides internationally recognised guidelines for import risk analyses.*

### 3. IMPORT RISK ANALYSIS

#### a. Introduction

Import risk analysis (IRA) is the process of identifying the pests and diseases relevant to a particular import proposal, assessing the risks posed by them and, if those risks (the 'unrestricted risk estimate') are unacceptable, determining what measures can reduce the risks to an acceptable level (the 'restricted risk estimate'). Such measures include processing, testing, treatment and quarantine. Where available measures cannot reduce the risks to an acceptable level, imports should not be permitted.

There is an important distinction between the general epidemiological definition of risk and that used for import risk analyses:

- In general epidemiology, risk is simply the probability of occurrence of an adverse event during a specified time period.

- In IRAs, however, the magnitude of the consequences and the likelihood of the adverse event are each incorporated into the definition. Under the IRA definition of risk, an adverse event, which is unlikely to occur, may still be regarded as important because the consequences of the event may be quite catastrophic. For example, white spot syndrome virus (WSSV) can cause so much damage to a country's cultured shrimp industry that those countries which are free may wish to minimise the probability of an outbreak caused by importation of infected commodities.

Some of the terms used in IRA are listed in Figure 1. They are modifications of the definitions provided in Section 1.3 of the OIE Terrestrial Animal Health Code.

**Acceptable risk:** Risk level judged by OIE Member Countries to be compatible with the protection of animal and public health within their country, taking into account epidemiological, social, and economical factors.

**Commodity:** Animals, animal products, animal genetic material, feedstuffs, biological products and pathological material.

**Consequence assessment:** A description of the potential consequences of a given exposure and an estimate of the likelihood that each will occur.

**Exposure assessment:** A description of the biological pathways necessary for the exposure of animals and humans in the importing country to the hazards released from a given risk source, and an estimation of the probability of this occurring.

**Hazard:** In the context of the Code, hazard is a pathogenic (and usually infectious) agent.

**Hazard identification:** The process of identifying the pathogenic agents, which could potentially be introduced in the commodity, considered for importation.

**Qualitative risk assessment:** An assessment where the outputs on the likelihood of the outcome or the magnitude of the consequences are expressed in qualitative terms such as high, medium, low or negligible.

**Quantitative risk assessment:** An assessment where the outputs of the risk assessment are expressed numerically.

**Release assessment:** A description of the biological pathways necessary for an importation activity to 'release' (that is, introduce) pathogenic agents into a particular environment, and an estimation of the probability (qualitative or quantitative) of the complete process occurring.

**Risk:** The likelihood (probability or chance) of the occurrence and the likely magnitude of the consequences of an adverse event to animal or human health in the importing country during a specified time period.

**Risk analysis:** The process composed of hazard identification, risk assessment, risk management and risk communication.

**Risk assessment:** The evaluation of the likelihood and the biological and economic consequences of entry, establishment, and/or spread of a pathogenic agent within the territory of an importing country (i.e. the process of estimating the risk presented by a hazard, in qualitative or quantitative terms).

**Risk communication:** The process by which information and opinions regarding hazards and risks are gathered from potentially affected and interested parties during a risk analysis, and by which the results of the risk assessment and proposed risk management measures are communicated to the decision makers and interested parties in the importing and exporting countries.

**Risk estimation:** An integration of the results of the release assessment, exposure assessment and consequence assessment to produce an overall measure of the risk associated with each identified hazard.

**Risk management:** The process of identifying, selecting and implementing measures that can be applied to reduce the level of risk.

**Sanitary measure:** Measures such as those described in each Chapter of the Code, which are used for risk reduction and are appropriate for particular diseases.

**Sensitivity analysis:** The process of examining the impact of the variation in individual model inputs on the model outputs in a quantitative risk assessment.

**Transparency:** Comprehensive documentation of all data, information, assumptions, methods, results, discussion and conclusions used in the risk analysis. Conclusions should be supported by an objective and logical discussion and the document should be fully referenced.

**Uncertainty:** The lack of precise knowledge of the input values which is due to measurement error or to lack of knowledge of the steps required, and the pathways from hazard to risk, when building the scenario being assessed.

**Variability:** A real-world complexity in which the value of input is not the same for each case due to natural diversity in a given population.

Figure 1. A glossary of terms used in import risk analyses

## b. Qualitative versus quantitative

Although detailed methodologies for risk analyses are not considered here, it is worthwhile briefly discussing the differences between qualitative and quantitative methods before outlining the risk analysis process.

Qualitative risk assessment is an important part of all risk analyses. It provides a characterisation of the risk and a summary of all the available scientific information. Essentially, it is a scientific discussion of the biology and epidemiology of potential hazards associated with the relevant commodities being considered for importation. It is suitable for the majority of import risk analyses and is commonly used for routine import decisions. The lack of mathematics in a qualitative approach to risk assessment means that it is easy to adopt and the results are understandable to a non-scientific audience. However, it can be difficult to maintain objectivity and consistency between decisions (Vose, 2000). Inevitably qualitative risk assessments rely on phrases such as 'probable' and 'unlikely', which are open to differing interpretations. Qualitative assessments are generally used as the 'first step' of a IRA process. Further quantitative methods would generally only be justified if qualitative methods suggest that data are available and the risk is non-negligible.

Quantitative risk assessment uses probability and sometimes economic theory to estimate the probability and consequences of a risk. This approach is far more demanding of data and other resources compared with qualitative methods. The data required for quantitative risk assessments are largely absent for aquatic diseases, and expert opinion is therefore frequently required. The development of Monte Carlo simulation software packages, such as @Risk (Palisade Corporation, Ithaca, NY, USA) has made quantitative risk assessment a more realistic option. Inputs can be described as probability distributions and thus reflect the uncertainty associated with their values when based, say, on expert opinion. Quantitative methods also provide a mechanism for identifying the most important factors through sensitivity analyses. The use of numbers in a quantitative analysis does not necessarily add objectivity and precision, and interpretation and communication can be more difficult than for qualitative approaches in some circumstances.

Semi-quantitative methods combine qualitative and quantitative approaches. For example, probabilities may be estimated quantitatively and combined with qualitative estimates of the consequences.

Both methods have a degree of subjectivity and are heavily influenced by the opinions and experience of those involved in the analysis, and the decision makers who use the results.

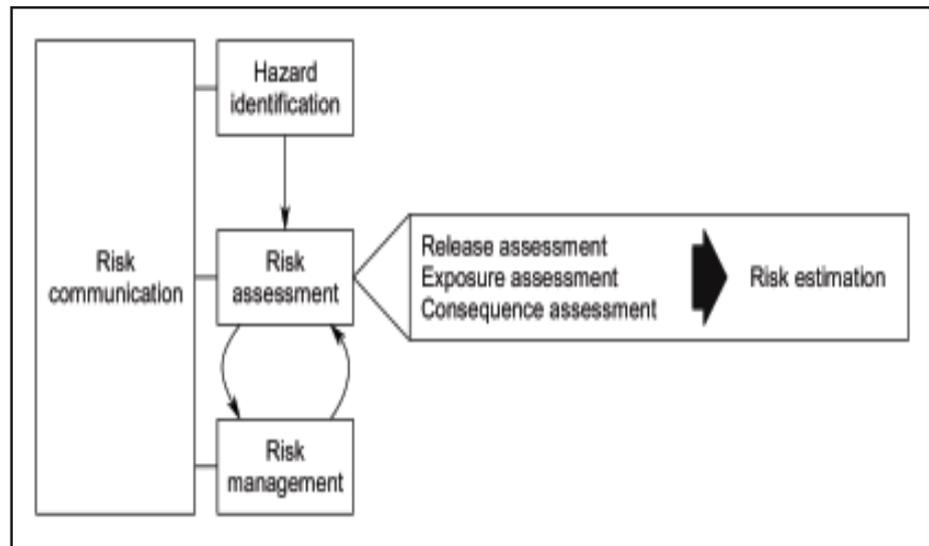


Figure 2. The components of an import risk analysis

## c. The components of an import risk analysis

Under the Code, risk analysis has four major components:

- hazard identification,
- risk assessment (which is further divided into four steps: release assessment, exposure assessment, consequence assessment and risk estimation),
- risk management, and
- risk communication.

The broad relationships among the components and steps are shown in Figure 2.

The majority of IRA are undertaken for trade purposes, thus the IRA process begins with a decision to conduct a risk assessment in response to a request to import a commodity. The starting point of the analysis is the commodity. A full description of the commodity proposed for import and the likely annual quantity of trade of the proposed importation should be documented. It must be recognised that whilst an accurate estimate of the anticipated quantity of trade is desirable to incorporate into the risk estimate, it may not be readily available, particularly where such trade is new.

Hazard identification is an essential step, which must be conducted before the risk assessment. If no hazards are identified, then a risk assessment is not required. The report from the risk assessment forms the basis for the development of risk management strategies and risk communication with stakeholders.

The process of an IRA may also need to take into consideration the results of an evaluation of competent authorities responsible for aquatic animal health services, zoning and surveillance systems in place for monitoring of animal health in the exporting country. These are described in separate Chapters in the Code.

*In IRAs, risk incorporates both the likelihood of occurrence and the magnitude of the consequences.  
Both qualitative and quantitative methods can be validly used in IRA.*

Table 1. Identification of hazards associated with the importation of salmonid carcasses to Australia (from Kahn *et al.*, 1999)

<b>Salmonid disease agents</b>						
DISEASE AGENT/PEST	1 DISEASE AGENT IS INFECTIOUS	2A AGENT OR STRAIN EXOTIC TO AUSTRALIA	2B CONTROL PROGRAM IN AUSTRALIA	3A OE-LISTED	3B SIGNIFICANT DISEASE	FURTHER CONSIDERATION OF DISEASE AGENT IS REQUIRED
<b>Viruses</b>						
Erythrocytic necrosis virus	Y	Y	N	N	Y	Y
Herpes virus salmonis type 1	Y	Y	N	N	N	N
Infectious haematopoietic necrosis virus	Y	Y	N	Y	Y	Y
Infectious pancreatic necrosis virus	Y	Y <sup>a</sup>	N	Y	Y	Y
Infectious salmon anaemia virus	Y	Y	N	Y	Y	Y
New Japan virus	Y	Y	N	N	Y	Y
<i>Oncorhynchus masou</i> virus	Y	Y	N	Y	Y	Y
Pacific salmon anaemia virus — erythrocytic inclusion body syndrome	Y	Y	N	N	Y	Y
Salmon leukaemia virus — plasmacytoid leukaemia	Y	Y	N	N	Y	Y
Salmon pancreas disease virus/sleeping disease of rainbow trout	Y	Y	N	N	Y	Y
Viral haemorrhagic septicaemia virus	Y	Y	N	Y	Y	Y
<b>Bacteria</b>						
<i>Aeromonas salmonicida</i> — atypical	Y	Y <sup>a</sup>	N <sup>e</sup>	N	Y	Y
<i>Aeromonas salmonicida</i> — typical	Y	Y	N	N	Y	Y
<i>Edwardsiella tarda</i>	Y	N	N	N	Y	N
<i>Piscirickettsia salmonis</i>	Y	Y	N	Y	Y	Y
<i>Renibacterium salmoninarum</i>	Y	Y	N	Y	Y	Y
<i>Vibrio anguillarum</i>	Y	Y <sup>a</sup>	N	N	Y	N <sup>e</sup>
<i>Vibrio ordalii</i>	Y	N	N	N	Y	N
<i>Vibrio salmonicida</i>	Y	Y	N	N	Y	Y
<i>Yersinia ruckeri</i> (Hagerman strain)	Y	Y	N	N	Y	Y
<b>Protozoans</b>						
<i>Ceratomyxa shasta</i>	Y	Y	N	N	Y	Y
<i>Dermocystidium</i> spp	Y	Y	N	N	N	N
<i>Enterocytozoon salmonis</i>	Y	Y	N	N	Y	Y
<i>Henneguya salminicola</i>	Y	Y	N	N	Y	Y
<i>Hexamita salmonis</i>	Y	Y	N	N	Y	Y
<i>Kudoa thyrssites</i>	Y	N	N	N	Y	N
<i>Loma salmonae</i>	Y	Y	N	N	Y	Y
<i>Microsporidium takedai</i>	Y	Y	N	N	Y	Y
<i>Myxobolus cerebralis</i>	Y	Y	N	N	Y	Y
<i>Parvicapsula</i> spp	Y	Y	N	N	N	N
Proliferative kidney disease agent	Y	Y	N	N	Y	Y
<b>Idiopathic diseases</b>						
Nervous mortality syndrome	Y	Y	N	N	Y	Y
Rosette agent	Y	Y	N	N	Y	Y
<b>Metazoans</b>						
<i>Gyrodactylus salaris</i>	Y	Y	N	Y	Y	Y
<i>Lepocephtheirus salmonis</i>	Y	Y	N	N	Y	Y
<i>Caligus elongatus</i>	Y	N	N	N	Y	N
Other metazoans	Y	N <sup>b</sup>	N	N	N	N

Y = yes; N = no

a A non-IPNV aquabirnavirus has been reported.

b Some strains occur.

c Numerous species have been reported but few identified at species level.

d This pathogen was rated 'Y' — for further consideration — in the draft of this report. The rationale for changing this rating is set out in the text.

e No movement controls apply to non-viable fish/fish products.

