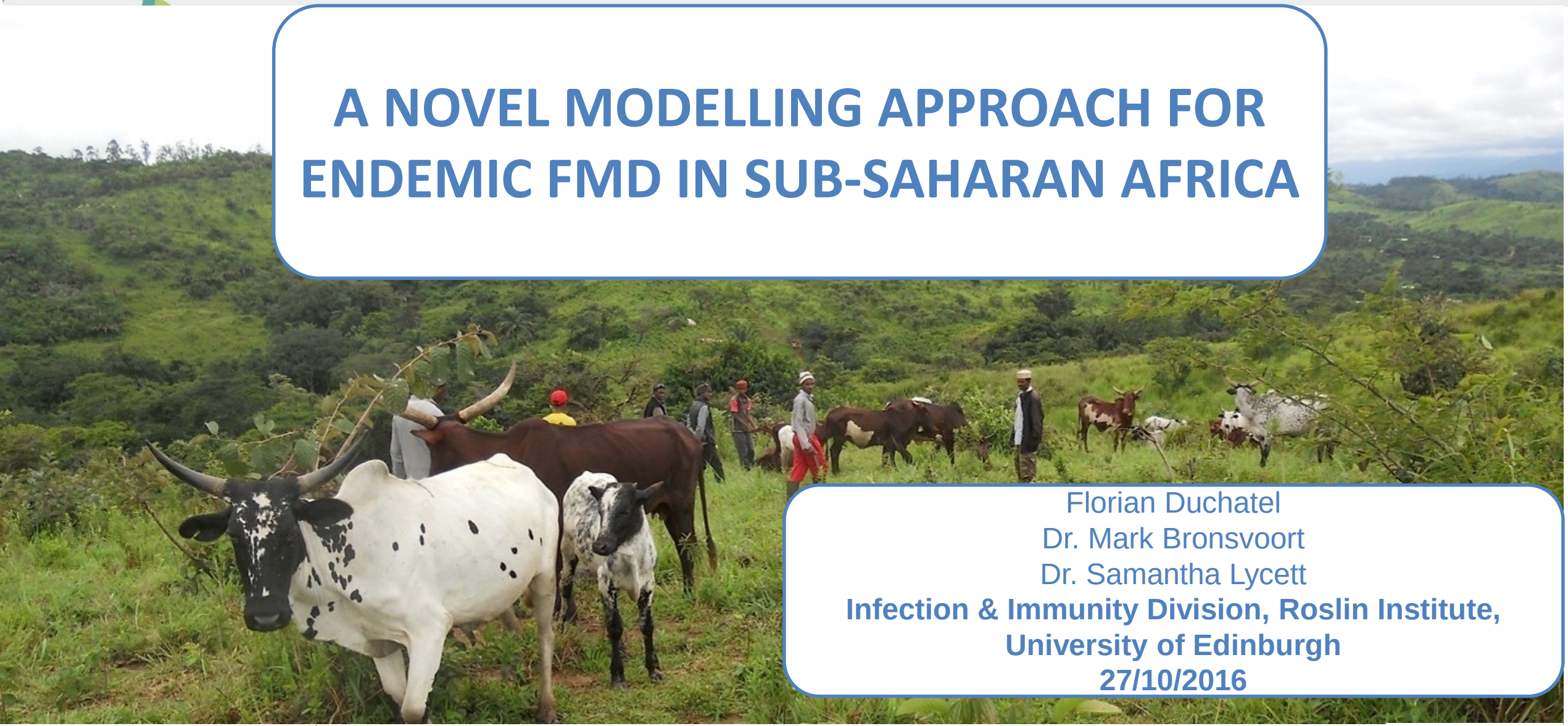
A NOVEL MODELLING APPROACH FOR ENDEMIC FMD IN SUB-SAHARAN AFRICA

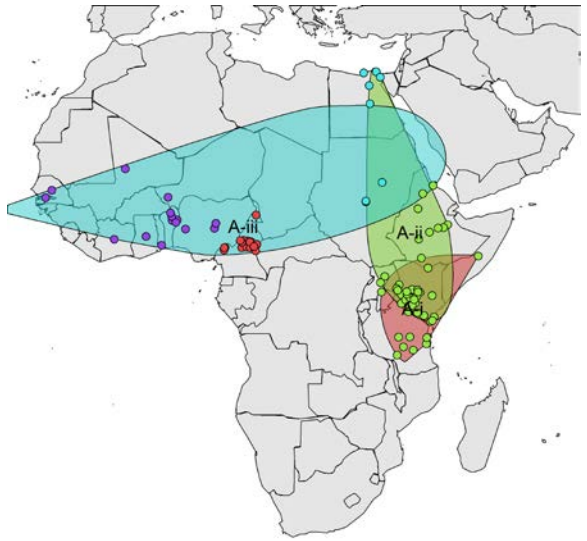


Florian Duchatel
Dr. Mark Bronsvoort
Dr. Samantha Lycett
Infection & Immunity Division, Roslin Institute, University of Edinburgh
27/10/2016

