Te Kunenga ki Pūrehuroa

Massey University

JOHNES DISEASE RESEARCH CONSORTIUM

JDRC Epidemiology 5.2 Modelling

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Milestones

- Test validation
  - **Individual deer**
  - Pooled faecal culture and Elisa (sheep, cattle, deer)
- Multispecies prevalence over time
- Transmission between farms: network analysis

Test evaluation: individual deer

- Reasons
  - Monitoring: herd classification based on normal yearling deer
  - Need test performance at animal level first
  - Adjusting apparent prevalence of baseline survey
- Methods
  - 2 populations: NI, SI
  - 3 tests: IFC, Paralisa
  - Latent class analysis
    - Panel of gold standard tests likely biased towards highly infected/affected animals
    - No gold standard in live animals
    - Bayesian methods require lower sample size

Results from IFC and ELISA

737 paired samples (20/herd):

South Island: 20 herds, 401 animals

North island: 18 herds, 336 animals

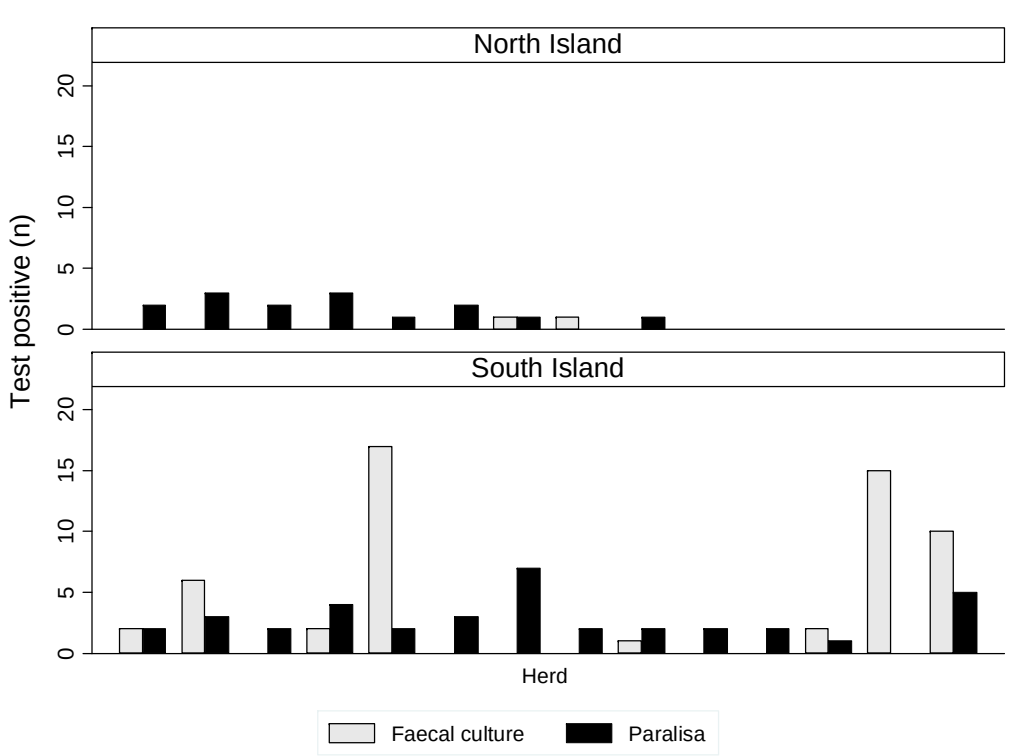
North Island

	IFC +	IFC-
ELISA +	1	14
ELISA -	1	320

South Island

	IFC +	IFC -
ELISA +	10	27
ELISA -	45	319

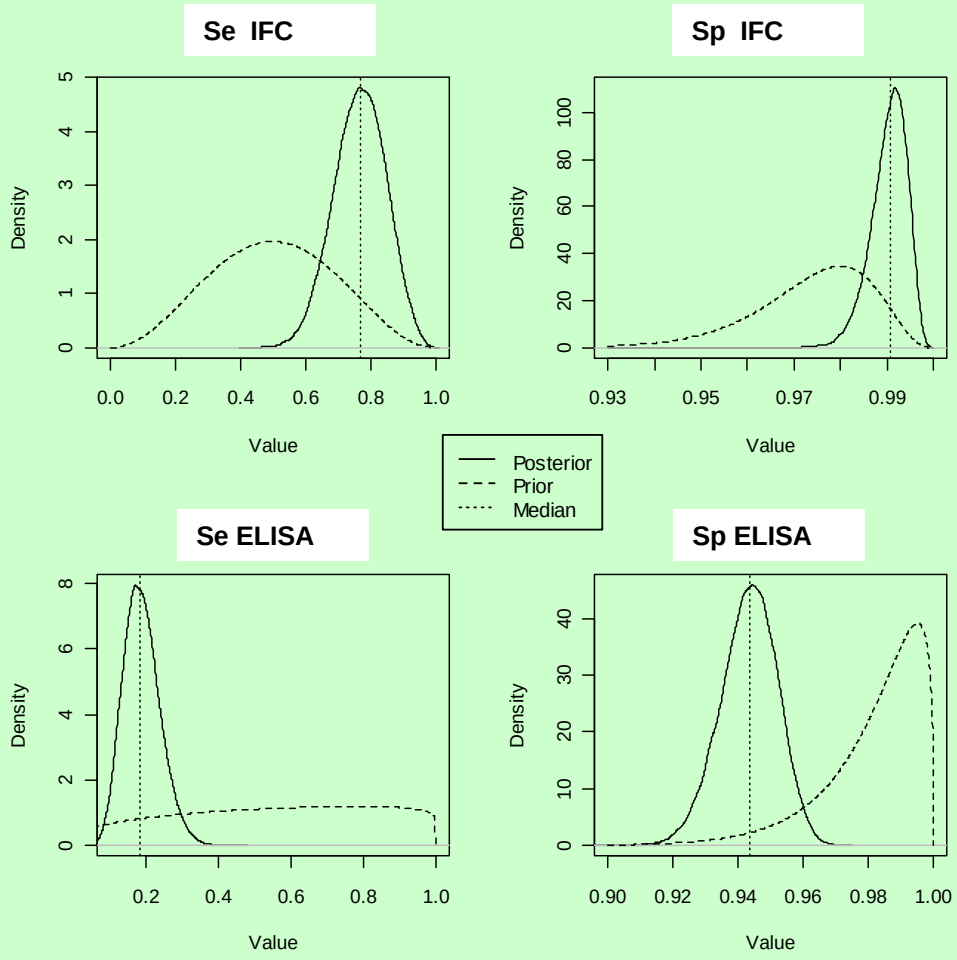
Herd-level results



IFC pos = 2 herds in NI, 8 herds SI

ELISA pos = 8 herds NI, 13 SI

Prior and posterior distributions



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Herd test performance

	Test Protocol	Sheep	Beef Cattle	Deer
H-sensitivity	PFC normal	80% (68-89)	57% (44-69)	52% (33-78)
	PFC normal + suspect	88% (79-94)	77% (66-86)	65% (45-89)
	PFC normal + Elisa	98% (95-100)	97% (93-99)	87% (68-99)
	PFC normal+suspect+Elisa	99% (97-100)	99% (95-100)	91% (73-99)
H-specificity	PFC normal	100% (98-100)	99% (98-100)	99% (95-100)
	PFC normal + suspect	99% (97-100)	98% (97-99)	98% (95-99)
	PFC normal + Elisa	82% (75-87)	97% (92-99)	43% (27-56)
	PFC normal+suspect+Elisa	81% (74-87)	97% (91-99)	43% (27-56)