## 4. HAZARD IDENTIFICATION

Hazard identification involves identifying the pathogenic agents, which could potentially produce adverse consequences associated with the importation of a commodity.

The potential hazards identified would be those appropriate to the species being imported, or from which the commodity is derived, and which may be present in the exporting country. It is then necessary to identify whether each potential hazard is already present in the importing country, and whether it is a notifiable disease or is subject to control or eradication in that country. In other words, the question must be asked for each potential hazard: 'Is this pathogenic agent of quarantine significance to the importing country?' If the agent is not of quarantine significance, then it is probably not a hazard.

Hazard identification is a categorisation step, identifying pathogenic agents dichotomously as potential hazards or not. This step can be reported using a single table (Table 1), with column headings representing the classification criteria used to decide if a particular agent is a hazard or not. For each pathogen, the classification criteria could include susceptible species, exporting country occurrence and control measures, and importing country

occurrence and control measures. An example, the hazards associated with the importation of salmonid carcasses to Australia, is presented in Table 1.

The evaluation of the Veterinary Services, surveillance and control programs and zoning systems are important inputs for assessing the likelihood of hazards being present in the animal population of the exporting country.

The risk assessment may be concluded if any of the following apply:

- no potential hazards are identified associated with the importation;
- potential hazards are identified which are disease agents listed in the Code and the importing country decides to permit the importation using the risk management measures recommended in the Code; or
- potential hazards are identified, but, because they are not disease agents listed in the Code and not considered be significant, the importing country decides not to apply risk management measures. Note that a country can apply risk management measures to diseases that are not listed in the Code.

*Hazard identification lists the potentially important pathogens to be considered in the risk assessment.*

## 5. RISK ASSESSMENT

### 5.1 Overview

The risk assessment is the component of the analysis, which evaluates the risks associated with a hazard. As previously discussed, risk assessments may be qualitative or quantitative. Qualitative assessment does not require mathematical modelling skills to carry out, and so is often the type of assessment used for routine decision making. No single method of risk assessment has proven applicable in all situations, and different methods may be appropriate in different circumstances.

sources, including expert opinion. Consistency in risk assessment methods is encouraged and transparency is essential in order to ensure fairness and rationality, consistency in decision-making and ease of understanding by all the interested parties. Risk assessments should document the uncertainties, the assumptions made, and the effect of these on the final risk estimate.

Figure 3 highlights the key role of risk assessment, within an overall IRA process. The linkages to risk communication are not shown as this is an ongoing process undertaken during all IRA stages. Risk assessment should be flexible enough to deal with the complexity of real life situations. No single method is applicable in all cases. Risk assessment must be able to accommodate the variety of animal commodities, the multiple hazards that may be identified with an importation and the specificity of each disease, detection and surveillance systems, exposure scenarios and types and amounts of data and information.

A range of factors will determine whether qualitative or quantitative methods are more appropriate. A qualitative assessment may be undertaken for all the hazards, which allows the hazards to be ranked. A quantitative assessment may then be undertaken for the highest ranked hazards, provided relevant data are available. In either case, the risk assessment should be based on the best available information that is in accord with current scientific thinking. The assessment should be well documented and supported with references to the scientific literature and other

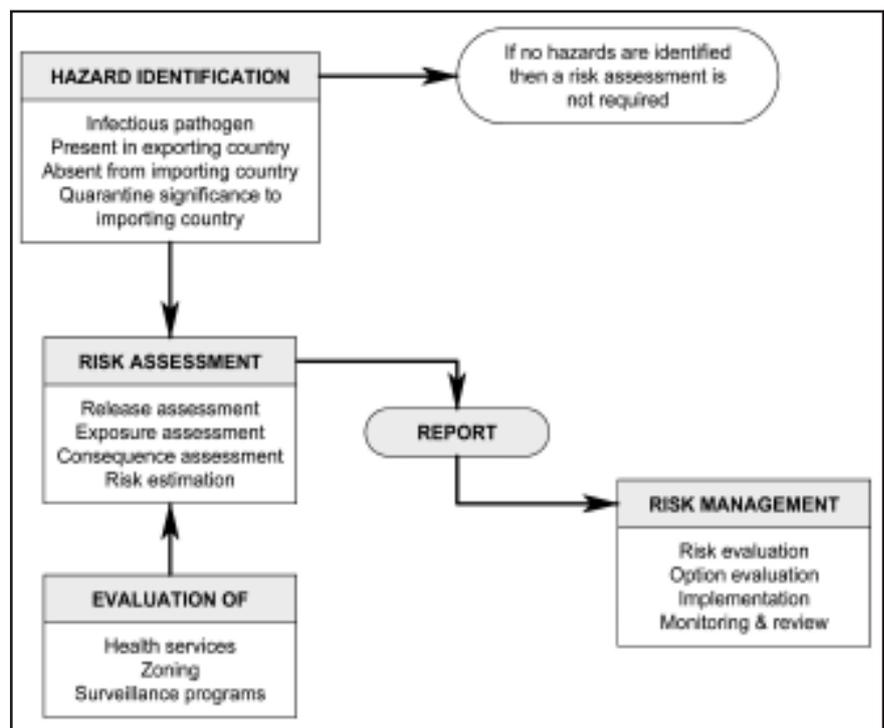


Figure 3. The key role of risk assessment, within an overall import risk analysis process

## 5.2 The sequential steps

- The risk assessment process consists of four sequential steps:
- Release assessment,
- Exposure assessment,
- Consequence assessment, and
- Risk estimation.

The four steps clarify the stages of the risk assessment, describing them in terms of the series of events necessary for the identified potential risk(s) to occur, and facilitate understanding and evaluation of the outputs. The product is the risk assessment report, which is used in risk communication and risk management. The first three steps of the risk assessment leading to risk estimation are illustrated in Figure 4. Pathways of entry into the importing country and exposure of susceptible animals are developed in the release and exposure assessments respectively, while outbreak scenarios are frequently used to assist in estimating the consequences. These will be more fully explained later.

Table 2: Qualitative descriptions of likelihood

Likelihood statement	Qualitative description
Very high	Event would be expected to occur
High	Likelihood of event occurring is approximately even
Moderate	Event is unlikely to occur
Low	Event would occur rarely
Very low	Event extremely unlikely to occur
Negligible	Likelihood of event occurring is so small that it can be ignored in practical terms

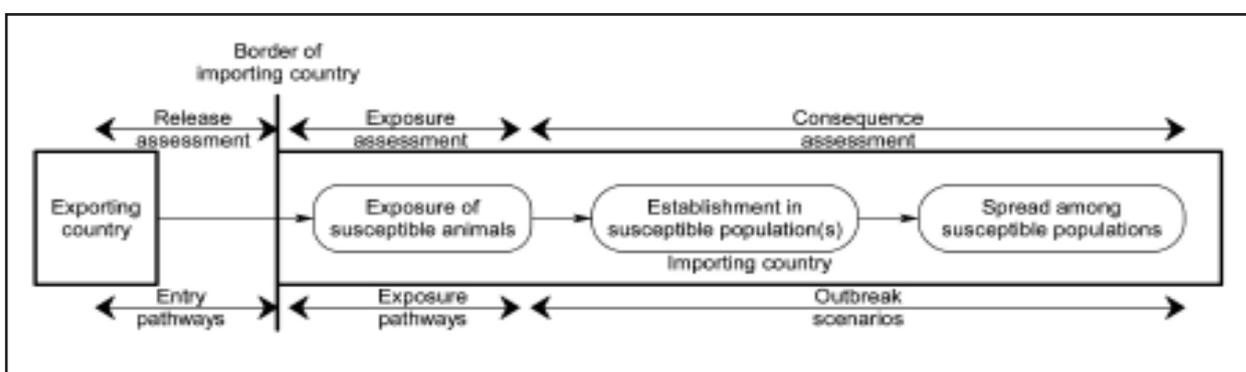


Figure 4. The steps of risk assessment leading to risk estimation

The likelihood that an identified hazard will enter an importing country with the proposed importation is estimated in the release assessment. The likelihood that susceptible animals will then be exposed to an infectious dose of that agent contained in the imported commodity is estimated in the exposure assessment. Next, the likelihood of establishment and spread, and biological and economic consequences of introducing the agent, are estimated in the consequence assessment. The risk assessment for each identified hazard concludes with risk estimation where the likelihoods and consequences are combined to provide what is known as the unrestricted risk estimate. The unrestricted risk estimate is the estimate of the risk prior to the application of any risk management measures.

## 5.3 Estimating likelihood

Both release and exposure assessments result in estimates of the likelihood of events. Essentially, likelihood can be estimated either qualitatively or quantitatively. Qualitative methods use verbal descriptions (Table 2) while quantitative methods use mathematical terms to describe likelihoods.

It is important to appreciate that when estimating likelihoods, the time period and unit (e.g. a consignment) of interest must each be stated. In the case of an IRA, the period is usually one year. Also, since the likelihood of release (introduction) and exposure (establishment) of a hazard increases with increasing volume of the commodity imported, the risk assessment should be amenable to updating when additional information becomes available.

## 5.4 Release assessment

The release assessment consists of describing the biological pathway(s) necessary for an importation activity to release (that is,

introduce) biological agents (hazards) into a particular country or location, and estimating the probability of that complete process occurring, either qualitatively (in words) or quantitatively (as a numerical estimate). Diagrams of potential pathways are useful in this regard. They ensure that all the steps necessary for the release (and exposure) are identified in a sequence that is logical in time and space. In Figure 5, the pathways for the introduction of the parasite, *Cyrodactylus salaris* are illustrated. The release assessment describes the probability of the release of each of the potential hazards (the infectious pathogens) under each specified set of conditions with respect to amounts and timing, and how these might change as a result of various actions, events or measures.

Examples of the kind of inputs that may be required in the release assessment include:

- Biological factors**
  - species, age and strain of animals
  - agent predilection sites
  - vaccination, testing, treatment and quarantine.
- Country factors**
  - incidence/prevalence
  - evaluation of animal health services, surveillance and control programs and zoning systems of the exporting country.
- Commodity factors**
  - quantity of commodity to be imported
  - ease of contamination
  - effect of processing
  - effect of storage and transport.

If the release assessment demonstrates an acceptable risk, then the risk assessment can be concluded at this stage.

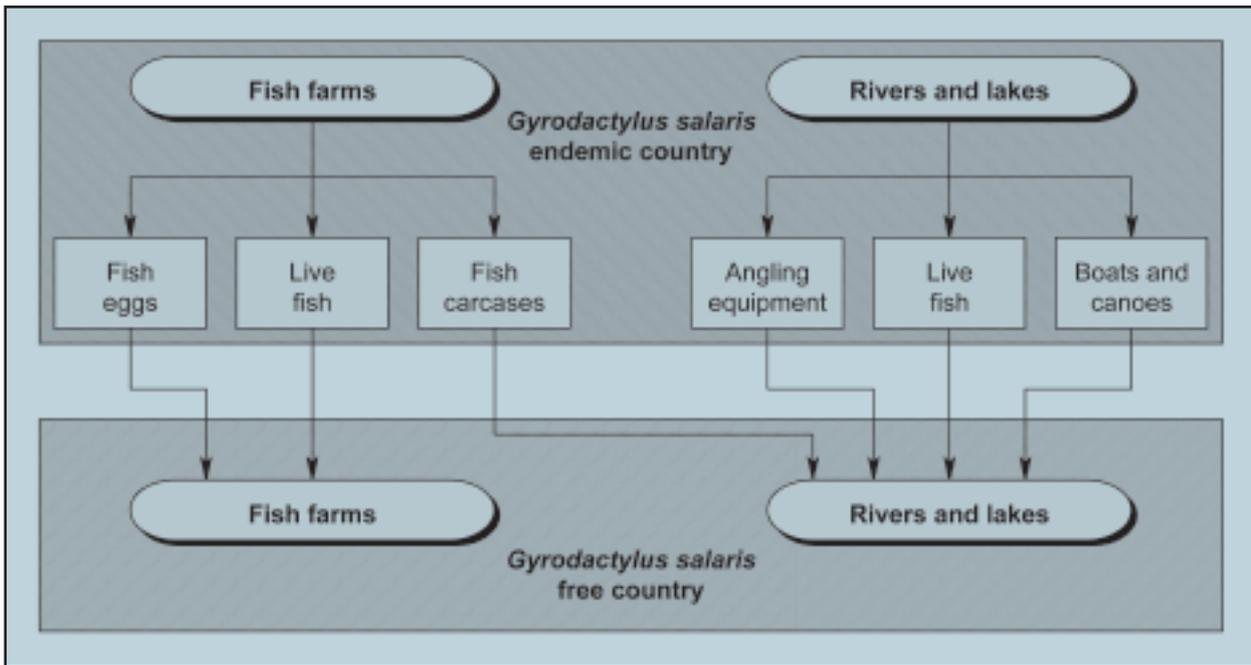


Figure 5. Possible routes of introduction for *Gyrodactylus salaris* from an endemically infected country to a country free from infection