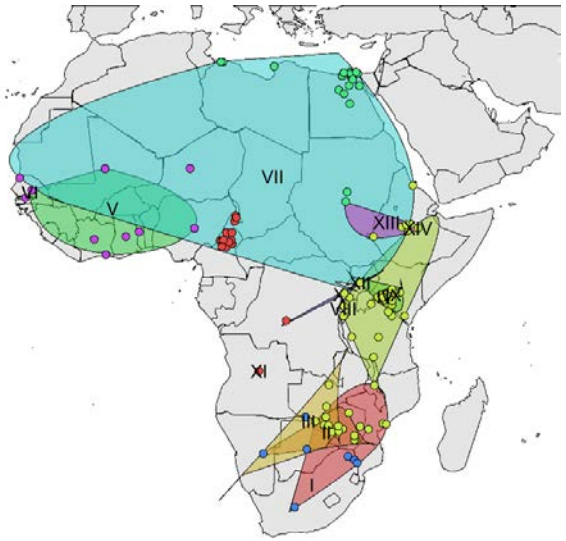
Introduction

FMD subtypes and topotypes in Africa

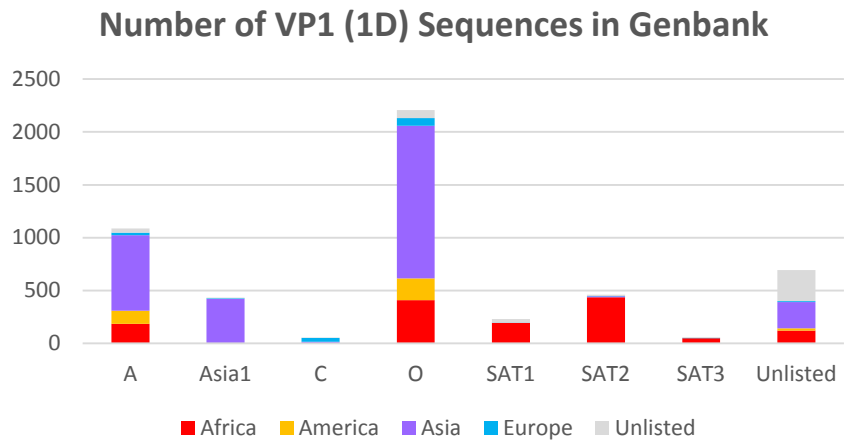
- Control of foot-and-mouth disease
  - ➔ understand the epidemiology of the disease
- Interested in :
  - **Transmission** rates between **locations**
  - Number of transition between locations
  - **Effect** of anthropological/ environmental **variable**
- Overlap in FMDV serotypes and topotypes in **West, Central and East Africa**
  - Serotypes O, A, SAT 1, SAT 2
  - Great circulation between countries
- Epidemiology of FMD in Africa **still unclear**
  - ➔ Role of livestock and wildlife?
  - ➔ Lack of data



FMDV A clades distribution in Africa



FMDV SAT2 topotypes distribution in Africa



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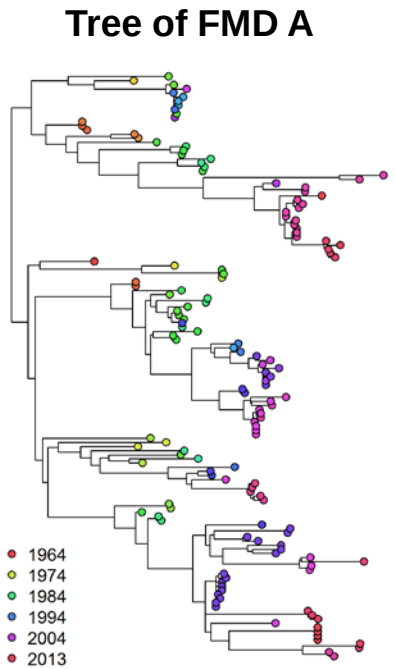
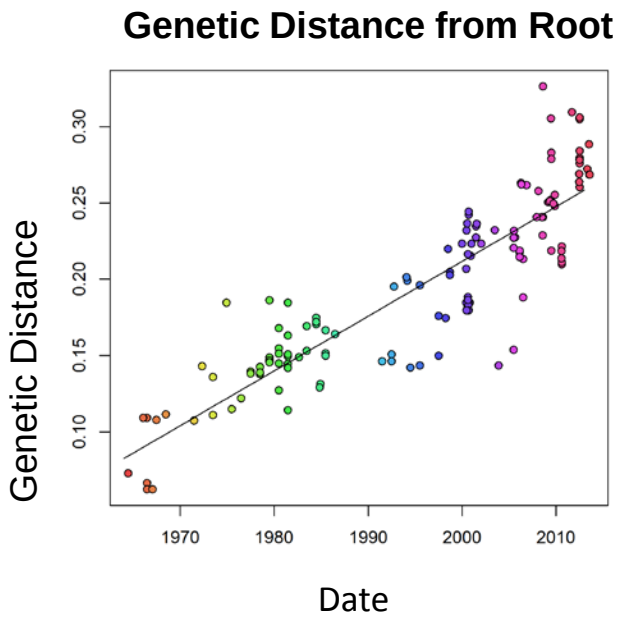
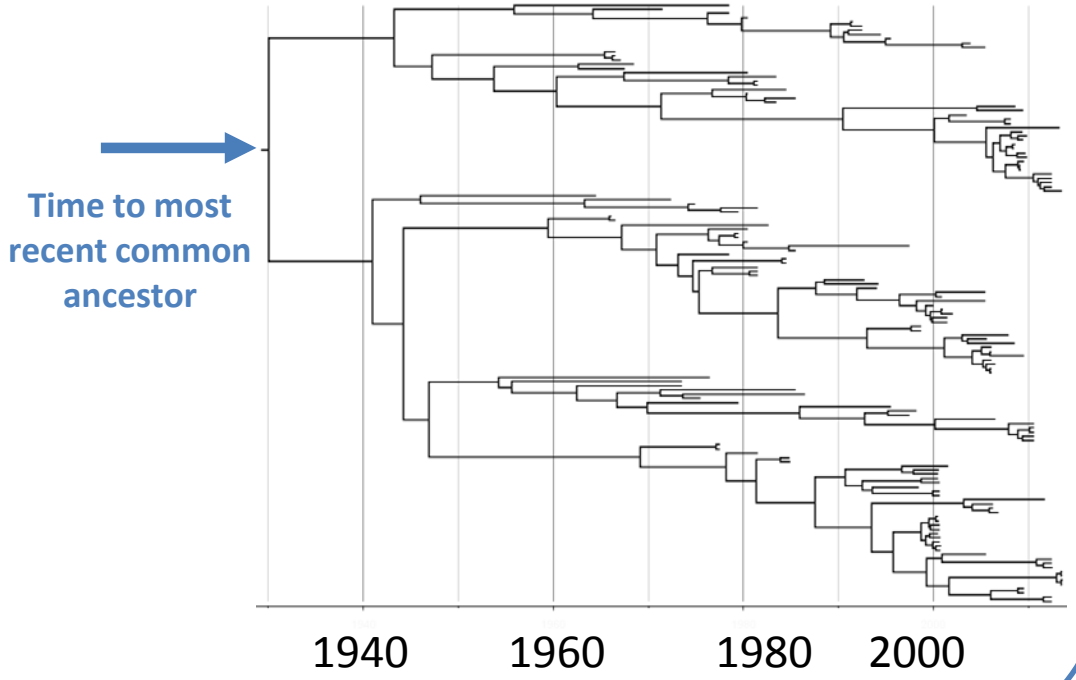
Pathogen sequences accumulate mutations over time





