

S. J. Lycett¹, G. Russell², G. Gunn³, R. Zadoks^{1,2}, R. R. Kao¹

¹Boyd Orr Centre for Population and Ecosystem Health, University of Glasgow,

²Moredun Research Institute, ³Scotland's Rural University College

Introduction

- BVD is endemic in Scotland and the rest of GB
- Calves may become persistently infected in utero
- Movement of infected animals spreads the disease
- BVD Eradication Programme in Scotland

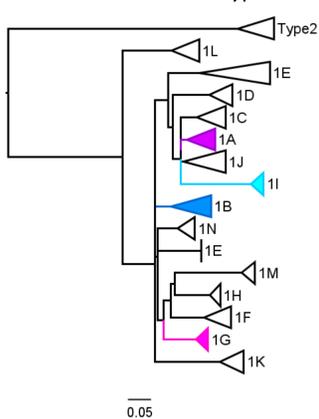
Bovine Viral Diarrhoea Virus

- Pestivirus genus includes BVDV, Border Disease Virus and Classical Swine Fever Virus
- Single Stranded positive sense RNA virus
- One open reading frame coding for a polyprotein
- Evolutionary rate approximately 2×10^{-3} per site per year

5'UTR | Npro | Structural Proteins | Non Structural Proteins

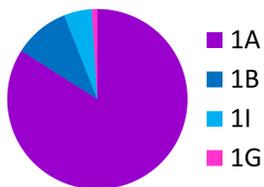
Sequences from GB

5'UTR Tree of BVDV Types



- Isolates submitted for field testing are sequenced
- 600 isolates 2011-2014
- 5'UTR and Npro regions sequenced

Types found in GB



Principles of Phylodynamics

Forensic Scenario

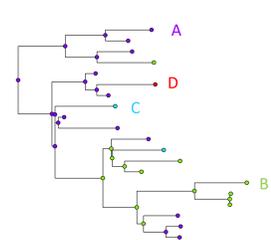
- For outbreak situations
- Who infects who?
- Dense sampling required

Transmission Pattern

- For endemic diseases
- Quantify transmission routes
- Surveillance required

Discrete Traits Model

Tree with Location Traits

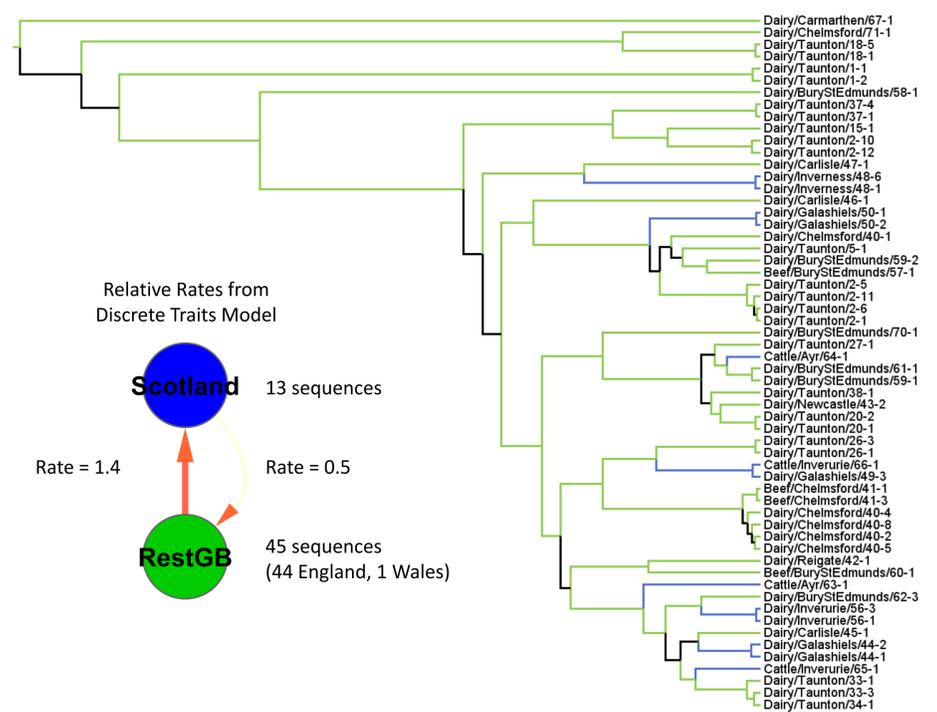


Transition Rate Matrix

	A	B	C	D
A	-	R(A-B)	R(A-C)	R(A-D)
B	R(B-A)	-	R(B-C)	R(B-D)
C	R(C-A)	R(C-B)	-	R(C-D)
D	R(D-A)	R(D-B)	R(D-C)	-

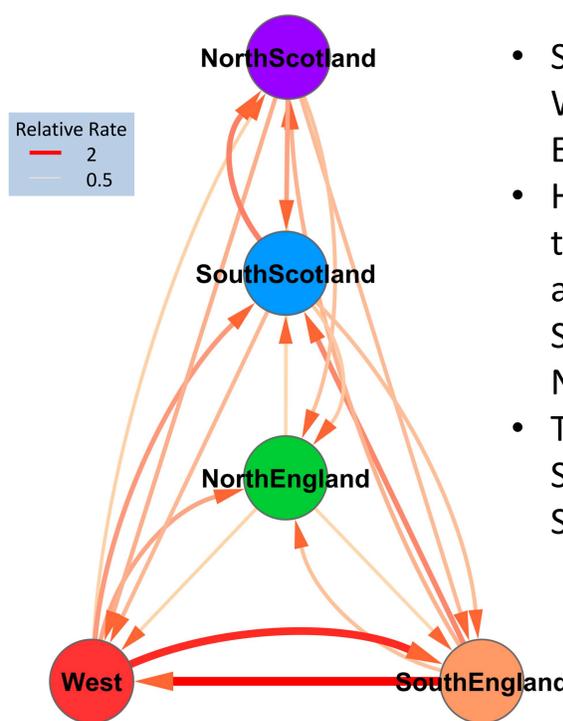
- Add locations to phylogenetic tree
- Estimate transition rates between locations along branches of tree
- Transmission pattern between locations inferred using asymmetric continuous time Markov chain Discrete Traits Model in BEAST

Transmission into Scotland



- Multiple incursions into Scotland from the rest of GB
- 8 different events in 6 years

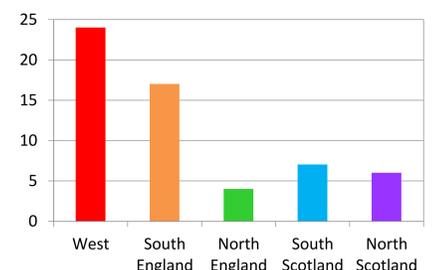
Transmission around GB



- Strongest links between West and Southern England
- Higher apparent rate of transmission from West and South into Southern Scotland than from Northern England
- Transmission from Southern to Northern Scotland important

Phylodynamic Data Set

- BVDV-1 sequences from 2005-2011 study in GB
- Place of origin available
- No recombination detected in this set
- 58 unique 5'UTR+Npro sequences



Booth et al. *Veterinary Research* 2013, 44:43