5.5 Exposure assessment

Exposure assessment begins by describing the biological pathway(s) necessary for exposure of animals and humans in the importing country to the hazards (in this case the biological agents) released from a given risk source. The pathways for the exposure to the aquatic environment of pathogens introduced with the importation of shrimp are illustrated in Figure 6. For aquatic animal diseases the probability of sufficient quantities or concentrations of the biological agent entering the aquatic environment to eventually cause establishment of the disease in a susceptible population must be considered. In contrast, the OIE terrestrial animal code considers establishment of the pathogen under the consequence assessment. The probability of exposure to the identified hazards is estimated for specified exposure conditions with respect to amounts, timing, frequency, duration of exposure, routes of exposure (e.g. ingestion, skin penetration, gill exposure), and the number, species and other characteristics of the animal and human populations exposed. The probability of the exposure(s) occurring can be expressed either qualitatively (in words) or quantitatively (as a numerical estimate). Examples of the kind of inputs that may be required in the exposure assessment are:

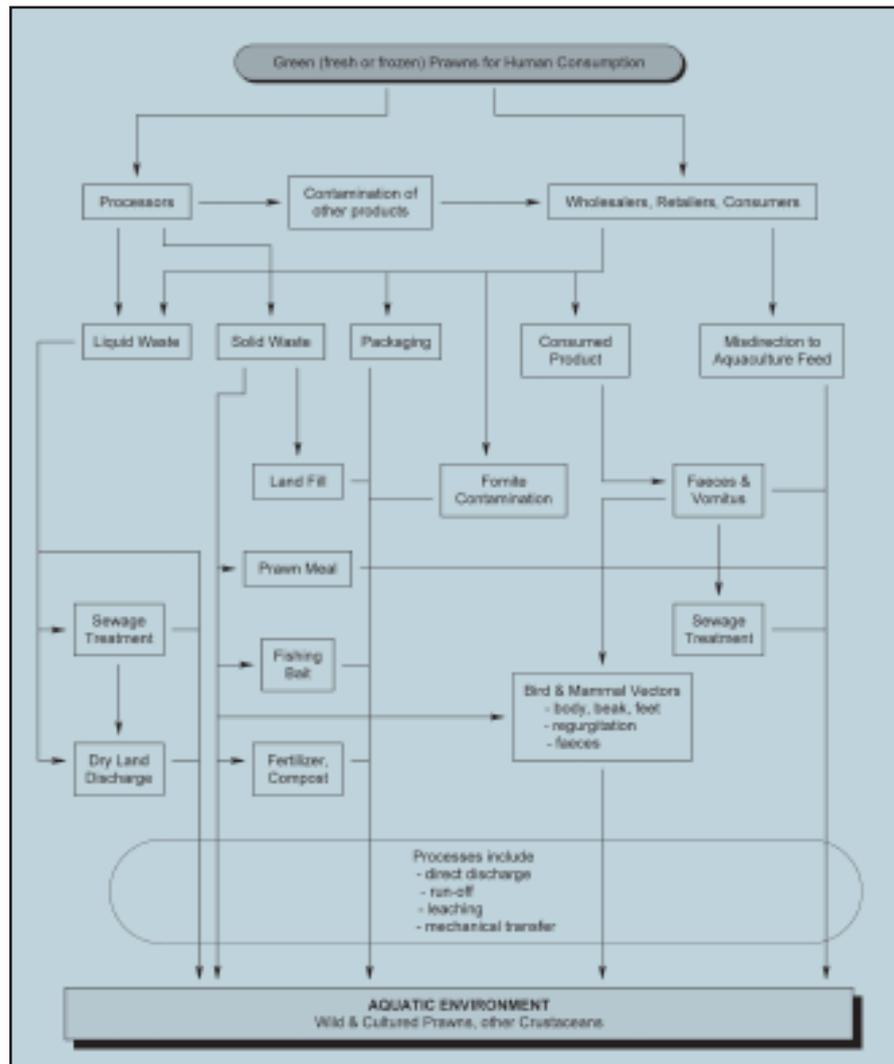


Figure 6. Example of diagram to show potential pathways for the exposure of pathogens introduced with imports of fresh prawns (shrimp) into Australia

## a. Biological factors

- properties of the agent

## b. Country factors

- presence of potential vectors
- human and animal demographics
- customs and cultural practices
- geographical and environmental characteristics

## c. Commodity factors

- quantity of commodity to be imported
- intended use of the imported animals or products
- disposal practices

If the exposure assessment demonstrates no significant risk, then the risk assessment can be concluded at this stage.

## 5.6 Consequence assessment

Consequence assessment consists of describing the relationship between specified exposures to a biological agent (hazard) and the consequences of those exposures. A causal process must exist by which exposures produce adverse health or environmental consequences, which may in turn lead to socio-economic consequences. The consequence assessment describes the potential consequences of a given exposure and estimates the probability of them occurring. This estimate may be either qualitative (in words) or quantitative (a numerical estimate). Outbreak scenarios may be used to illustrate the range of possible consequences that could be experienced in the importing country and to provide quantitative biological data for economic analyses where these are considered necessary. Examples of consequences include:

## a. Direct consequences

- animal infection, disease, and production losses
- public health consequences.

## b. Indirect consequences

- surveillance and control costs
- compensation costs
- potential trade losses
- adverse consequences to the environment.

An example of how different levels of impact of consequences might be described is shown below. A particular country may wish to define the different levels of significance of consequences in a totally different manner. However, it is important for any particular IRA to define the terms used and also to be consistent with other IRAs undertaken for similar commodities and hazards:

- a *very high (also called catastrophic or extreme) impact* is associated with the establishment of diseases that would be expected to significantly harm economic performance at a national level, or cause serious, irreversible harm to the environment.
- a *high impact* is associated with the establishment of diseases that would have serious biological consequences (e.g. high mortality or high morbidity and significant pathological changes in affected animals) over a prolonged period and are not amenable to control or eradication. Such diseases would be expected to significantly harm economic performance at an industry or national level. Alternatively or in addition, they may cause serious harm to the environment.
- a *moderate impact* is associated with the establishment of diseases that either have less pronounced biological consequences or would harm economic performance significantly at an enterprise/regional level. Such diseases would not be expected to significantly harm economic performance at the industry/national level. These diseases may be amenable to control or eradication, at a significant cost or

their effects may be temporary. They may affect the environment, but such effects would not be serious or may be reversible.

- a *low impact* is associated with the establishment of diseases that have mild biological consequences and would normally be amenable to control or eradication. Such diseases would be expected to affect economic performance at the enterprise/regional level but to have only minor significance at the industry or national level. Effects on the environment would be minor or, if more pronounced, would be temporary.
- a *very low impact* is associated with the establishment of diseases that have very mild biological consequences and/or are readily amenable to control or eradication. Though there may be moderate economic effects at an enterprise level, there would be little impact at an industry or national level. Effects on the environment would be minor and transient.
- a *negligible impact* is associated with the establishment of diseases that have no significant biological consequences, may be transient and/or that are readily amenable to control or eradication. The economic effects would be expected to be low at an individual enterprise level, and insignificant at an industry or national level. Effects on the environment would be negligible.

If the consequence assessment demonstrates a negligible impact, then the risk assessment can be concluded at this stage although this will depend on the importing country's acceptable level of protection which is explained later.

## 5.7 Risk estimation

Risk estimation consists of integrating the findings from the release assessment, exposure assessment and consequence assessment to produce overall measures of risk associated with the hazards identified at the outset. Thus risk estimation takes into account the whole of the risk pathway from hazard identified to unwanted outcome.

For a quantitative assessment, the final outputs may include:

- estimated numbers of animals, farms or people likely to experience health impacts of various degrees of severity over time;
- probability distributions, confidence intervals, and other means for expressing the uncertainties in these estimates;
- portrayal of the variance of all model inputs;
- a sensitivity analysis to rank the inputs as to their contribution to the variance of the risk estimation output; and
- analysis of the dependence and correlation between model inputs.

For a qualitative assessment, there may be some representation (graphical or other) of the combinations of likelihoods (probability of occurrence) and consequences. A relatively straightforward way to qualitatively combine the likelihood of introduction and establishment with the impact of the consequences for each identified hazard is to use a risk estimation matrix (also called a probability-impact table; Vose, 2000). An example is shown in Figure 7. The cells of this matrix describe the product of likelihood and consequences which are the different levels of 'risk'. When interpreting the risk estimation matrix, it should be remembered that although the descriptors for each axis are similar ('low', 'moderate', 'high', etc.), the vertical axis refers to 'likelihood' and the horizontal axis refers to 'consequence'. One implication of this is that a 'negligible' probability combined with 'very high' consequences, is not the same as a 'very high' probability combined with 'negligible' consequences; in other words, the matrix is not symmetrical. Another implication is that 'risk' is expressed in the same units as are used to estimate consequences. Thus, 'risk' is not a likelihood in IRA.

<b>Likelihood of entry and exposure</b>	<i>Very high likelihood</i>	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Very high risk
	<i>High</i>	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Very high risk
	<i>Moderate</i>	Negligible risk	Negligible risk	Very low risk	Low risk	Moderate risk	High risk
	<i>Low</i>	Negligible risk	Negligible risk	Negligible risk	Very low risk	Low risk	Moderate risk
	<i>Very low</i>	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk	Low risk
	<i>Negligible likelihood</i>	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk
		<i>Negligible impact</i>	<i>Very low</i>	<i>Low</i>	<i>Moderate</i>	<i>High</i>	<i>Very high impact</i>
<b>Consequences of entry and exposure</b>							

Figure 7. A matrix of risk estimation, combining likelihoods and consequences

*The risk associated with each identified hazard is evaluated in the risk assessment.*

*Likelihoods of release and exposure are usually estimated for a one year period and may change as annual volume of imports changes.*

*Release assessment considers the likelihood of a hazard being introduced into a country.*

*Exposure assessment considers the likelihood of susceptible animals being exposed to a hazard if it is introduced into a country.*

*Consequence assessment considers the potential impacts of a hazard if it becomes established in a country.*

## 6. RISK MANAGEMENT

Risk management is the process of deciding upon and implementing measures to achieve the Member Country's appropriate level of protection (ALOP), whilst at the same time ensuring that negative effects on trade are minimised. The objective is to manage risk appropriately to ensure that a balance is achieved between a country's desire to minimise the likelihood of disease incursions and their consequences and its desire to import goods and fulfil its obligations under international trade agreements. Each Member Country has the right to set its own ALOP which is consistent with the animal health status of that country and which is consistent with the principles of the SPS Agreement. Thus, different countries will have different ALOPs. It is important to note that the SPS Agreement does not require a country to have a scientific basis for its ALOP determination.

The risk estimation matrix shown in Figure 7 can be used to visualise a country's ALOP. For example, a country may be willing to accept only a very low risk or less for all hazards. However, the ALOP must be consistent for all imports. For example, it would not be acceptable to permit the import of a particular commodity for use as fishing bait while at the same time refusing the import of a similar commodity for human consumption from the same country. Similarly, if a hazard is present in both importing and exporting country, the importing country can only expect the exporting country to apply the same level of control and surveillance that it applies.

The international standards of the OIE are the preferred choice of sanitary measures for risk management. The application of these sanitary measures should be in accordance with the intentions in the standards.

The four steps used in deciding upon and then introducing appropriate risk management strategies are summarised below:

- *Risk evaluation*, the process of comparing the risk estimated in the risk assessment with the Member Country's appropriate level of protection.
- *Option evaluation*, the process of identifying, evaluating the efficacy and feasibility of, and selecting measures in order to reduce the risk associated with an importation in line with the Member Country's ALOP. The efficacy is the degree to which an option reduces the likelihood and/or magnitude of adverse biological and economic consequences. Evaluating the efficacy of the options selected is an iterative process that involves their incorporation into the risk assessment and then comparing the resulting level of risk with that considered acceptable. The evaluation for feasibility normally focuses on technical, operational and economic factors affecting the implementation of the risk management options.
- *Implementation*, the process of following through with the risk management decision and ensuring that the risk management measures are in place.
- *Monitoring and review*, the ongoing process by which the risk management measures are continuously audited to ensure that they are achieving the results intended.