Evolutionary tree timescale by a molecular clock

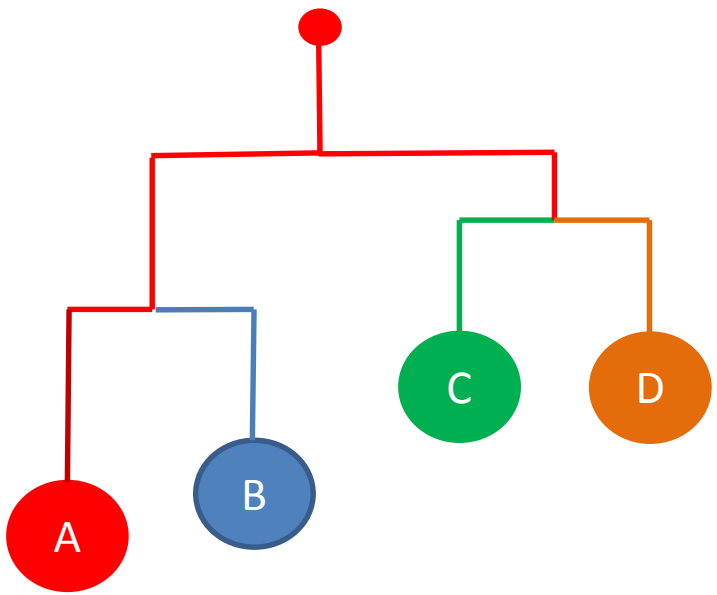


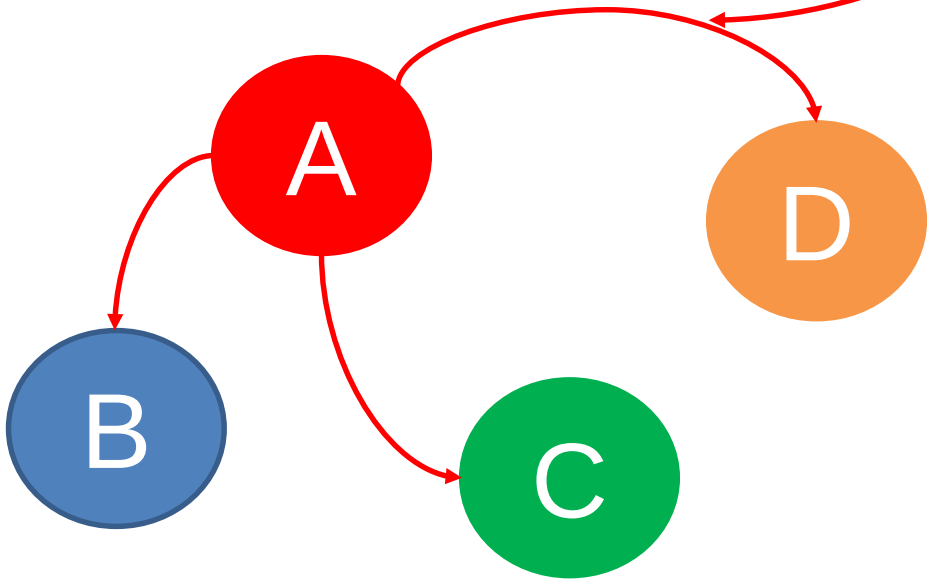
Phylogeographic inference

Integration of spatial data

- Add **locations** to phylogenetic tree ➔ evolutionary trait
- Estimate transition rates between **locations** along branches
- Transmission pattern between **locations** represented by rate matrix

