ROSLIN

Genetic correlations between susceptibility to *Mycobacterium bovis* infection and performance in Irish Holstein Friesian dairy cows

M.L. Bermingham, S.J. More, M. Good,
A.R. Cromie, I. M. Higgins and D.P. Berry

THE UNIVERSITY OF EDINBURGH · eagasc Agriculture and Food Development Authority · UCD DUBLIN · Department of Agriculture, Fisheries and Food An Roinn Talmhaíochta, Iascaigh agus Bia · ERAD Eradication of Animal Disease Board · R(D)SVS

Introduction

Bovine tuberculosis (bTB)

- Infectious respiratory disease
- wide range of animals
- including man
- tubercles (g*ranuloma)*

Mycobacteria bovis

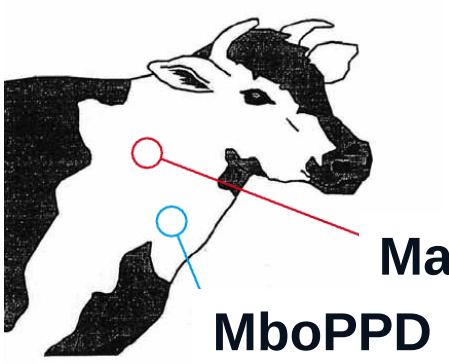
- The primary agent of bTB

Introduction

Active surveillance

- **Single intradermal comparative tuberculin test (SICTT)**

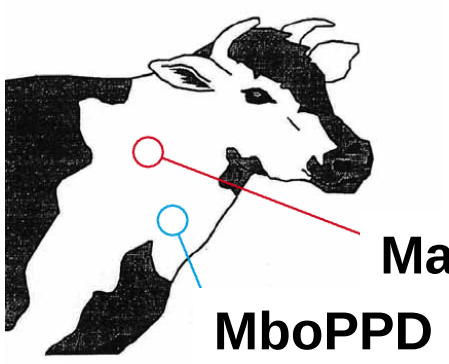
- **Annually in Republic of Ireland (ROI)**



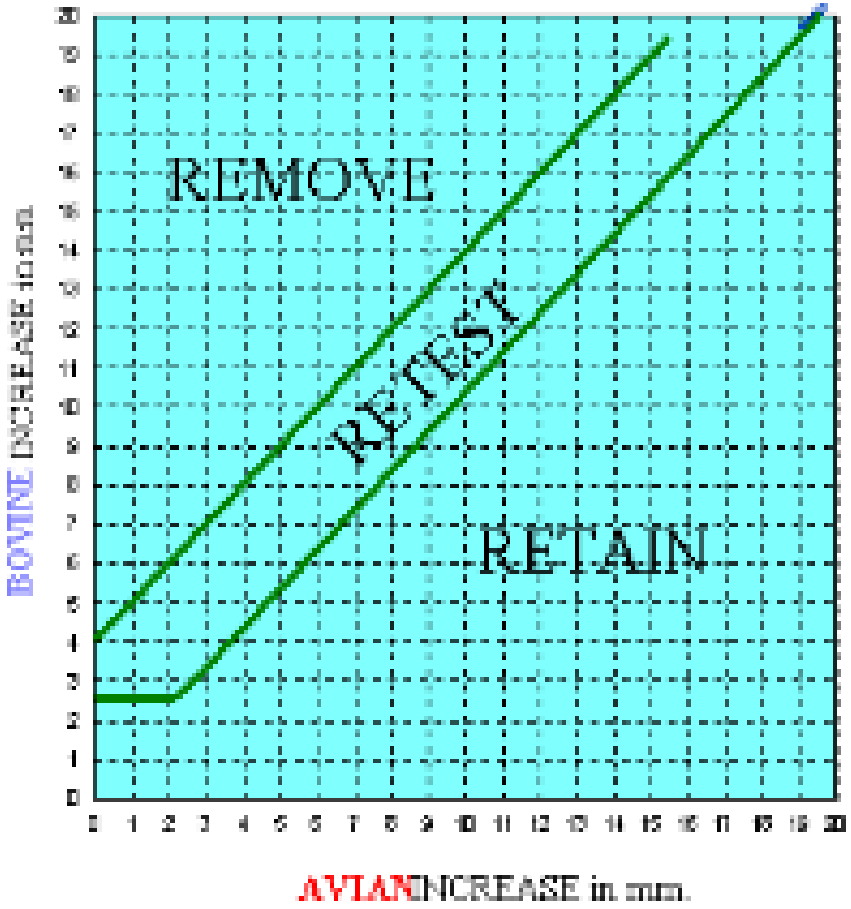
M. bovis purified protein derivative - MboPPD
***M. avium* purified protein derivative - MavPPD**