For some hazards, the 'unrestricted risk' (the risk prior to the application of risk management measures) may exceed a country's ALOP. In these circumstances, risk can be reassessed in the light of the different options for management. The selected option should be that which brings the risk to the ALOP value and no lower (the 'restricted' risk).

For example, a country considering a proposal to import live goldfish may have identified goldfish haematopoietic necrosis virus (GFHNV) as a hazard, and estimated the likelihood of release and exposure as low and the consequences of establishment as high. Reference to the risk estimation matrix in Figure 7 shows that the qualitative unrestricted risk for GFHNV based on these estimates is low. If the importing country has a conservative ALOP and only accepts risks that are very low or lower, the unrestricted GFHNV

risk estimate exceeds the ALOP and risk management measures are required. The types of measures which might be considered include:

- certification of the health status of the source populations,
- inspection prior to export and after arrival, and
- observation in a post-entry quarantine facility.

If it could be shown that these measures would reduce the risk to the level of very low (the restricted risk estimate), then the imports could proceed with the appropriate management measures in place for GFHNV.

*A country sets its own ALOP, which must be consistent for all imports.  
Risk management measures are applied to bring risks to a level consistent with a country's ALOP.*

## 7. RISK COMMUNICATION

Risk communication is the process by which information and opinions regarding hazards and risks are gathered from potentially affected and interested parties during a risk analysis. The results of the risk assessment and proposed risk management measures are then communicated to the decision-makers and interested parties in the importing and exporting countries. It is a multidimensional and iterative process, and should ideally begin at the start of the risk analysis process and continue throughout.

The principles to be followed as recommended in the Code are:

- A risk communication strategy should be put in place at the start of each risk analysis.
- The communication of risk should be an open, interactive, iterative and transparent exchange of information that may continue after the decision on importation.
- The principal participants in risk communication include the authorities in the exporting country and other stakeholders such as domestic and foreign industry groups, domestic livestock producers and consumer groups.
- The assumptions and uncertainty in the model, model inputs and the risk estimates of the risk assessment should be communicated.
- Peer review is a component of risk communication in order to obtain scientific critique and to ensure that the data, information, methods and assumptions are the best available.

## 8. FURTHER READING

Detailed information on the concepts and methodology of import risk analysis for aquatic animals is available in the Aquatic Animal Health Code (World Organisation for Animal Health, 2007). Detailed guides on import risk analysis for terrestrial animals are also available (Murray, 2004a,b). A detailed review of the application of risk analysis in aquatic animal health management is presented by Peeler *et al.* (2007). This review provides an historical perspective, a summary of risk analyses conducted in this field, and a critical overview of current problems and future challenges.

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## A CRITICAL EVALUATION OF SURVEILLANCE AND CONTROL MEASURES WITHIN THE NATIONAL BRUCELLOSIS ERADICATION PROGRAMME IN THE REPUBLIC OF KOREA DURING 2000 TO 2006

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### ABSTRACT

Bovine brucellosis has recently emerged as a major animal health problem in the Republic of Korea. The incidence of human cases of brucellosis has also risen rapidly since 2002. This study seeks to critically evaluate the brucellosis eradication programme in Korea, focusing on the effectiveness of surveillance (identifying new cases) and control (clearing known cases) measures, during the period from 2000 to 2006. Using data from AIMS (the national animal infectious disease data management system), we conducted separate descriptive analyses, initially using farm and then episode as our unit of interest. An episode was defined as a period of compulsory trading restriction, following detection of infection with *Brucella abortus* in one or more cattle. We also identified risk factors for episode duration (logistic generalised estimating equation model) and time to re-restriction (Cox's proportional hazard model). There were 8,530 and 52,739 reactor farms and reactor cattle, respectively, during 2000 to 2006. There was a substantial increase in new outbreaks during 2004-2006. In beef cattle, the probability of a prolonged episode (>150 days) increased with herd size and size of the outbreak (measured as within-herd incidence during the first 30 days of the episode). Similarly, the hazard of a second episode increased with herd size, was higher in 2005 compared with other years, and was higher in the southeast of Korea compared with other provinces. The hazard also increased with the size of the outbreak (measured as within-episode incidence). The results from 2004-2006 suggest rapid spread of infection to previously non-infected farms, particularly in the beef sector. In large part, however, this increase can be directly attributed to increased surveillance effort, noting that there had been minimal surveillance for brucellosis in beef cattle prior to 2004. The current control strategy appears to have been effective, leading to rapid clearance of infection, on most farms. Control becomes problematic with increasing herd size and increasing percentage of animals infected. This work provides a detailed insight into the national brucellosis eradication programme in Korea, and should assist both policy-makers and field veterinarians to improve the effectiveness of national control efforts.

### 1. INTRODUCTION

Bovine brucellosis, due to infection with *Brucella abortus*, remains a significant animal health problem in many countries, causing reproductive failure, most commonly abortion, in cows and potential sterility in bulls (Abernethy et al., 2006). The status of bovine brucellosis in regions and countries varies considerably (Radostits et al., 2007). Detailed country reviews have been produced (see *Veterinary Microbiology* volume 90, 2002), and regular updates are available using World Animal Health Information Database (WAHID) Interface, maintained by the World Organisation for Animal Health (OIE) (Anon., 2008a). Human brucellosis, due to infection with *B. abortus*, *B. melitensis*, *B. suis* and *B. canis*, is the most-common zoonotic infection worldwide (Pappas et al., 2006).

Bovine brucellosis has recently emerged as a major animal health problem in the Republic of Korea (Kakoma et al., 2007; Wee et al., 2008). Bovine brucellosis was first reported in Korea among imported dairy cattle in 1955 (Park and Lee, 1959). Although initially a sporadic problem, there has been a steady increase in confirmed cases in dairy cattle since the mid-1980s. In beef cattle, there has been a dramatic increase in confirmed cases since 2000, rising to 15,524 confirmed cases in 2005 (Wee et al., 2008). There has also been an associated rise in human cases of brucellosis. The first human case of brucellosis in Korea was detected in 2002, in a livestock worker following the ingestion of unpasteurised milk (Park et al., 2003). Subsequently, the incidence of human brucellosis has risen rapidly (Park et al., 2005; Kim et al., 2006); following the single case in 2002, 10 human cases were reported to the Korean Centre

for Disease Control and Prevention in 2003, 47 in 2004, 158 in 2005 and 215 in 2006 (Anon., 2006).

There has been a national brucellosis eradication programme, based on test-and-slaughter of infected cattle, in Korea since the 1960s (Wee et al., 2008). Prior to 2000, control efforts mainly focused on infection in dairy herds, based on four-yearly (in 2005, changed to six-yearly) milk ring testing. In recent years, a range of national control measures for beef animals have been introduced, including:

- pre-movement testing of cows (to markets, between farms) (May 2004),
- mandatory annual surveillance in high prevalence areas (November 2004),
- mandatory testing on high-risk farms (with epidemiological links to confirmed infection) (November 2004),
- routine slaughterhouse surveillance (March 2005),
- mandatory testing of bulls prior to trade (June 2005), and
- mandatory biannual testing on all farms with 10 or more beef animals (June 2006).

In 2008, the surveillance effort will be broadened to include annual testing of all female cattle older than 12 months of age on all beef farms.

This study seeks to critically evaluate the brucellosis eradication programme in Korea, focusing on the effectiveness of surveillance (identifying new cases) and control (clearing known cases) measures, during the period from 2000 to 2006.

## 2. MATERIALS AND METHODS

### 2.1 Data

This study considers events during 2000 to 2006. It was conducted using data from AIMS (animal infectious disease data management system), which is managed by the National Veterinary Research and Quarantine Service (NVRQS). In the national database, data are available for each positive brucellosis testing event (one or more cattle positive at a single bleed), including the date of laboratory diagnosis at NVRQS, the name of farmer, the farm address (therefore, farms could be assigned to defined administrative areas [see below]; farm geographic coordinates were not available), the farm type (beef, dairy), the number of reactor animals, and – according to the field veterinarian – whether the outbreak was new or recurrent. A positive testing event was classified on the basis of serological results only. A range of additional data are held regionally, including all negative brucellosis testing events (for example, a herd test in which all animals test negative) and dates of de-restriction. However, these are currently not maintained in AIMS, and therefore were not available for this study.

In Korea, administrative areas are tiered: primary areas are termed do [province], gwangyeoksi [metropolitan city] and teukbyeolsi [special city]; secondary areas si [city], gun [county] and gu [district]; and tertiary areas eup [town], myeon [township], dong [neighbourhood] and ri [village]. Under different circumstances, there are differences in the hierarchy of administrative areas; for example: do, si, gu, dong; but: do, gun, eup, ri.

Data on the number of cattle per administrative area (current to 2006) were obtained from the National Agricultural Products Quality Management Service within the Korean Ministry of Agriculture and Forestry (Anon., 2008b).

### 2.2 Data analyses

#### 2.2.1 General

Data analyses were conducted using Microsoft Excel (Redmond, WA, USA), SAS version 9.1 (Cary, NC, USA), STATA release 10 (Stata Statistical Software, College Station, TX, USA) and ArcGIS version 9.0 ArcMap (ESRI, Redlands, CA, USA). A map of Korea, current to 2002, was obtained in polygon format (a series of .shp files for 4,250 administrative areas). Throughout Korea, apart from 39 si, gun or gu, data were available to the level of the eup, myeon or dong.

AIMS data were imported into Excel, with each record representing a unique testing event. To facilitate SAS programming, key text fields were translated from Korean to English. Each farm was given a unique identifier, after combining farmer name and farm address (a combination of secondary [si, gun, gu] and tertiary [eup, myeon, dong] administrative areas), which was later used to link the geographic (polygon) and disease datasets. A detailed review of the database was made, to identify (and either correct or remove) records with missing, implausible or otherwise unusable data.

#### 2.2.2 Descriptive analyses

##### a. Reactor farms

Initially, farm was considered the unit of interest. A reactor farm was defined as a single epidemiological unit (one or more farms with the same farm owner) with at least one positive testing event during each period of interest. The exact geographic coordinates for each reactor farm were not available; therefore, unless stated otherwise, the farm was assigned to the centroid of the smallest

associated administrative area for which polygon data were available. We calculated the number of reactor farms (that is, farms with at least one positive testing event), the number of positive testing events, and the number of reactor animals on these reactor farms, by year, by production type (dairy, beef) and area (primary administrative area) during 2000 to 2006. We also determined the number of reactor farms per area (tertiary administrative area, where available) each year, and used these data to develop choropleth maps using ArcMap. A kernel density analysis was conducted at the level of the tertiary administrative area using the Spatial Analyst extension in ArcMap to map the number of reactor farms per km<sup>2</sup> per year. Farm location, both of reactor farms and of farms-at-risk, in each administrative area was not available.

##### b. Brucellosis episodes

We then considered episode (rather than farm) as the unit of interest. A brucellosis episode was defined as a period of compulsory trading restriction, following detection of infection with *Brucella abortus* in one or more cattle. As part of the national control programme, prior to 15 July 2006 a herd was able to resume trading following two negative herd tests, with an interval between tests of between 30 and 60 days. From 15 July 2006, this was changed to at least three negative tests, with an interval between tests of no greater than 70 days. An episode started on the date of the first positive testing event following a period without trading restriction, and ended following an interval of 120 days (if the last positive test was conducted prior to 15 July 2006) or 210 days (if otherwise) without a positive testing event. Although testing data were available from 1 January 2000 (but not before), it was not possible to distinguish whether positive testing events during January to April 2000 were associated with a new or existing episode. Therefore, we created an episode-level dataset, with each record representing a unique episode starting at some point between 1 May 2000 and 31 December 2006. For each episode, we assigned farm identifier, episode number on each farm during 2000 to 2006 (1 for first restriction due to brucellosis, 2 for second, etc), start date, end date (if no later than 31 December 2006; otherwise, the episode was considered right-censored), location (tertiary administrative area, where available), number of testing events and number of reactor cattle during episode. These calculations concern the period of trade restriction, and not necessarily the period of infection or infectiousness.

Using the episode-level dataset, we calculated measures of surveillance (number of cases of brucellosis on previously unaffected farms [new cases], equivalent to the number of episode 1 restrictions) and control (number of episodes per farm, number of testing events per episode, number of reactor animals per episode, reactor incidence, episode duration, inter-episode interval), by do [province], year and (for all but the first measure) episode number. When calculating reactor incidence, we divided the total number of reactors detected during an episode by the maximum number of animals tested at any test during that episode. The spatial distribution of episode 1 restrictions and of episode 2+ restrictions, by year and tertiary administrative area, where available, were presented using choropleth maps. We created a visual representation of the outbreak, after assigning each episode 1 restriction to a randomly selected geographic location within each associated tertiary administrative area. Yearly results were overlaid on a choropleth map of cattle density in Korea. We then investigated the possibility of spatial clustering among episode 1 restrictions using SaTScan version 7.0 (available without cost from The USA National Cancer Institute, <http://www.satscan.org/>). In this analysis, each tertiary administrative area was assigned a yearly status: positive or negative, based on the presence or absence in that year of at least one episode 1 restriction, respectively. During each year, we first examined the data for clusters, by varying the maximum population size window from 5

to 25%. We then used the Bernoulli option, within each arbitrary spatial window, to compare the locations of positive and negative areas each year.