	A	B	C	D
A	0	λab	λac	λad
B	λba	0	λbc	λbd
C	λca	λcb	0	λcd
D	λda	λdb	λdc	0





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BSSVS and Markov jump

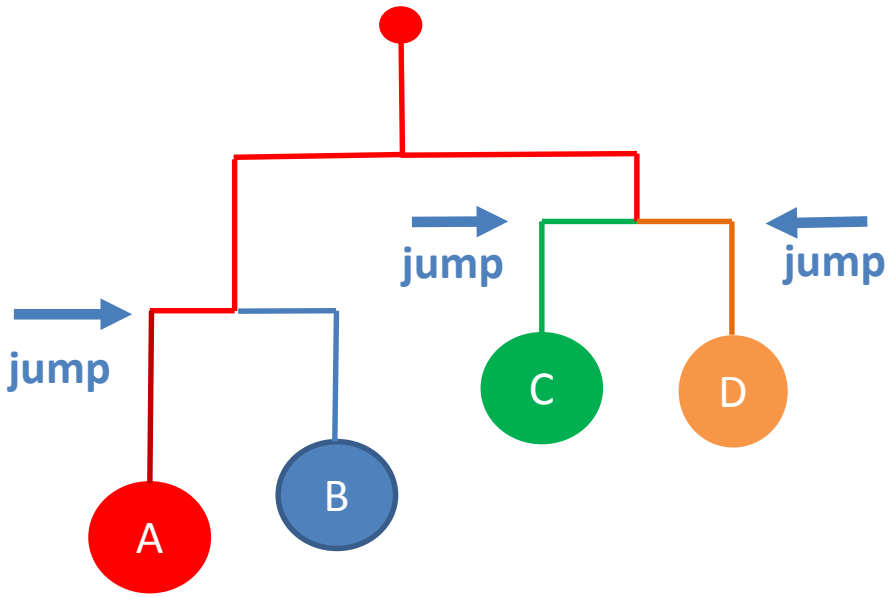
BSSVS (Bayesian Stochastic Search Variable Selection)

- Determine well supported location transmission rate
- Many location transitions are unlikely ➔ reduce the number of rates
  - Model augmented with indicator variables Δijk.
    Δijk =0 ➔ rate between states j and k is 0.
    Δijk =1 ➔ rate between states j and k is λijk
- Provide a **B**ayes **F**actor ➔ tests for well supported individual rates

	A	B	C	D
A	0	Δab λab	Δac λac	Δad λad
B	Δba λba	0	Δbc λbc	Δbd λbd
C	Δca λca	Δcb λcb	0	Δcd λcd
D	da λda	Δdb λdb	Δdc λdc	0

Markov jump

- Estimate the number of **location** transitions (Markov jumps) along the branches of the unknown tree



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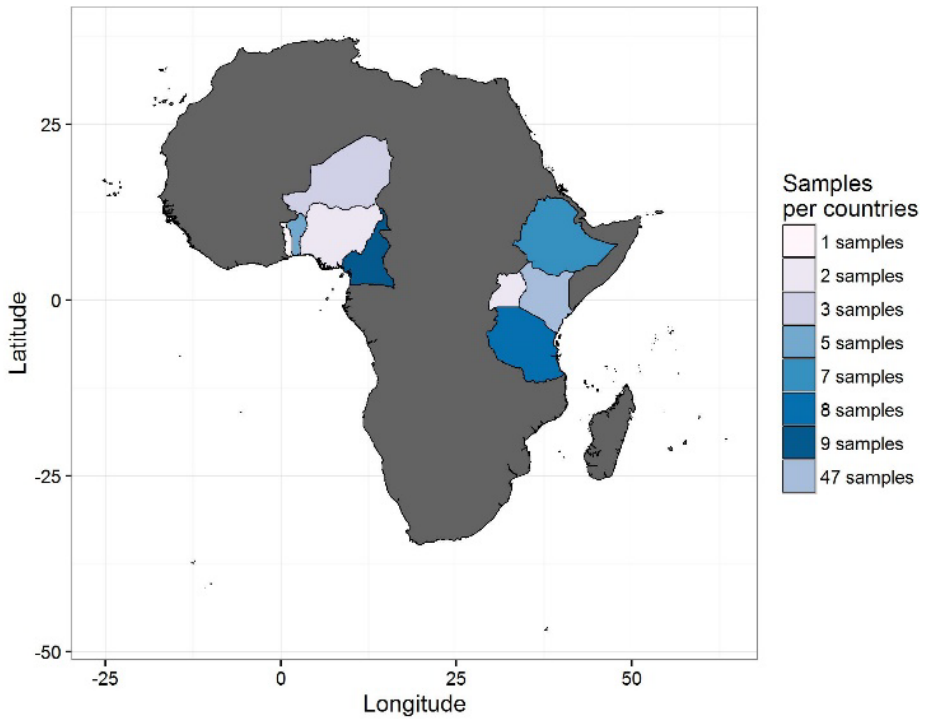
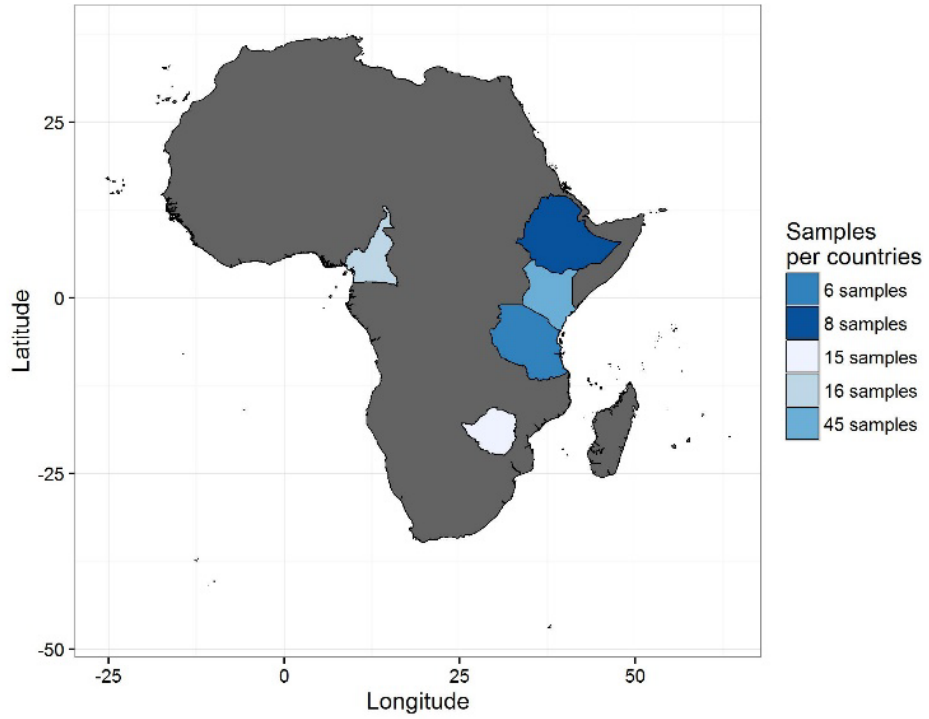
Datasets