Introduction

SICTT Interpretation



Standard Interpretation



Introduction

Non bTB-free status

- Ireland/other countries
- Transmission
  - wildlife-to-cattle
  - cattle-to-cattle

Introduction

Genetic selection

- ↑ resistance to bTB in cattle
- complement eradication efforts

Two recent studies

- Exploitable variation exists among GB and ROI HF dairy cows for resistance to tuberculosis

Heritabilities:	GB data	ROI data
Responsiveness to the SICTT	0.16 (0.012)	0.14 (0.025)
Abattoir-confirmed *M. bovis* infection	0.18 (0.044)	0.18 (0.041)
	Brotherstone et al. 2010	Bermingham et al. 2009

Genetic correlation ~1.0

- ROI dairy cows
- ↑ resistance to confirmed *M. bovis* infection
- via SICTT data

Introduction

Genetic correlations

- **-ve: susceptibility to confirmed *M. bovis* infection**
  vs. milk yield (UK)
- **antagonistic: risk of clinical mastitis**
  vs. milk yield
- **inconsistent: susceptibility to other diseases**
  vs. performance

Impact of selection of economically important traits

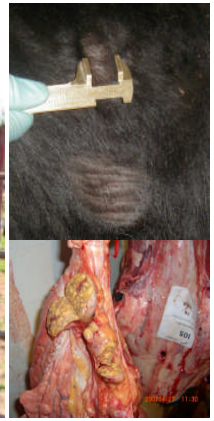
- Genetic resistance to *M. bovis* infection

- ROI dairy cattle needs to be determined

R(D)SVS

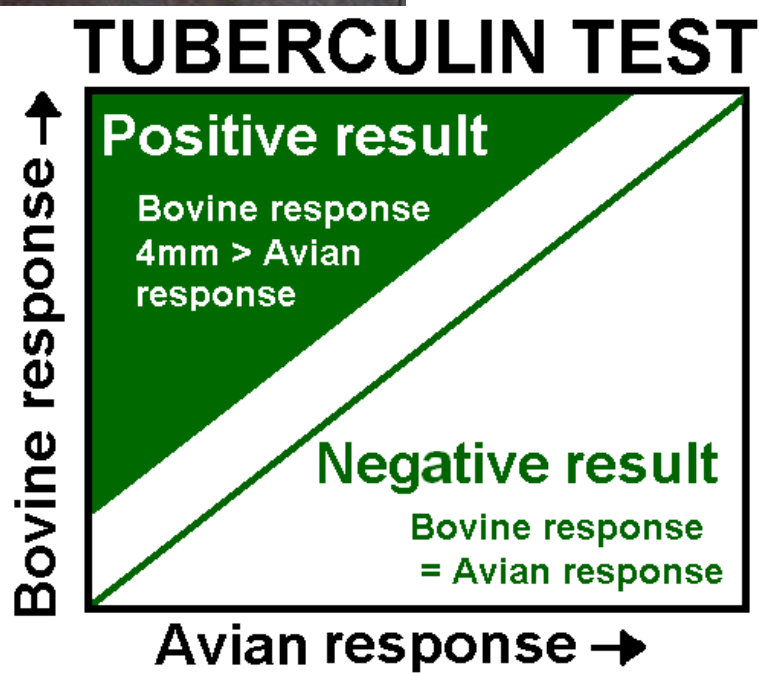
Objective

- **To estimate the genetic correlations between susceptibility to *M. bovis* infection and economically important traits**