### 2.2.3 Multivariable analyses

#### a. Episode duration

We developed a logistic generalised estimating equation (GEE) model. The outcome measure was whether an episode was prolonged (>150 days) or not, and the episode was the unit of interest. The analysis was run separately for dairy and beef cows. The independent variables included in each model were year (YEAR), episode number (EPI), herd size (HS), province (PROV) and within-herd incidence during the first 30 days of the episode (I\_30). We used a GEE model with compound symmetry, noting that there could be more than one episode per herd. Further, we chose a GEE model with a compound symmetry correlation structure, rather than a random effects model, to produce population averaged parameter estimates (Dohoo et al., 2003). We checked for collinearity by examining correlations between pairs of continuous variables. None of the variables were strongly correlated ( $r < 0.75$ ). We used a backward selection procedure, to eliminate terms from the model based on the generalised score test ( $p > 0.05$ ). We fitted the model using the GENMOD procedure in SAS v9.1 (SAS Institute Inc., 2003). We considered 2-way interactions between HS x I\_30, YEAR x PROV and EPI x YEAR since these were deemed to be biologically plausible. We obtained consistent estimates of coefficient standard errors using the empirical covariance matrix of parameter estimates resulting from the GEE method. The two continuous variables, HS and I\_30, were categorised into four groups according to the corresponding quartiles (which were different for dairy and beef cattle).

#### b. Time to re-restriction

The outcome measure was the time from the end of the first episode in a herd to the start of a second episode or until 31 December 2006, whichever occurred first. Herds that did not have a second episode were treated as censored at 31st December 2006. Herds were not allowed to re-enter the study following the second episode. Univariate and multivariate survival analysis were carried out using Cox's proportional-hazard models, using STCOX in STATA. The independent variables considered in the analysis included YEAR, HS, PROV and within-herd incidence during the first episode (I). The analysis was run separately for beef and dairy herds. We considered 2-way interactions between HS x I and YEAR x PROV since these were deemed to be biologically plausible. We used a backward selection procedure, to eliminate terms from the model based on a likelihood ratio test ( $p > 0.05$ ). HS and I were categorised into 4 groups according to the corresponding quartiles (which were different for dairy and beef cattle). We checked the proportional-hazard assumption visually using a plot of  $-\log(-\log)$  survival lines to examine whether the different covariate groups were parallel. In addition, we checked if the hazard ratio varied over time by analysing the chi-squared Schoenfeld residuals, if significant ( $p < 0.05$ ), we included the exposure time as a time-varying covariate.

## 3. RESULTS

### 3.1 Descriptive analyses

#### 3.1.1 Reactor farms

A total of 8,530 reactor farms (farms with at least one testing event in a defined calendar year, farms with more than one testing event may have been recounted in later years) in Korea during 2000 to 2006 (Table 1). During this period, there were 52,739 reactor cattle identified during 12,570 positive testing events, including 43,479 (83.5%) beef (beef, Korean beef and mixed) and 8,678 (16.5%) dairy cattle (Figure 1). The beef reactor animals were mainly identified in 2004 (4,043 animals), 2005 (15,765) and 2006 (23,210). The distribution of reactor farms in 2006 is presented as choropleth and density maps (Figure 2).

#### 3.1.2 Brucellosis episodes

A total of 8,179 brucellosis episodes were identified during 1 May 2000 to 31 December 2006, including 7,747 1<sup>st</sup> episodes, 407 (5.0%) 2<sup>nd</sup> episodes, 22 (0.3%) 3<sup>rd</sup> episodes and 3 (0.04%) 4<sup>th</sup> episodes. A substantial number of these episodes (3,476, 42.5%) were still active at the end of 2006; therefore, full (uncensored) episode data (including start and end) were available for 4,703 episodes. The distribution of 1<sup>st</sup> and 2+ (2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup>) episodes in Korea during 2006 is presented in Figure 3, each as a choropleth map, with the former overlaid with results from the SaTScan analysis (Figure 4).

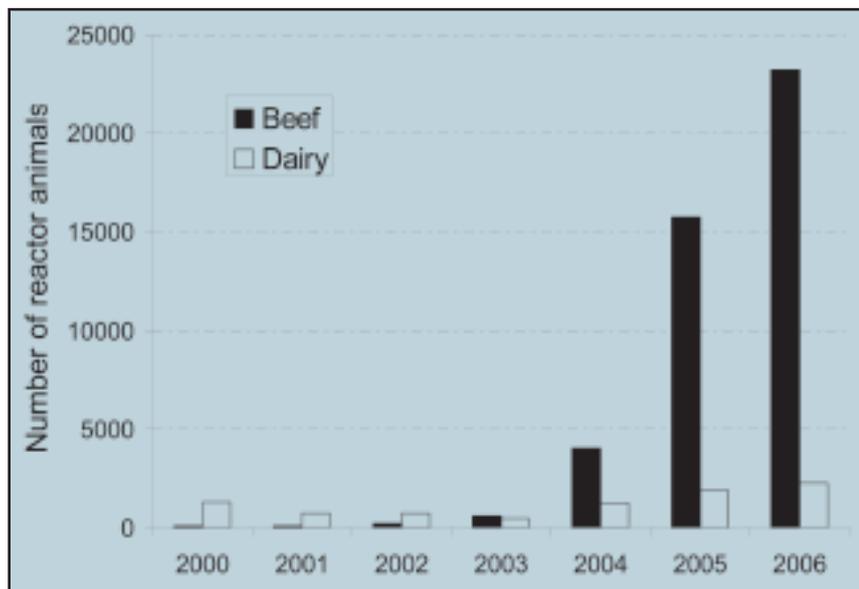


Figure 1. The number of brucellosis reactor animals in Korea during 2000 to 2006, by breed. Beef includes beef, Korean beef and mixed

#### a. Surveillance

The 7,747 new brucellosis outbreaks were reported in all primary administrative areas, apart from Seoul (Table 2, Figure 5). There was a substantial national increase in new outbreaks during 2004 (699), 2005 (2,515) and 2006 (4,236).

## SELECTED REPORTS

Table 1. The number of brucellosis reactor farms and reactor animals detected each year in Korea between 1 January 2000 and 31 December 2006, by primary administrative area. A reactor farm is defined as a farm with at least one testing event in a defined calendar year; therefore, farms with more than one testing event may have been recounted in later years

	2000		2001		2002		2003		2004		2005		2006		Total	
	Farms	Cattle														
<b>Special cities</b>																
Seoul															0	0
<b>Metro. Cities</b>																
Busan					2	10	5	17							7	27
Daegu					8	31	91	253							99	284
Daejeon									1	1	6	32	1	1	8	34
Gwangju	1	1									2	2	17	159	20	162
Incheon	4	40	6	64	9	78	3	24	4	22	9	15	24	86	59	329
Ulsan									83	405	233	1,199	176	796	492	2,400
<b>Provinces</b>																
Chungcheongbuk	10	128	4	14	6	67	13	144	71	801	311	1,938	592	3,039	1,007	6,131
Chungcheongnam	55	561	13	159	16	302	25	224	163	986	404	2,671	437	2,597	1,113	7,500
Gangwon	3	3	3	4			3	21	104	739	216	1,337	270	998	599	3,102
Gyeonggi	45	480	35	315	15	204	6	54	39	558	139	1,344	165	1,292	444	4,247
Gyeongsangbuk	3	17	2	24	5	203	8	72	115	811	534	3,553	1,253	7,429	1,920	12,109
Gyeongsangnam	7	40	1	4	2	11	3	24	72	521	316	1,687	732	3,079	1,133	5,366
Jeju	2	2							2	11				4	13	
Jeollabuk	13	73	11	147	3	29	16	444	50	284	129	1,042	328	1,572	550	3,591
Jeollanam	11	30	8	75	4	46	3	81	17	244	408	2,832	624	4,136	1,075	7,444
Total	154	1,375	83	806	60	940	80	1,088	721	5,383	2,717	17,693	4,715	25,454	8,530	52,739

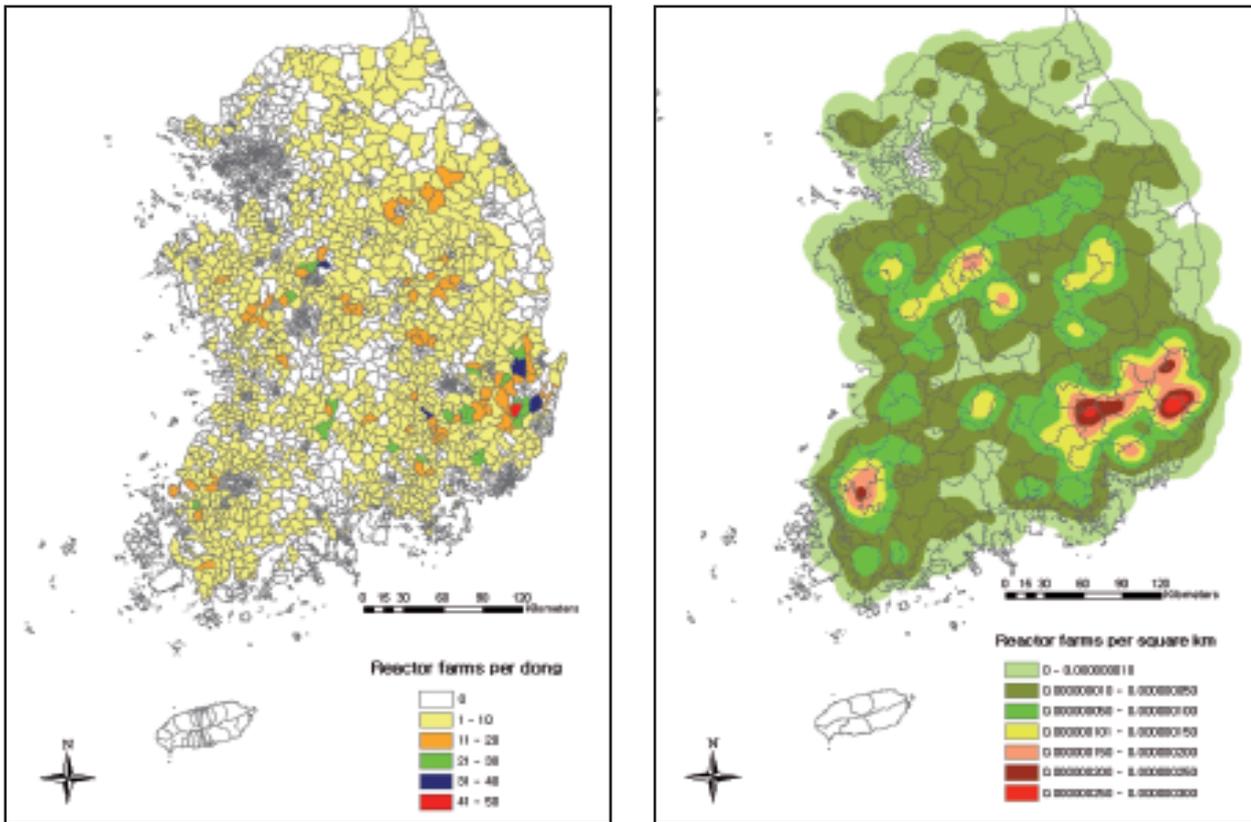


Figure 2. Distribution of brucellosis reactor farms in Korea during 2006, using choropleth (left) and density (right) maps. A reactor farm was defined as a single epidemiological unit (one or more farms with the same farm owner) with at least one positive testing event during each period of interest