FMDV A



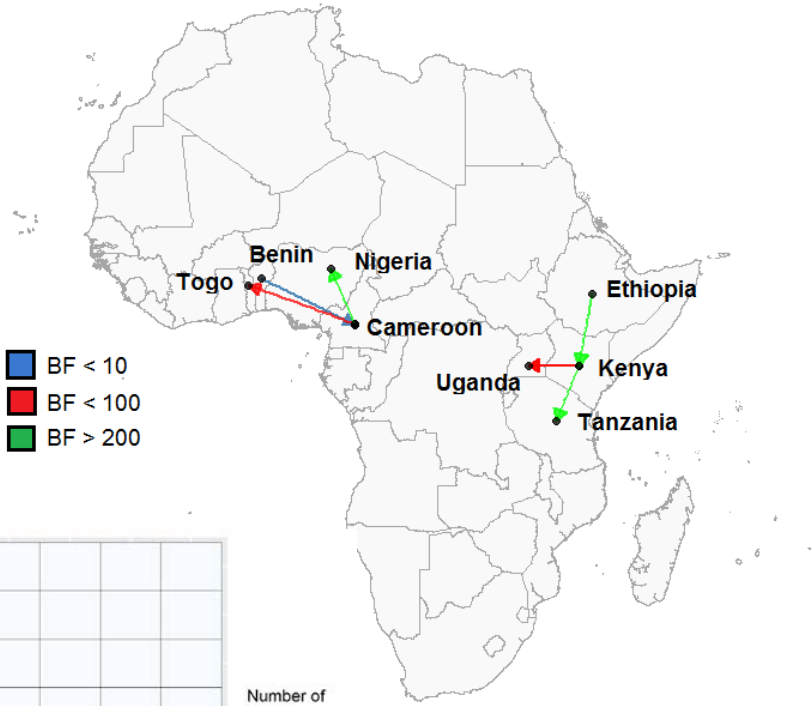
FMDV SAT2



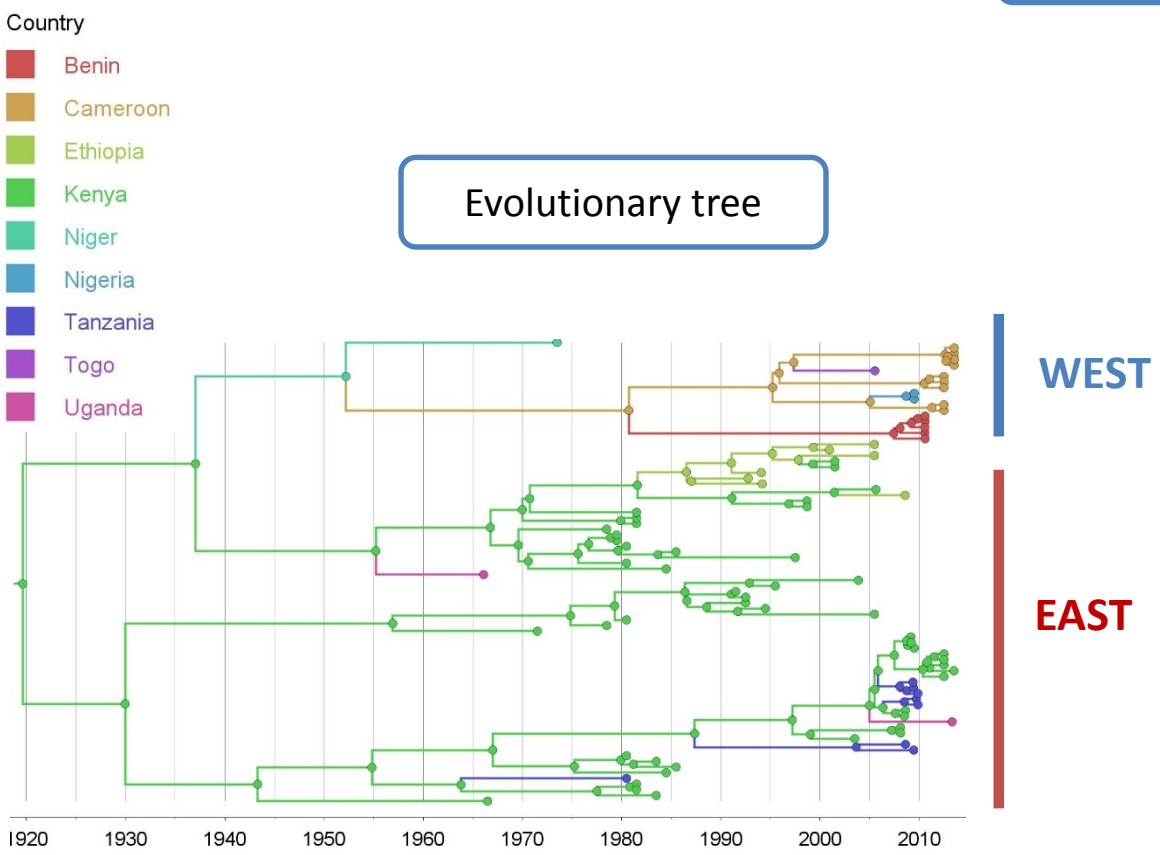
Pattern between countries

FMDV A

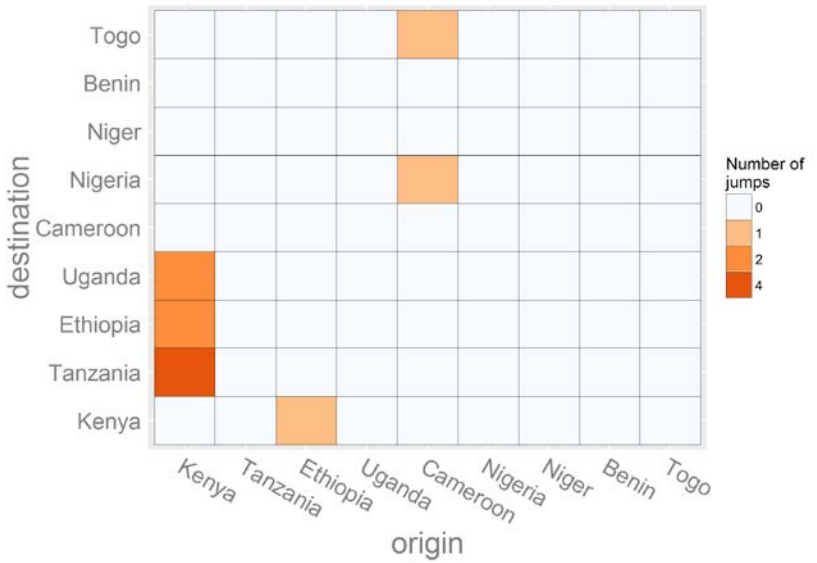
Supported routes of transmission



Evolutionary tree



Markov jumps



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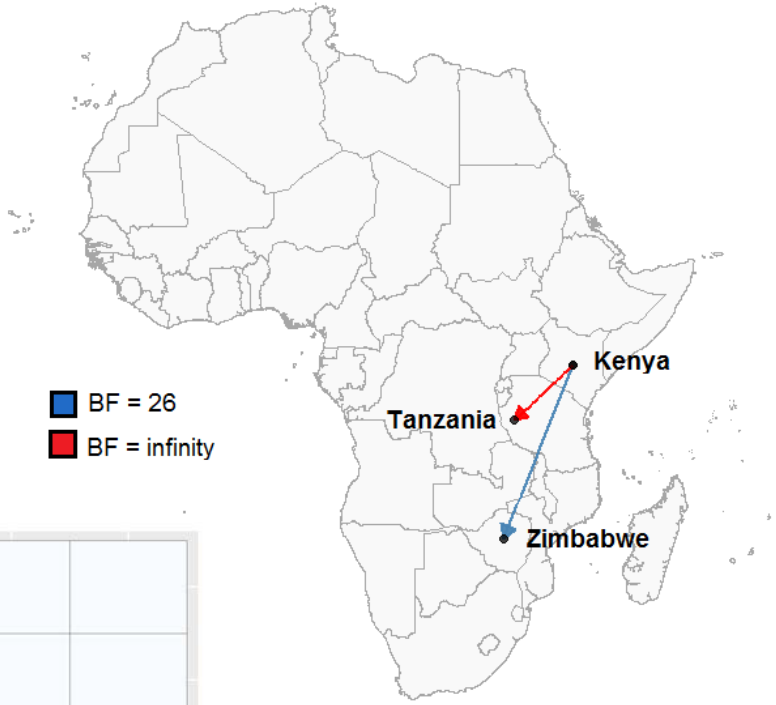
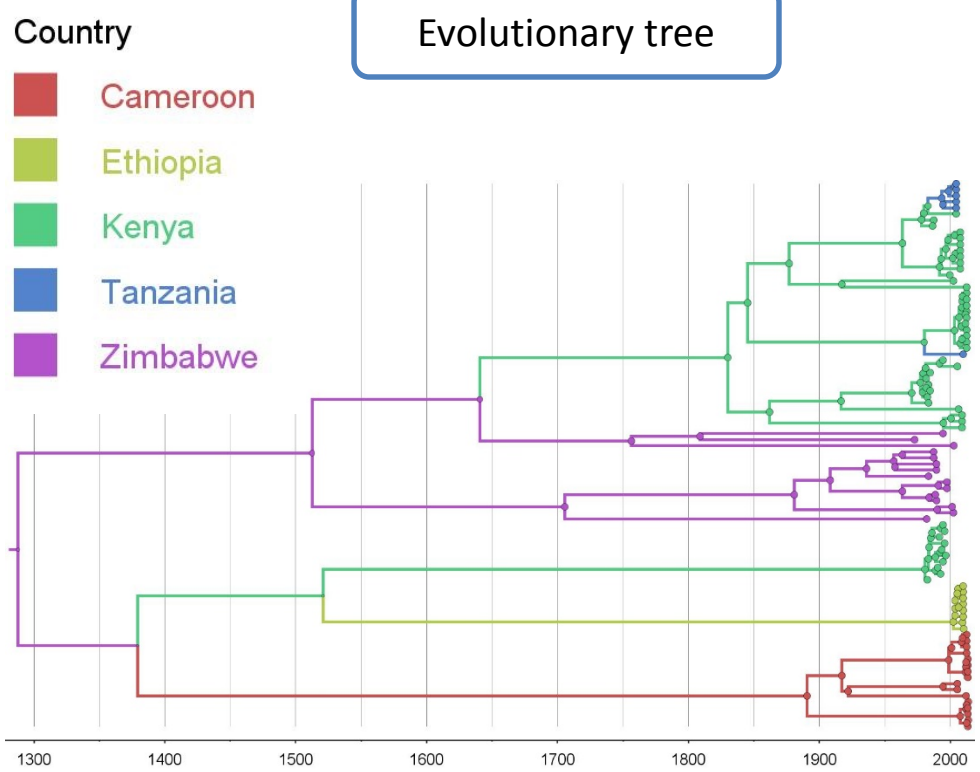
Pattern between countries

FMDV SAT2