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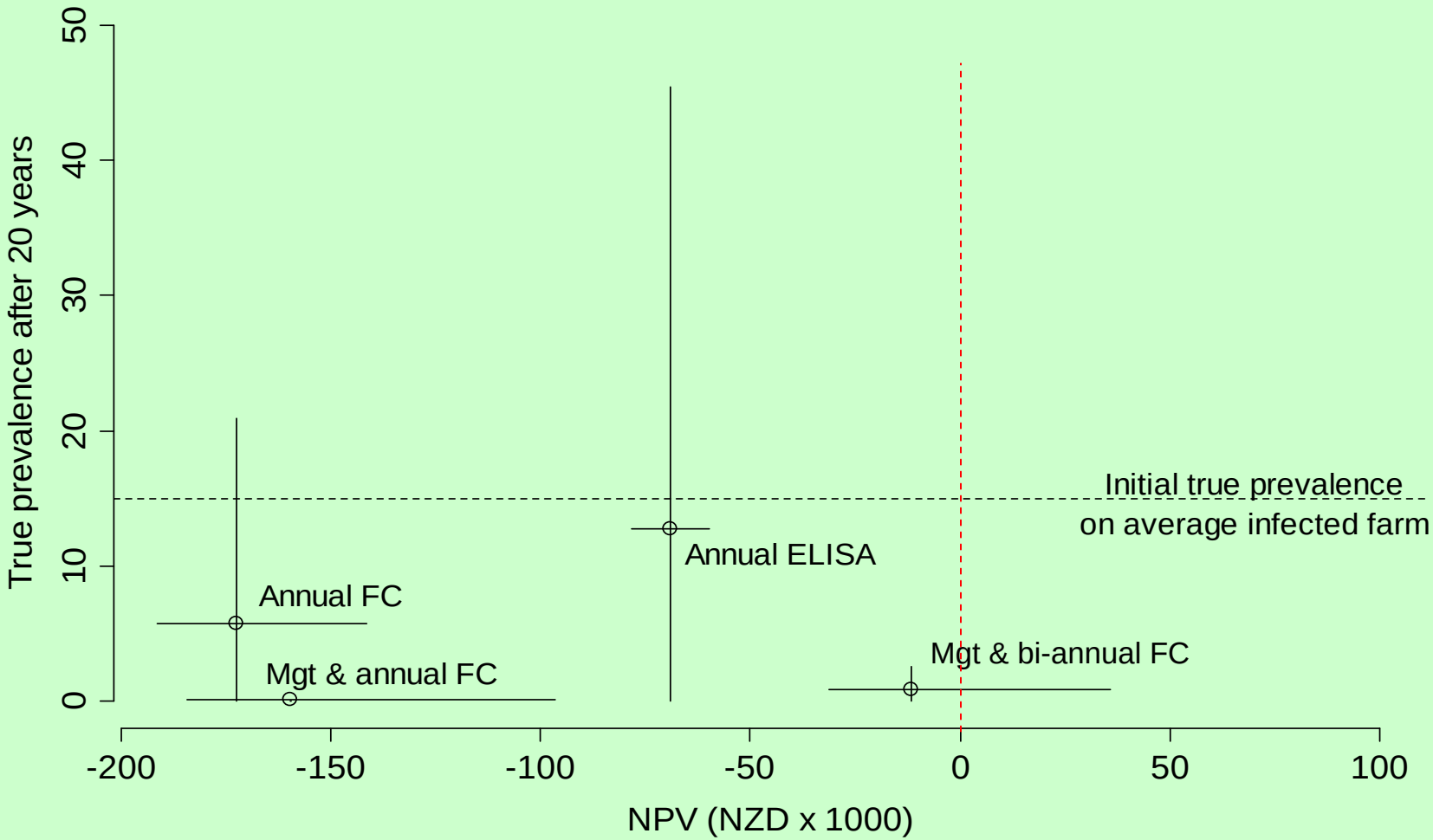
- **Multispecies prevalence simulation over time**
- Transmission between farms

Background

- Aim: estimate impact of management change on the prevalence of animals
  - infected
  - shedding
  - affected
  - clinically diseased
- Infection routes
  - (pseudo-)vertical
  - Faecal-oral from environment (= *pasture*)
    - within and across species
    - from other farms