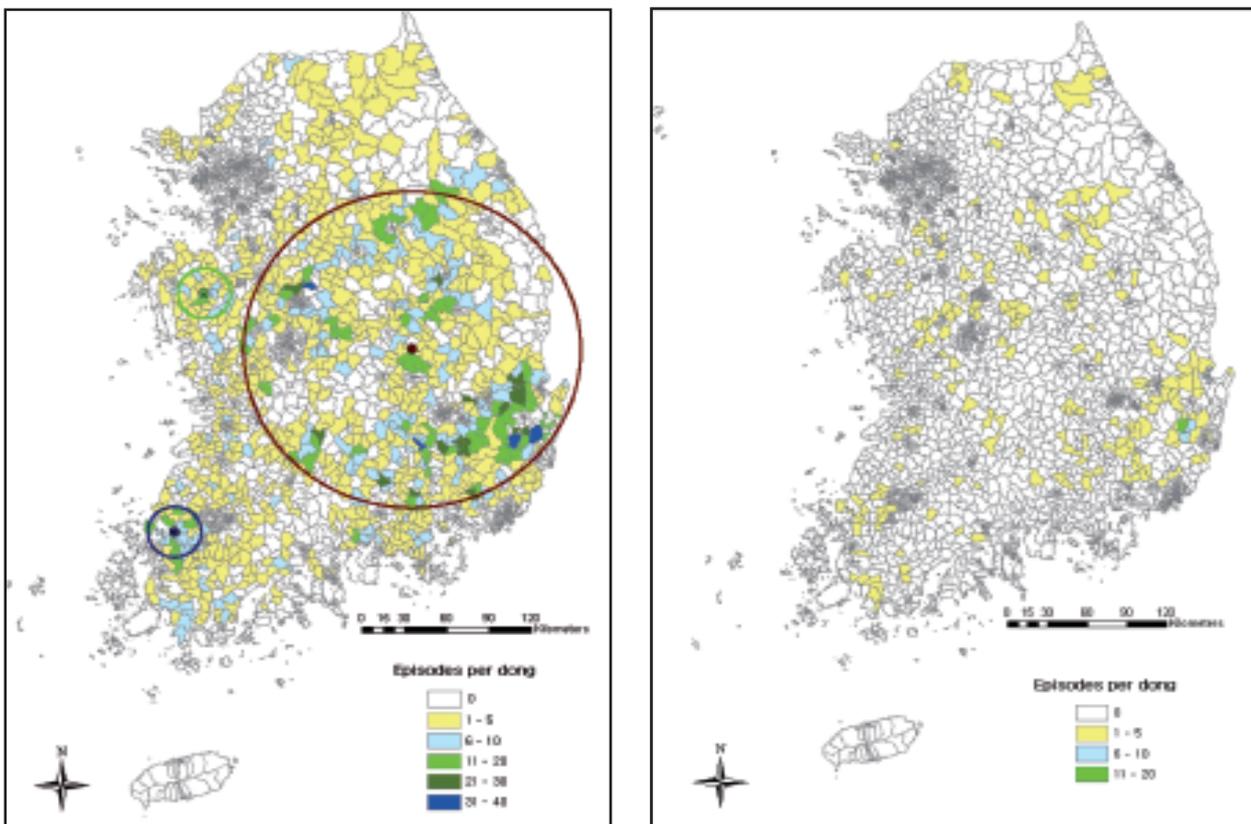


Figure 3. The distribution of 1<sup>st</sup> (left) and 2+ (2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup>; right) episodes in Korea during 2006, each as choropleth maps. The 1<sup>st</sup> episode distribution is overlaid with results from the SaTScan analysis

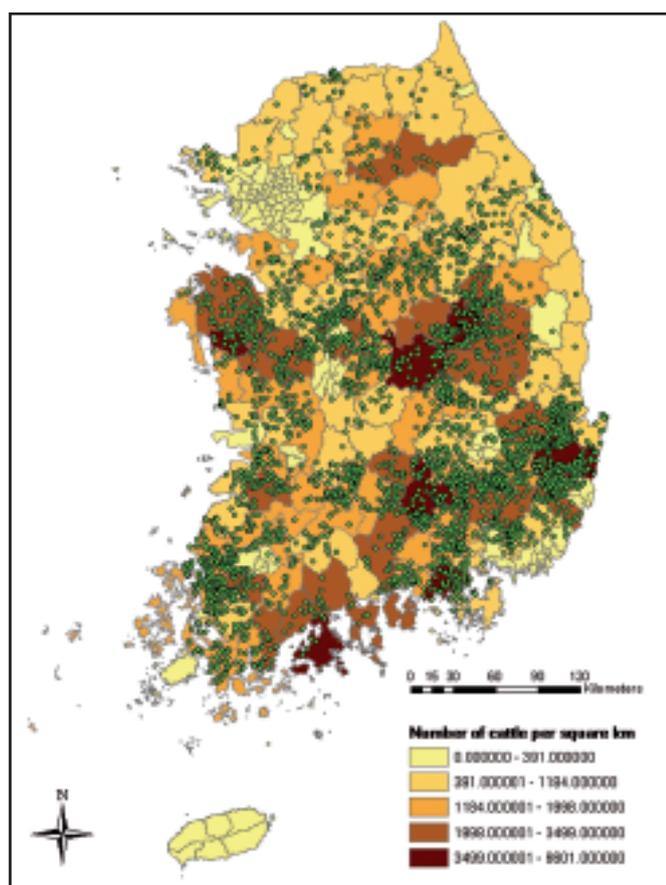


Figure 4. A visual representation of brucellosis episodes (green dots) on previously non-infected cattle farms in Korea during 2006, after assigning each episode 1 restriction to a randomly selected geographic location within each associated tertiary administrative area. The results overlay a choropleth map of cattle density in Korea

Table 2. The number of new brucellosis outbreaks in Korea between 1 May 2000 and 31 December 2006, by year and primary administrative area. A new outbreak is defined as the outbreak of brucellosis on a previously unaffected farm (no brucellosis had been diagnosed from 1 January 2000, when records became available)

	2000	2001	2002	2003	2004	2005	2006	Total
Special cities								
Seoul								
Metro. cities								
Busan						2	5	7
Daegu						8	91	99
Daejeon					1	6	1	8
Gwangju	1					2	16	19
Incheon	4	5	4	1	4	9	22	49
Ulsan					83	191	131	405
Provinces								
Chungcheongbuk	10	3	6	11	66	296	524	916
Chungcheongnam	51	10	10	19	155	363	382	990
Gangwon	2	3		2	104	194	246	551
Gyeonggi	34	25	8	5	38	130	137	377
Gyeongsangbuk	3	1	5	7	111	507	1,151	1,785
Gyeongsangnam	7	1	2	1	71	282	678	1,042
Jeju	2				2			4
Jeollabuk	13	7	2	15	47	120	300	504
Jeollanam	11	3		3	17	405	552	991
Total	138	58	37	64	699	2,515	4,236	7,747

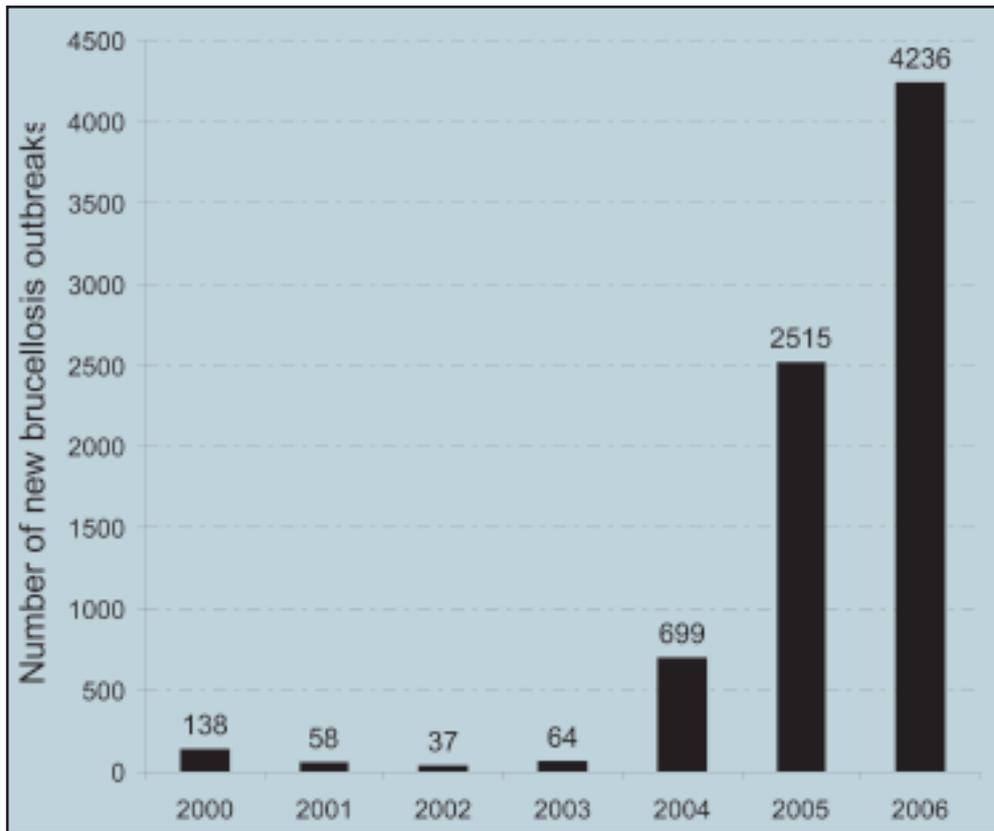


Figure 5. Number of new outbreaks of brucellosis in Korea during 1 May 2000 and 31 December 2006, by year. A new outbreak is defined as the outbreak of brucellosis on a previously unaffected farm (no brucellosis had been diagnosed from 1 January 2000, when records became available)

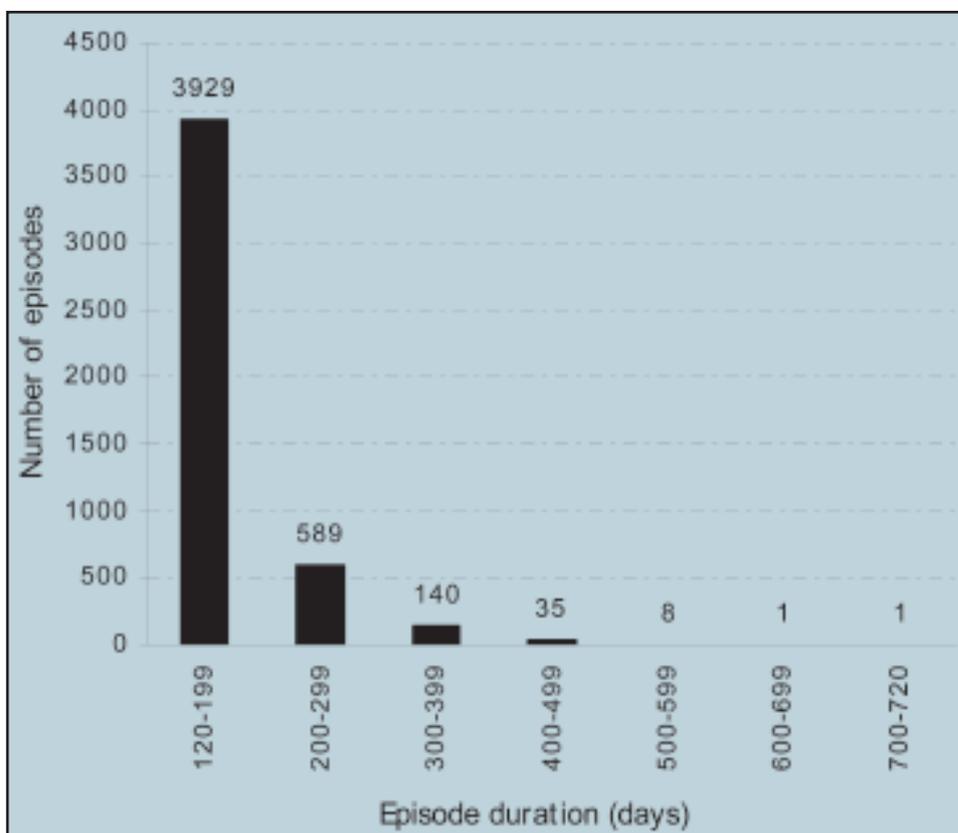


Figure 6. The duration of the 4,703 uncensored brucellosis episodes in Korea during 1 May 2000 to 31 December 2006