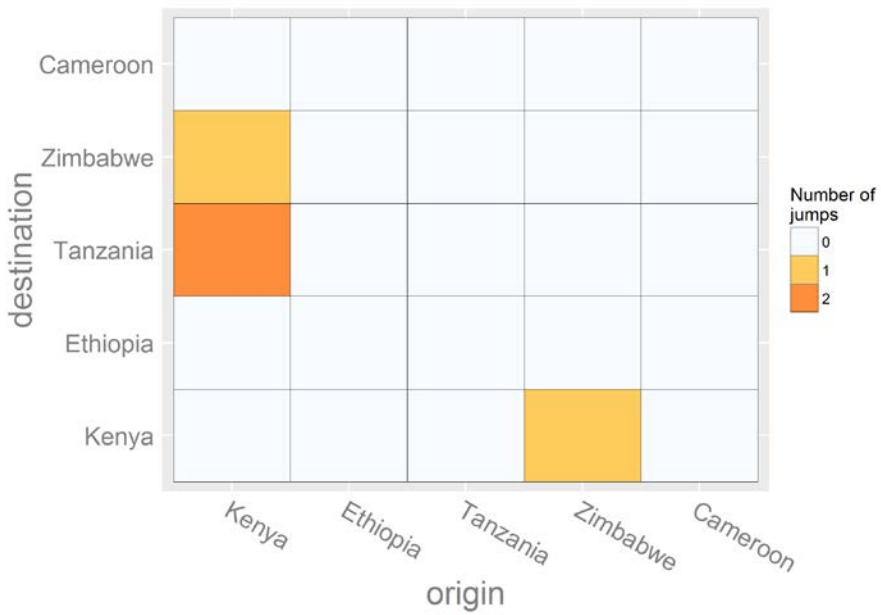
Supported routes of transmission



Evolutionary tree



Markov jumps



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Drivers of transmission

Predictors

- Different anthropological and environmental variables might affect the transmission of FMD in Africa
- Determination of the role played by the cattle density , human density and land use in the virus transmission

GLM

- Use of a Generalised Linear Model to parameterise the rates of transmission between two locations
- Rate as a linear function of one or more predictor variables.

Transition Rate Matrix

	A	B	C	D
A	0	λab	λac	λad
B	λba	0	λbc	λbd
C	λca	λcb	0	λcd
D	λda	λdb	λdc	0

For i=1 to n predictors

Predictor Rate Matrix

$$\log \Lambda = \sum_i \partial_i \beta_i \log R_i$$

(for each MCMC step, propose βi's and δi's)

Indicator variable, delta dirac (0 or 1)