Materials and Methods

Measure of bovine susceptibility *M. bovis* infection



Materials and Methods

Eight performance traits

- **Milk yield**
- **Fat yield**
- **Protein yield**
- **Somatic cell score**
- **Calving interval**
- **Survival**
- **Body condition score**

SICTT responsiveness

Data

- 108,000 SICTT herd summary records
- 2,000,000 SICTT results
- November 2000 to December 2007

Data Edits

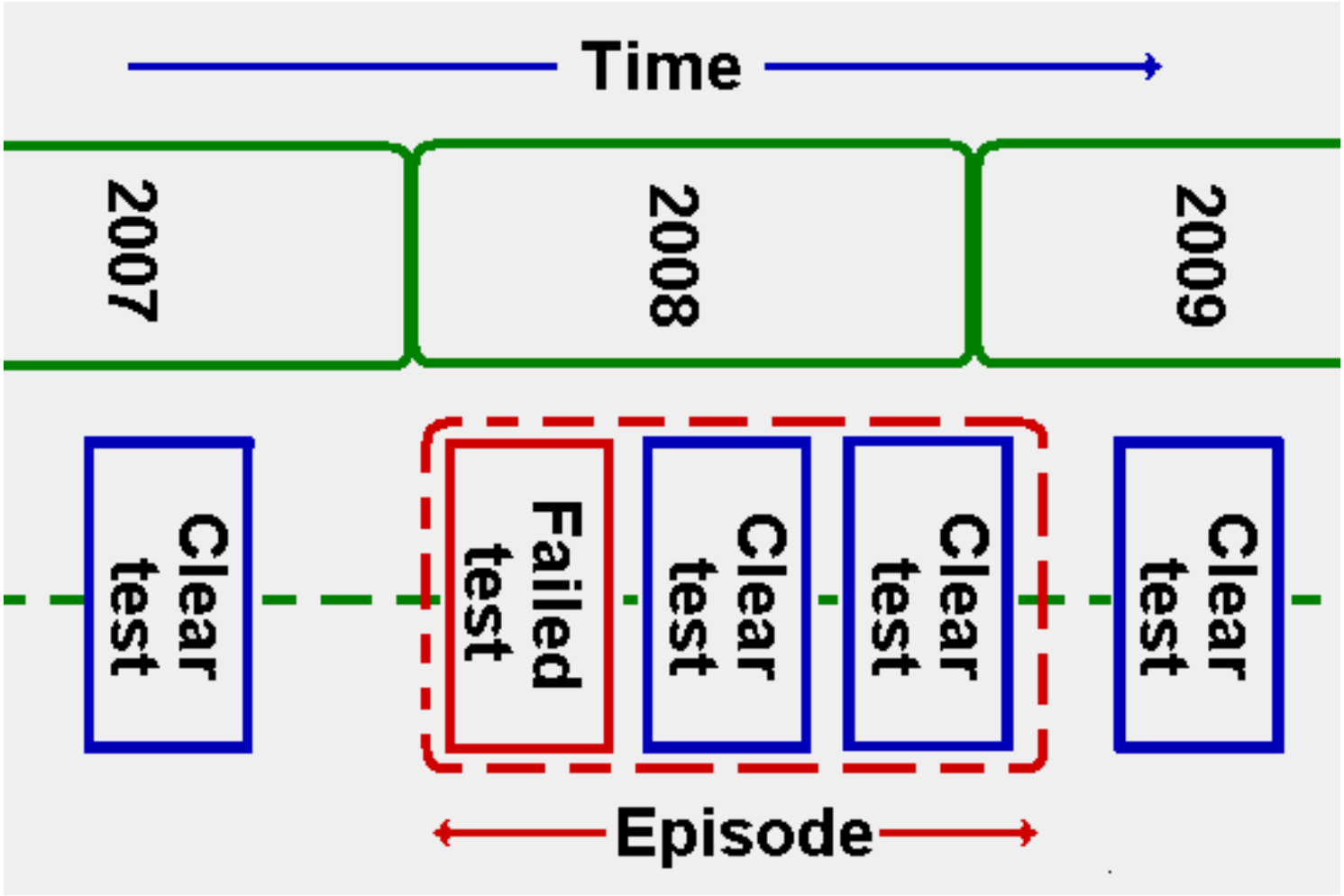
- Episodes
  - High likelihood of exposure to *M. bovis*
  - SICTT herd summary records