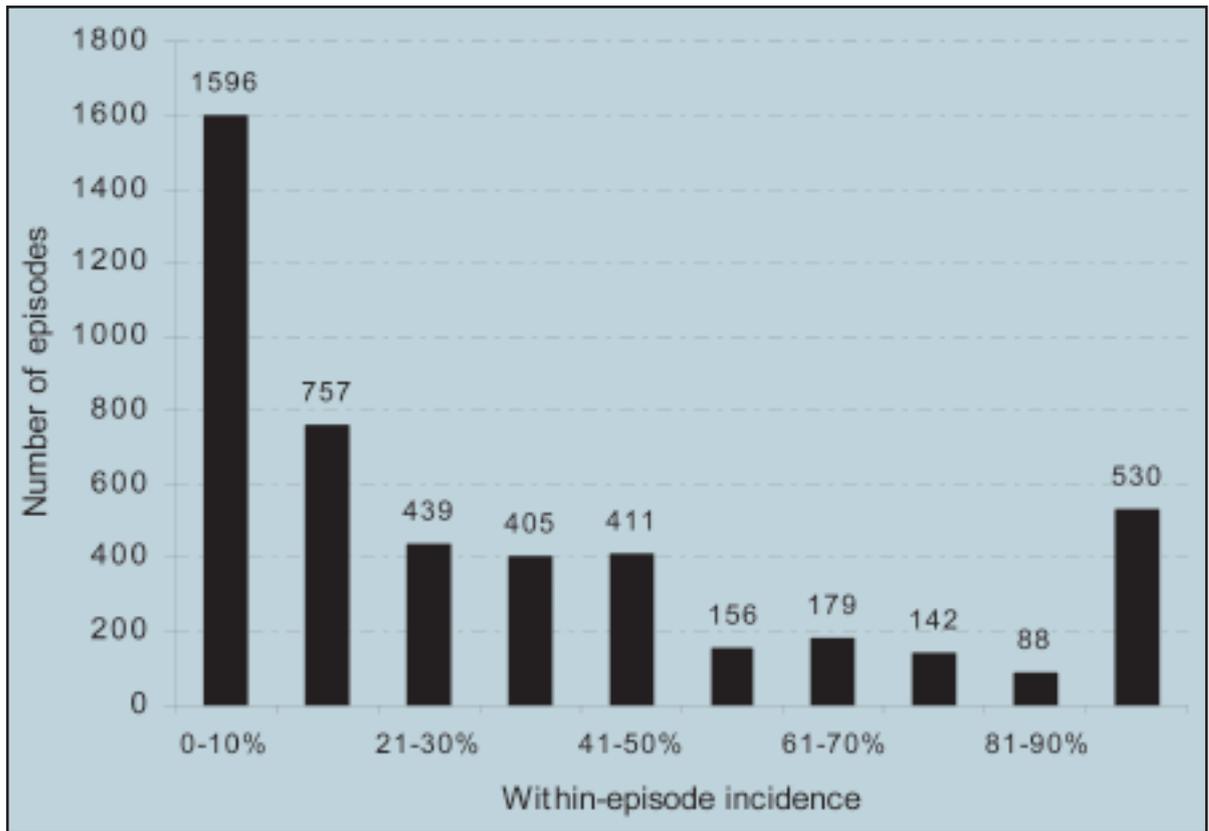


Figure 7. The within-episode incidence in 4,703 uncensored brucellosis episodes in Korea between 1 May 2000 and 31 December 2006

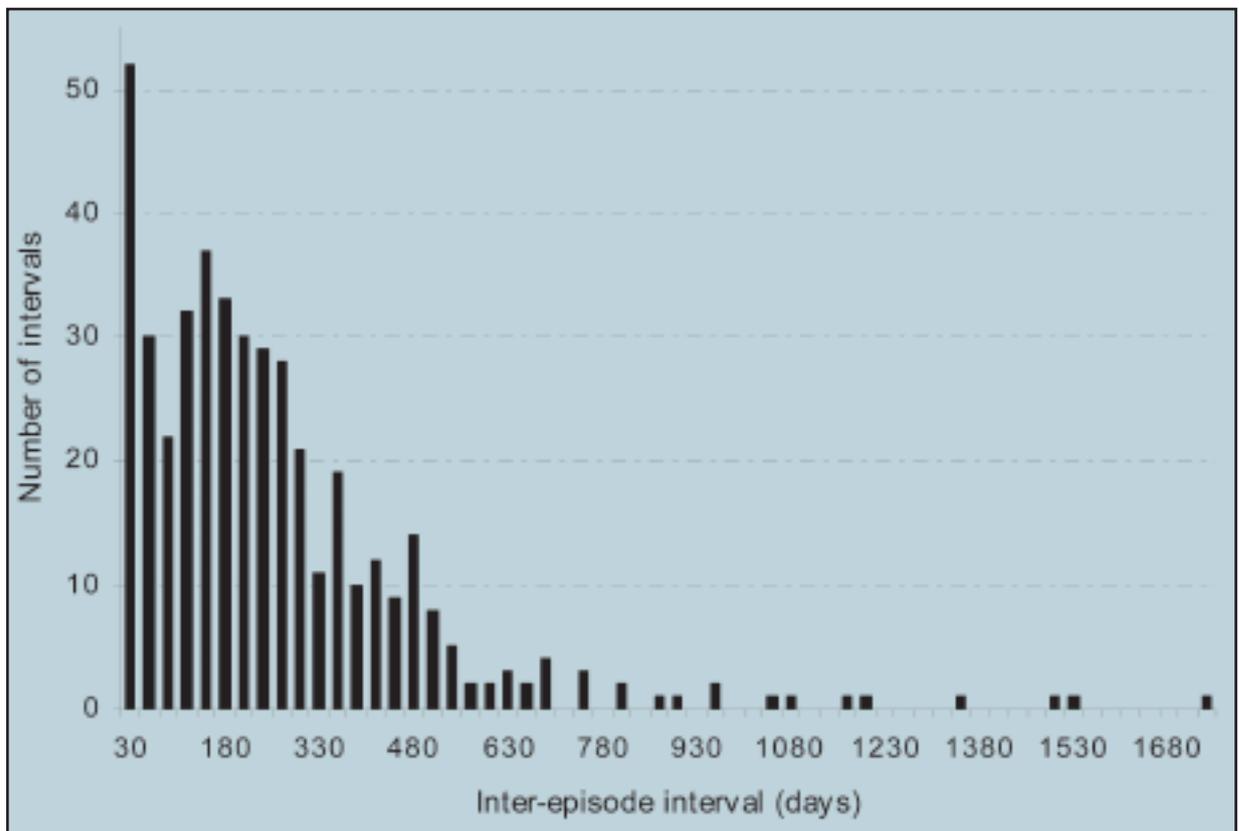


Figure 8. The interval (in days) between 432 brucellosis episodes in Korea between 1 May 2000 and 31 December 2006

## b. Control

There were 4,703 uncensored brucellosis episodes in Korea during 1 May 2000 and 31 December 2006, with an average episode duration of 149.6 days (median 120, minimum 120, maximum 703 days) (Figure 6). Each of these episodes had an average of 1.6 (median 1, minimum 1, maximum 12) positive testing events per episode and, on average, 7.4 (median 2, minimum 1, maximum 193) reactor animals. The average within-episode incidence [number of reactor cattle during the episode divided by the maximum number of cattle at any testing event during the episode] was 33.4% (median 21, minimum 0, maximum 100) (Figure 7). In total, 432 inter-episode intervals were observed in Korea during 1 May 2000 and 31 December 2006 including 407, 22 and 3, preceding a 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> episode, respectively. The average inter-episode interval was 242.3 (median 187, minimum 1, maximum 1719) (Figure 8).

## 3.2 Multivariable analyses

### 3.2.1 Episode duration

#### a. Beef cattle

Multivariable modelling was conducted using data from 4,106 episodes which correspond to 3,962 herds. Since there were few beef cattle tested prior to 2004, YEAR was re-categorised into 3 groups:  $\leq 2004$ , 2005 and 2006. Similarly, since there were few beef cattle that had more than 2 episodes, EPI was categorised into 2 groups (1 and  $\geq 2$ ). The interactions between YEAR x P and EPI x YEAR were not significant, along with the main effects of YEAR and

EPI. From the final model (Table 3), the predicted probability of a prolonged episode occurring was highest in P=1 (Gyeongsangnam province, Busan, Ulsan) and P=2 (Chungcheongbuk province, Daejeon) and lowest in P=7 (Gyeonggi province, Incheon), P=6 (Jeollanam province, Gwangju) and P=3 (Chungcheongnam province). The probability of a prolonged episode ( $>150$  days) increased with increasing herd size and increasing within-herd incidence during the first 30 days of the episode, except when within-herd incidence was  $>50\%$  (Figure 9). The intra-herd correlation from fitting a compound symmetry correlation structure was -0.06.

#### b. Dairy cattle

Multivariable modelling was similarly conducted using data from 595 episodes which corresponded to 530 dairy herds. Since there were few dairy cattle that had more than 2 episodes, EPI was categorised into 2 groups (1 and  $\geq 2$ ). The model would not converge when interactions were tested between YEAR x PROV and HS x I\_30. YEAR was re-categorised into 2 groups (2000-2003, 2004-2006), and the retested interaction was not significant. Similarly, I\_30 was regrouped into 2 groups ( $\leq 3.4$ ,  $>3.4$ ), however, the model would still not converge when the interaction HS x I\_30 was included in the model. This term was not considered further. The interaction between YEAR x EPI was not significant, along with the main effects of EPI and PROV. From the final model (Table 4), the predicted probability of a prolonged episode occurring was significantly higher in 2000 compared to 2006. The risk of a prolonged episode increased with herd size and the incidence at the start of the breakdown. The intra-herd correlation from fitting a compound symmetry correlation structure was -0.05.

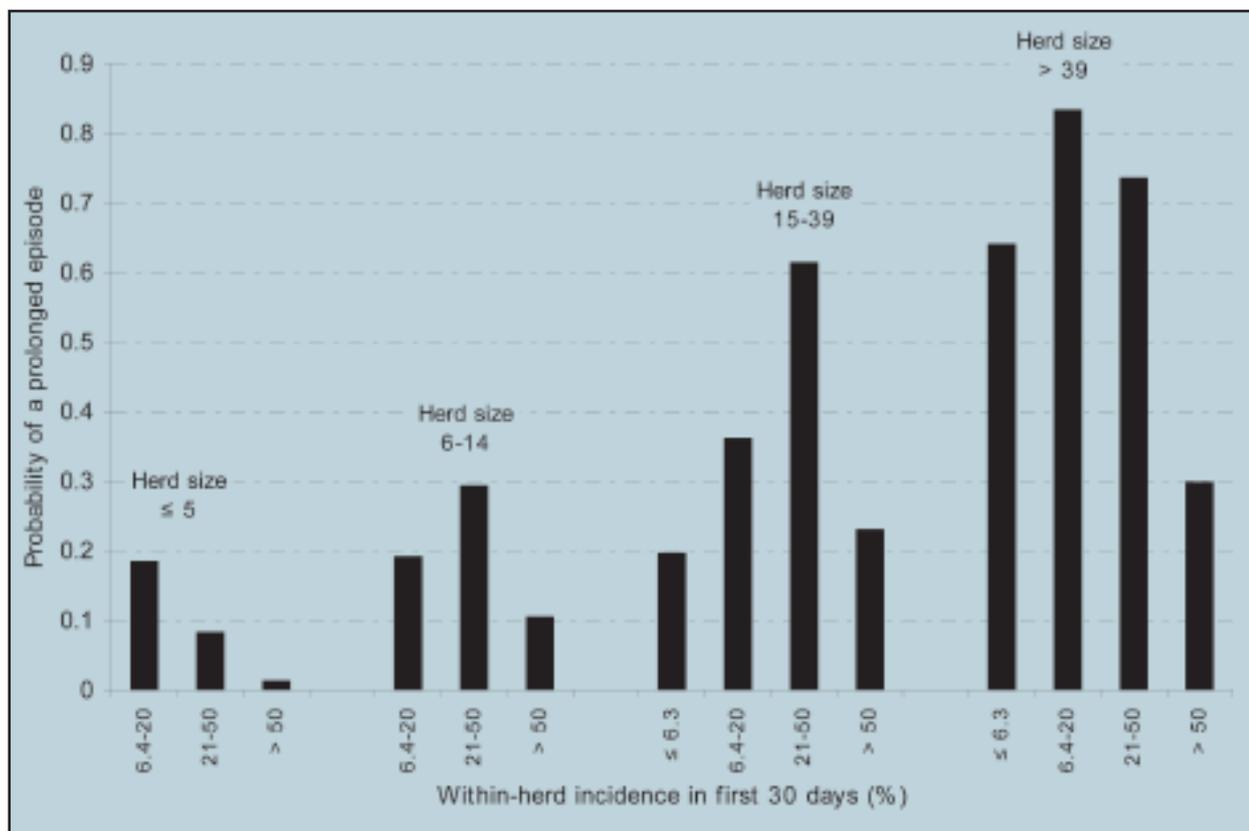


Figure 9. The probability of a prolonged brucellosis episode ( $>150$  days) in Korean beef herds during 2000 to 2006, by herd size and within-herd incidence during the first 30 days of the episode

Table 3. Estimates from the logistic GEE model for variables associated with a prolonged brucellosis episode (a restriction of greater than 150 days) in beef cattle in Korea during 2000 to 2006