Coefficient of predictor matrix

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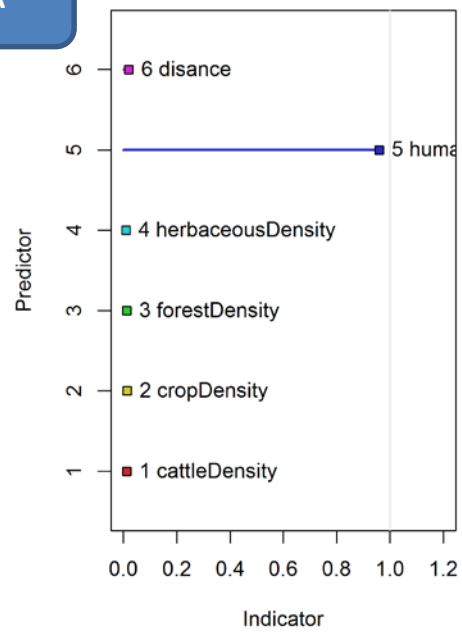
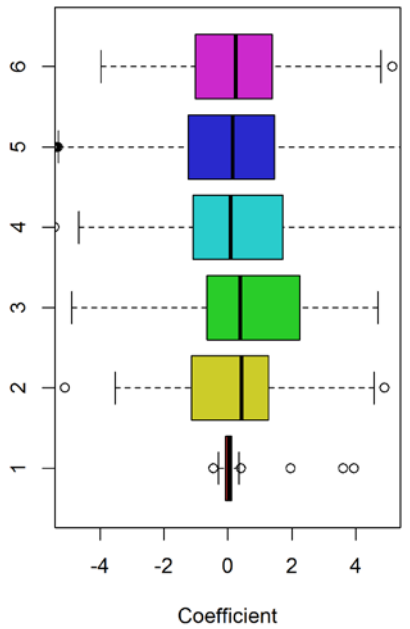
Results of the GLM analysis

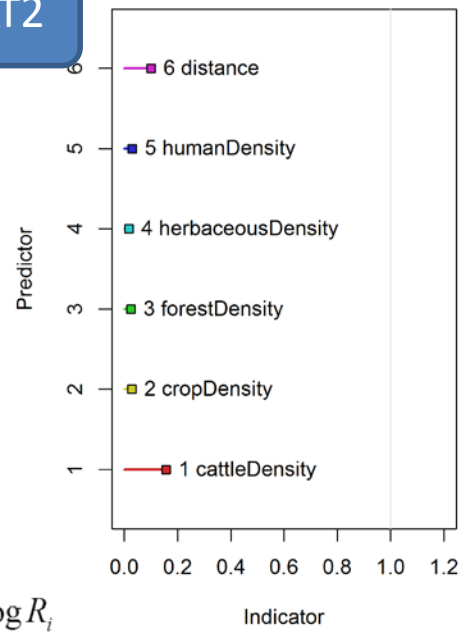
FMDV A

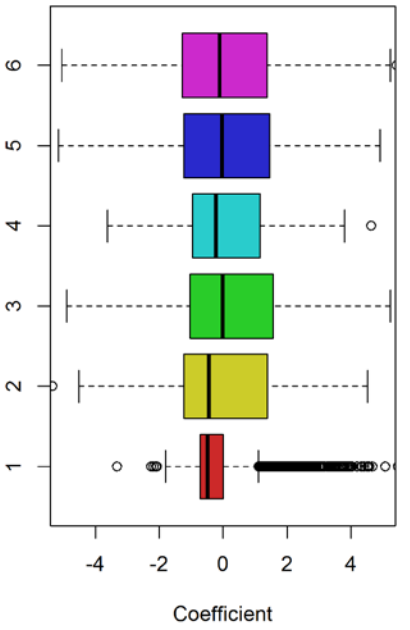




Predictors	BF
Cattle density	0,03
Crop density	0,03
Forest density	0,03
Herbaceous density	0,02
Human density	58
Distance	0,04

FMDV SAT2





$$\log \Lambda = \sum_i \partial_i \beta_i \log R_i$$

indicator coefficient

Predictors	BF
Cattle density	0,4
Crop density	0,03
Forest density	0,06
Herbaceous density	0,06
Human density	0,07
Distance	0,2

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Conclusions

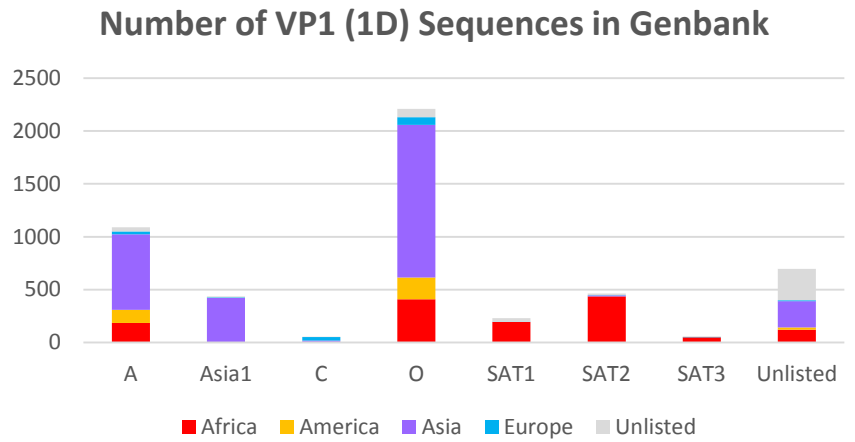
FMDV A

- Clear separation between the two African coasts for recent circulation
- Detection of well supported routes of transmission
- Effect of human density on the transmission

FMDV SAT2

- Circulates for a longer time than FMDV A
- Detection of well supported routes of transmission
- Small effect of distance and cattle density on the transmission

- Need for new FMD sequences



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Thanks for your attention

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S. Lycett
S. Mazeri
Institute of Evolutionary Biology, University of Edinburgh
M. Hall
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D. King
V. Mioulet
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