    → divide data

SICTT responsiveness

ROSLIN

Episode



SICTT responsiveness

Data Edits

- **Deleted animals**
  - No known pedigree data
  - Outside the normal age for a given parity
  - Inconclusive SICTT results
  - Moved into the herd - 6 weeks of SICTT

- **Retained episodes**
  - 1 standard reactor
  - 10 or more animals

Data records

- 17,178 SICTT responsiveness
- 598 episodes

Performance traits

ROSLIN

Data

- 3,600,000 305-day milk, fat & protein yield & SCC
- 6,500,000 calving date and calving interval (CI)
- 86,000 1st parity body condition score (BCS)
  - Irish cattle breeding federation database
  - calvings January 1985 to December 2007

Data Edits

- Cow survival lactation 1-2, 2-3 & 3-4
- Deleted Cows
  - CIs < 300 > 800 days
  - Unknown parity
  - <15 months of age
  - Outside the normal age for a given parity
  - <75% Holstein-Friesian
  - No known sire

Performance traits

Data records

- **105,064 production**
  - **2,185 *M. bovis* infection records**
- **112,337 CI**
  - **2,389 *M. bovis* infection records**
- **104,044 survival**
  - **2,895 *M. bovis* infection records**
- **57,250 BCS**
  - **354 *M. bovis* infection records**

Analysis

Genetic & residual (co) variance components

- **Responsiveness to the SICTT**
  vs. performance
  - **bivariate linear-linear sire model**
  - **bivariate threshold-linear sire models**
- **Statistical package ASREML**
- **Significance: Likelihood ratio test**

Results

Trait	Responsiveness to the SICTT		
	Parity 1	Parity 2	Parity 3
Milk	0.23 (0.14)	0.24 (0.14)	0.13 (0.16)
Fat	0.32 (0.14)	0.39 (0.13)	0.23 (0.15)
Protein	0.16 (0.15)	0.32 (0.14)	0.06 (0.16)
SCS	-0.34 (0.14)	0.11 (0.15)	-0.14 (0.17)
CI	-0.07 (0.18)	0.00 (0.22)	-0.18 (0.29)
Survival	-0.08 (0.22)	-0.17 (0.23)	-0.62 (0.22)
BCS	0.36 (0.14)		

Significance of the difference from zero; $P < 0.05$

Results

Trait	*R*esponsiveness to the SICTT	
	LLM	TLM
Fat	0.39 (0.13)	0.37 (0.13)
SCS	-0.34 (0.14)	-0.29 (0.14)
Survival	-0.62 (0.22)	-0.67 (0.21)
BCS	0.36 (0.14)	0.35 (0.13)

The test of significance: t-test; P> 0.05

Discussion

- **Results from this study**

  - Based on

  → large datasets

  → alternative statistical approaches

  - Selection for

  → ↑ survival may indirectly ↓

  → ↓ SCS & ↑ fat production & BCS

  - **↑ susceptibility to *M. bovis* infection**
  - **ROI Holstein Friesian dairy herd**

Acknowledgements

Financial support from ERAD and BBSRC is gratefully acknowledged