

Bovine Tuberculosis Workshop

9-10 May 2013



University
of Glasgow



Organizers:

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Liliana Salvador (Liliana.Salvador@glasgow.ac.uk)

AP

Rowland Kao

Physics

- Mathematical models
- Methodological development
- Livestock networks and network analyses
- Bayesian Likelihood parameter inference
- Integration of molecular epidemiology
- Use of combined mathematical and genetic data ('phylodynamics')

AGENDA

Thursday, May 9th

12.00	Transport from Kelvin Hotel (Glasgow)
12.05	Transport from Belhaven Hotel (Glasgow)
12.45	Arrival and Lunch
13.45	Introductions including one slide per person/group
14.30	<u>Session 1</u> <i>Different stokes for different folks: tailoring risk-based surveillance for bovine Tuberculosis in cattle</i> Speaker: Paul Bessel Discussion about the various aspects of risk-based surveillance and how it can be tailored
15.45	Report back from first breakout
16.15	Coffee break
16.45	<u>Session 2</u> <i>Wildlife: are badgers really different?</i> Speakers: Clare Benton/ Aurelie Courcoul What makes badgers a (potentially) very good reservoir for bTB
18.15	Report back from second breakout
18.45	End of first day
19.00	Drinks
20.00	Dinner
22.30	Transport to Glasgow (Belhaven & Kelvin Hotels)

AGENDA

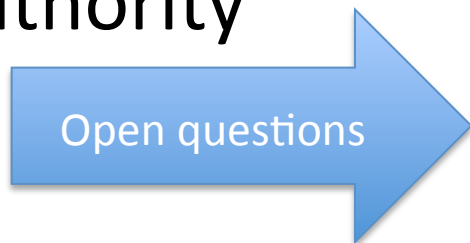
Friday, May 10th

08.00	Transport from Kelvin Hotel
08.05	Transport from Belhaven Hotel
08.45	Arrival of off-site participants
09.15	<u>Session 3</u> <i>What can whole genome sequencing do for you?</i> Speaker: Michael Deason Illustration of what we know about the resolution this technique offers and how it can improve our research
10.30	Report back from third breakout
11.00	Coffee break
11.20	<u>Session 4 (Final Session)</u> <i>The people speak: results from a survey of workshop participants</i> Speakers: Liliana Salvador/Rowland Kao Results of the survey sent to participants. Discussion about the most relevant questions
12.35	Report back from final breakout and summation
13.15	Lunch and departure (including transportation back to West End, Glasgow)
14.30	Transport to Belhaven Hotel

Adrian Muwonge	2	
Alberto Allepuz	1	
Andrew Conlan	5	
Andy Mitchell	4	
Ariadna Garcia Saenz	3	
Aurelie Courcoul	5	
Clare Benton	2	
Colin Birch	3	
Darrell Abernethy	1	rapporteur
Dez Delahay	1	
Edith Authie	1	
Fraser Menzies	4	rapporteur
Jan Muskens	3	
Jane Gibbens	4	
Javier Bezos	2	
Julian Drewe	3	
LI Siben	5	
Marian Price Carter	1	
Nick Coulson	2	
Paul Bessell	1	
Philip P Robinson	4	
Ricardo de la Rúa-Domenech	3	rapporteur
Robin Skuce	4	
Ron Crump	5	
Ruth Rushton	4	
Susanna Sternberg Lewerin	2	rapporteur
Tony Goodchild	3	
Tony Wilsmore	2	
William Wint	5	rapporteur

SOME GENERAL AIMS

- Bringing together people from different backgrounds, with disparate paradigms and ideas
- Bring forward 'grey literature' and expert opinions not found in peer reviewed publications
- Leading to arguments based on reason NOT authority



Hypothesis generation

Risk-based surveillance

What?

- Quantitative assessment of risk of herd breakdown
- Exploitation of statistical properties to target surveillance

Why?

1. To save money (same job, but cheaper)
2. To minimise onward risk (better job)
3. To identify problem herds (changing situations)
4. Other?

Things to think about

- What are the critical challenges to designing risk-based surveillance
- What are the critical challenges to implementing risk-based surveillance
- What are the critical risks associated with it, if implemented (give examples, if possible)?
- Give examples of risk factors and where they might be appropriate (contrast countries, situations, etc.)?

M. bovis in wildlife

- Why badgers?
- Perspectives on wildlife from other countries
 - Is the problem in GB special?
 - Does maintenance of bTB under test and slaughter require a reservoir host?
 - What other hypotheses may fit the available data?

Things to think about

- What are the main ways of identifying potential reservoirs?
- Why sometimes a reservoir and sometimes not?
- What is the signature of a reservoir host? i.e. when do you know when you've got one?
- What makes some potential reservoirs different than others?

Whole Genome Sequencing of *M. bovis*

- What are the scientific questions that WGS can be used to address in different ways?
- What can it do to change our understanding of the epidemiology
- What can it do to change our disease control paradigms?

Results of the survey

- Get an impression of what is important to people at the workshop
- Focus last discussion around an aspect of this