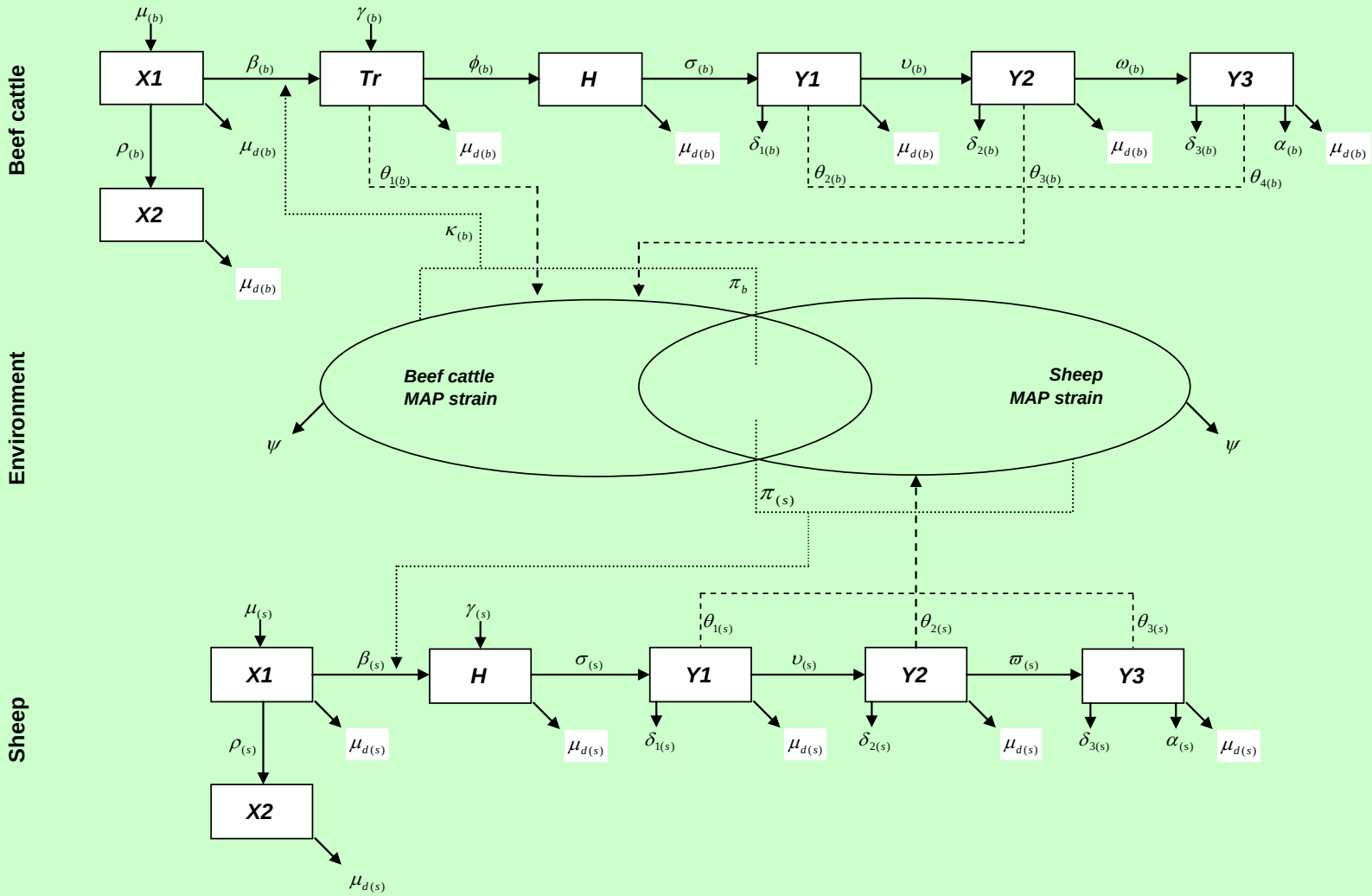
Mathematical modelling (20 yrs.)