Variable	b	SE	P	OR	95% confidence interval	
					Lower	Upper
Intercept	-2.56	0.39	<.001			
HS: Herdsize						
≤5 cattle	0.00	0.00	-	1.00		
6-14 cattle	0.05	0.32	0.883	1.05	0.56	1.95
15-39 cattle	0.92	0.32	0.004	2.51	1.34	4.69
>39 cattle	2.91	0.36	<.001	18.28	9.07	36.83
PROV: Province						
1: Gyeongsangnam province, Busan, Ulsan	0.23	0.20	0.241	1.26	0.86	1.85
2: Chungcheongbuk province, Daejeon	0.13	0.21	0.538	1.14	0.75	1.73
3: Chungcheongnam province	-0.14	0.20	0.479	0.87	0.58	1.29
4: Gyeongsangbuk province, Daegu	0.04	0.20	0.848	1.04	0.70	1.54
5: Gangwon province	0.09	0.23	0.692	1.09	0.70	1.70
6: Jeollanam province, Gwangju	-0.38	0.21	0.065	0.68	0.45	1.02
7: Gyeonggi province, Incheon	-0.51	0.26	0.045	0.60	0.36	0.99
8: Jeollabuk province	0.00	0.00	-	1.00		
I_30: Within-episode incidence (first 30 days)						
≤6.3%	0.00	0.00	-	1.00		
6.4-20%	0.84	0.19	<.001	2.32	1.61	3.34
21-50%	-0.08	0.39	0.848	0.93	0.43	2.00
>50%	-2.04	0.54	<.001	0.13	0.05	0.37
I_30 x HS						
I_30: ≤6.3%, HS: 15-39 cattle	0.00	0.00	-	1.00		
I_30: ≤6.3%, HS: >39 cattle	0.00	0.00	-	1.00		
I_30: 6.4-20%, HS: ≤5 cattle	0.00	0.00	-	1.00		
I_30: 6.4-20%, HS: 6-14 cattle	0.00	0.00	-	1.00		
I_30: 6.4-20%, HS: 15-39 cattle	0.00	0.00	-	1.00		
I_30: 6.4-20%, HS: >39 cattle	0.19	0.26	0.471	1.21	0.72	2.01
I_30: 20-50%, HS: ≤5 cattle	0.00	0.00	-	1.00		
I_30: 20-50%, HS: 6-14 cattle	1.48	0.40	<.001	4.38	2.01	9.56
I_30: 20-50%, HS: 15-39 cattle	1.95	0.40	<.001	7.02	3.23	15.27
I_30: 20-50%, HS: >39 cattle	0.52	0.45	0.242	1.68	0.70	4.03
I_30: >50%, HS: ≤5 cattle	0.00	0.00	-	1.00		
I_30: >50%, HS: 6-14 cattle	2.18	0.57	<.001	8.83	2.89	27.00
I_30: >50%, HS: 15-39 cattle	2.25	0.57	<.001	9.45	3.08	28.97
I_30: >50%, HS: >39 cattle	0.61	0.65	0.350	1.84	0.51	6.62

### 3.2.2 Time to re-restriction

#### a. Beef cattle

Multivariable survival analysis was conducted using data from 4,278 first episodes, including 338 where a second episode also occurred. Since there were few beef cattle tested prior to 2004, YEAR was categorised as ≤2004, 2005 and 2006. All of the main effects were significant, whereas the 2-way interactions were not. There was borderline evidence of non proportionality for PROV, based on both the Schoenfeld residuals test ( $\chi^2 = 25.11$ ,  $df = 15$ ,  $p = 0.049$ ) and the  $-\log(-\log)$  plot. However, PROV was kept as a fixed time effect, as a time varying covariate did not significantly improve model fit (Likelihood Ratio test  $p = 0.056$ ). The final multivariable model is shown in Table 5. The hazard of a second episode increased with herd size, was higher in 2005 compared with other years, and was higher in the southeast (P1: Gyeongsangnam province, Busan, Ulsan) compared to other provinces. The hazard increased as incidence increased, apart from the largest incidence category (>57%).

#### b. Dairy cattle

Multivariable survival analysis was conducted using data from 549 first episodes, including 68 where a second episode also occurred. YEAR was categorised as 2000-2001, 2002-2004, 2005 and 2006. YEAR, PROV and all 2-way interactions were not significant. There was no evidence of non proportionality, based on the Schoenfeld residuals test ( $\chi^2 = 4.26$ ,  $df = 6$ ,  $p=0.641$ ). The final multivariable model is shown in Table 6. The hazard of a second episode increased with herd size. The hazard also increased as incidence increased, apart from the largest incidence category (>16%).

Table 4. Estimates from the logistic GEE model for variables associated with a prolonged brucellosis episode (a restriction of greater than 150 days) in dairy cattle in Korea during 2000 to 2006

Variable	b	SE	P	OR	95% confidence interval	
					Lower	Upper
Intercept	-4.75	0.75	<.0001			
YEAR: Year						
2000	1.26	0.60	0.035	3.53	1.09	11.35
2001	0.55	0.63	0.384	1.73	0.50	5.95
2002	0.91	0.73	0.212	2.47	0.60	10.25
2003	-0.38	0.68	0.570	0.68	0.18	2.57
2004	0.37	0.62	0.548	1.45	0.43	4.87
2005	0.55	0.59	0.349	1.74	0.55	5.53
2006	0.00	0.00	-	1.00		
HS: Herdsize						
≤38 cattle	0.00	0.00	-	1.00		
39-65 cattle	1.82	0.42	<.0001	6.17	2.73	13.95
66-130 cattle	3.99	0.44	<.0001	54.03	23.02	126.82
>130 cattle	6.52	0.58	<.0001	678.04	217.74	2,111.18
I: Within-episode incidence (first 30 days)						
≤1.6%	0.00	0.00	-	1.00		
1.7 - 3.4%	0.69	0.36	0.056	2.00	0.98	4.07
3.5 - 9.1%	1.14	0.40	0.005	3.14	1.43	6.92
>9.1%	1.49	0.42	0.000	4.44	1.97	10.03

Table 5. Estimates from the Cox's proportional hazards model for variables associated with time to episode recurrence in beef cattle in Korea during 2000 to 2006

Variable	Hazard ratio	SE	P	95% confidence interval	
				Lower	Upper
HS: Herd size					
≤5 cattle	1.00	0.00	-		
6-13 cattle	1.44	0.35	0.129	0.90	2.31
14-37 cattle	3.28	0.73	0.000	2.11	5.09
>37 cattle	3.82	0.87	0.000	2.44	5.98
I: Within-episode incidence					
≤9%	1.00	0.00	-		
10-25%	1.20	0.18	0.202	0.91	1.60
26-57%	1.16	0.18	0.320	0.86	1.56
>57%	0.65	0.14	0.044	0.43	0.99
PROV: Province					
1: Gyeongsangnam province, Busan, Ulsan	2.83	0.92	0.001	1.50	5.34
2: Chungcheongbuk province, Daejeon	2.41	0.81	0.009	1.25	4.66
3: Chungcheongnam province	1.60	0.54	0.164	0.83	3.10
4: Gyeongsangbuk province, Daegu	2.01	0.67	0.035	1.05	3.85
5: Gangwon province	1.23	0.46	0.574	0.60	2.55
6: Jeollanam province, Gwangju	1.52	0.52	0.226	0.77	2.98
7: Gyeonggi province, Incheon	2.26	0.85	0.030	1.08	4.74
8: Jeollabuk province	1.00	0.00	-		
YEAR: Year					
≤2004	0.60	0.17	0.070	0.34	1.04
2005	1.13	0.15	0.368	0.87	1.48
2006	1.00	0.00	-		

Table 6. Estimates from the Cox's proportional hazards model for variables associated with time to episode recurrence in dairy cattle in Korea during 2000 to 2006

Variable	Hazard ratio	SE	P	95% confidence interval	
				Lower	Upper
<b>HS: Herd size</b>					
≤37 cattle	1.00	0.00	-		
38-65 cattle	1.69	0.71	0.217	0.74	3.87
66-127 cattle	1.41	0.62	0.429	0.60	3.33
>127 cattle	2.93	1.09	0.004	1.41	6.09
<b>I: Within-episode incidence</b>					
≤3%	1.00	0.00	-		
4-6%	1.24	0.47	0.569	0.59	2.63
7-16%	1.72	0.57	0.100	0.90	3.30
>16%	0.48	0.22	0.116	0.20	1.20

#### 4. DISCUSSION

Korea is currently experiencing a serious outbreak of bovine brucellosis, following a rapid rise in the number of brucellosis reactors from 2003 (Figure 1). Infection was introduced into Korea in the late 1950s, and until very recently was an ongoing, but relatively minor, problem in the national dairy herd (Wee et al., 2008). Since 2004, however, the authorities have detected a large (and increasing) number of beef reactors, and a smaller rise in dairy reactors. In 2006, there were 23,210 beef reactors (91.2% of all bovine reactors that year, from a national beef herd of approximately 2 million animals) and 2,244 dairy reactors (8.8% of reactors, from a national dairy herd of approximately 465,000 animals). Wee et al. (2008) have highlighted a range of factors associated with the spread of infection from dairy to beef animals in Korea, including the increasing problem of brucellosis in the dairy sector, the close proximity between many dairy and beef farms, the use of dairy cattle in beef artificial breeding programmes and the establishment of colostrum banks (drawing from dairy herds) to assist in calf raising within Korean beef herds. In Korea, most cattle are held under 'zero-grazing' management.

This work was conducted using an episode-based approach. Within the constraints of the data available, this allowed us to disentangle progress in the very different activities of surveillance (detection of new cases) and control (clearing infection from known infected herds). This study has also enabled us to critically evaluate AIMS, the national database, highlighting areas where modifications may assist with surveillance and control efforts into the future. AIMS currently maintains only a subset of the data generated as part of the national disease control effort; the balance is currently held at a number of regional centres throughout the country. As a result, a number of strategies were developed to fill information gaps in the AIMS data, including the calculation of end-of-episode, in accordance with national policy, after identifying periods of freedom following each positive testing event. During the study period, farm details were recorded in AIMS without georeferencing, which limited the potential for spatial analysis, and using owner and address fields rather than an agreed national farm code, which proved problematic during the creation of the episode file. Each of these issues is currently under discussion. Implementation of a national animal identification and traceability system, which is currently underway, is expected to solve many of these issues.

The results from 2004-2006 are suggestive of rapid spread of infection to previously non-infected farms. Most of the cases during this period were beef animals, whereas earlier cases were mainly confined to the dairy sector. However, in large part this

increase can be directly attributed to increased surveillance effort, noting that there had been minimal surveillance for brucellosis in beef cattle prior to 2004 (Wee et al., 2008). As a result of the current epidemic, there have been substantial changes to brucellosis control policy and operations in the beef sector. Once these changes are fully implemented, including the introduction of annual testing for all female beef cattle greater than 12 months of age, it will be possible to accurately determine the full extent of the problem. Nonetheless, it is likely that the brucellosis epidemic is a recent phenomenon, given the close temporal association between the increases in human and cattle cases. Further, the worsening situation in dairy cattle in recent years would be consistent with recent spillover of infection from beef cattle. In Korea, beef and dairy cattle are generally managed under a zero-grazing management system, at times in common housing. As the surveillance effort is broadened to include all animals at risk, it will be important to maintain a continuous appraisal of surveillance efficiency, to assess the effectiveness of changes to national disease control policy. An ongoing measurement of  $R_h$  (the reproductive ratio between herds; Bouma et al., 2003) offers one means to monitor progress.

In Korea, brucellosis outbreaks have generally been managed through partial, rather than complete, depopulation of infected herds. Herds are re-bled at intervals, and test positive animals are removed. This control strategy appears to have been effective, leading to a rapid clearance of infection, on most infected farms. In 3,137 (66.6%) and 3,313 (70.4%) episodes, the duration of restriction was 120 days (the minimum length of restriction prior to 15 July 2006, following a single testing event) and no greater than 150 days, respectively. In both beef and dairy herds, we identified increasing herd size and increasing outbreak size (when considering episode duration, measured as within-herd incidence during the first 30 days of the episode; time to re-restriction: within-herd incidence throughout the episode) as the two key risk factors for problems with disease control, either through an increase in the odds of an extended episode (>150 days) or of the hazard of a further episode following de-restriction. Control is particularly problematic in large herds, particularly where a substantial number of infected animals are detected at the initial bleed. Note that the decreasing risk associated with high within-episode incidence (Tables 3 and 5, Figure 9) is the result of national policy: full depopulation is strongly encouraged if a substantial number of animals are identified as reactors at the start of an episode. These results are consistent with our understanding of the epidemiology of brucellosis. As part of a detailed review of factors associated with the dynamics of *Brucella* spp. infection, Salman and

Meyer (1984) highlighted the importance of population density, herd size, type and breed of animals (dairy or beef) and the type of husbandry system. In Kenya, increasing herd size and location (Kadohira et al., 1997), and in Eritrea, herd type (potentially a proxy for cattle purchases) and stocking density (cattle/m<sup>2</sup>) (Omer et al., 2000) were identified as important risk factors for brucellosis in cattle populations.

## 5. CONCLUSION

This work provides a detailed insight into the national brucellosis eradication programme in Korea, in particular the effectiveness of current surveillance and control measures. It is anticipated that this work will continue into the future, and should assist both policy-makers and field veterinarians to improve the effectiveness of national control efforts. Several additional studies are anticipated, focusing on the measurement of, and risk factors for, between-herd spread.

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