Prevalence vs. NPV (dairy)

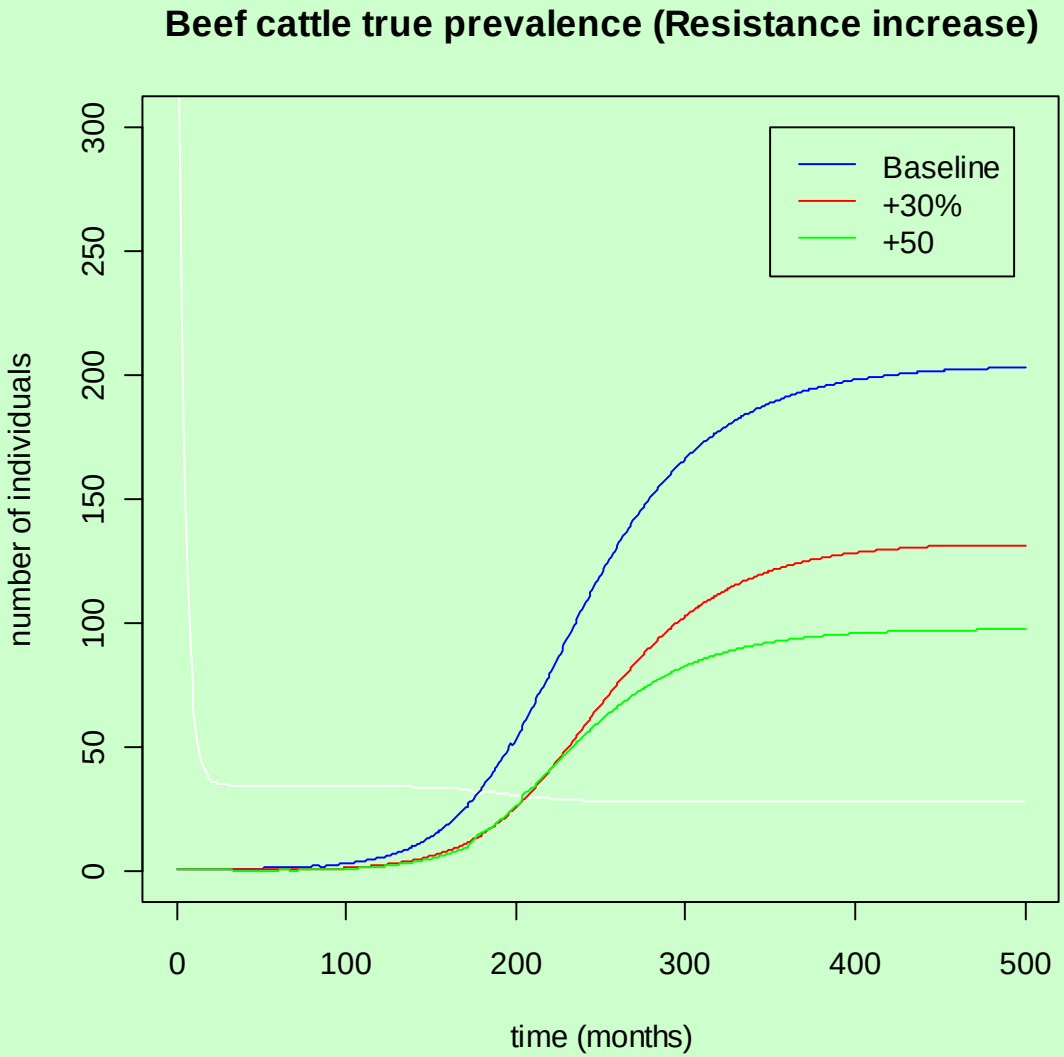


(Norton et al 2008)

Structure


Beef cattle
Environment
Sheep
X1
X2
Tr
H
Y1
Y2
Y3
Beef cattle MAP strain
Sheep MAP strain

Outputs


Beef cattle true prevalence (Resistance increase)
Baseline
+30%
+50
number of individuals
0
50
100
150
200
250
300
0
100
200
300
400
500
time (months)

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- **Transmission between farms**

Network analysis

- Movement data received
  - Covering 12 months 2009/10
- Draft protocol
- First results expected by end June

Key points:

- Milestone 5.2 on target
- Prevalence model requires robust testing, some modifications
- Required information
  - Sub-clinical production effects
  - Predictive quality of diagnostic tests (T&C)
  - Discriminatory power of STs

Acknowledgements

- AgRes and DRL for testing samples
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