Welcome to the
Disease BioPortal

Molecular Epidemiology of FMDV in Southern Africa

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Research team

- UC Davis
- Onderstepoort Veterinary Institute
- CIRAD
- Plum Island Animal Disease Center

GFRA framework

Objective

To assess the epidemiological dynamics of FMD in buffalo at the molecular level.

Data

1) Epidemiological database

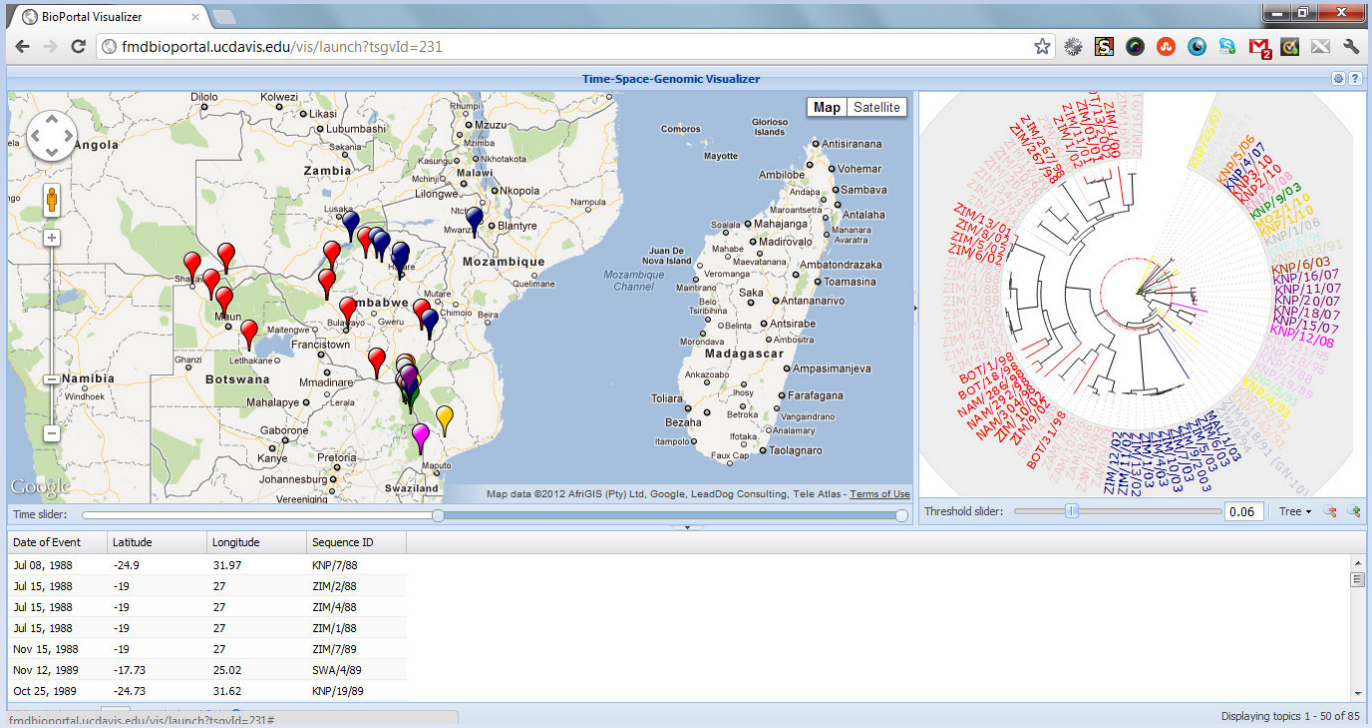
- 1825 records OVI and IAH (1934-2012)
- Serotype information
- Additional information of species, location, year and date of collection

2) 249 (14%) records have VP1 sequence information

- SAT 1=92
- SAT 2= 102
- SAT 3= 55

Preliminary analysis

- Data uploaded into Disease BioPortal: http://fmdbioportal.ucdavis.edu/
- Spatial visualization of serotype reports
- Phylogenetic temporal and spatial display of sequences



Date of Event	Latitude	Longitude	Sequence ID
Jul 08, 1988	-24.9	31.97	KNP/7/88
Jul 15, 1988	-19	27	ZIM/2/88
Jul 15, 1988	-19	27	ZIM/4/88
Jul 15, 1988	-19	27	ZIM/1/88
Nov 15, 1988	-19	27	ZIM/7/89
Nov 12, 1989	-17.73	25.02	SWA/4/89
Oct 25, 1989	-24.73	31.62	KNP/19/89

Proposed activities

a. Fill gaps in database

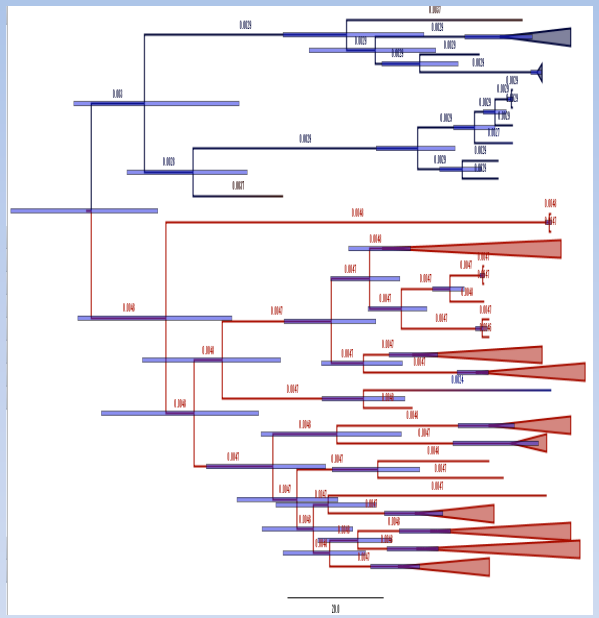
b. Analysis

1. Comparison of substitution rates
2. Estimation of virus population diversity in time
3. Estimate migration between virus populations

Phylogenetic analysis- Tree construction

Phylogenetic tree construction using Bayesian MCMC approaches

1. Selection of substitution priors using jModeltest (Posada, 2008)
2. Assessment of tree convergence using different tree models in BEAST (Drummong and Rambaut, 2007)
3. Association between variation and epidemiological parameters (Perez et al, 2008)

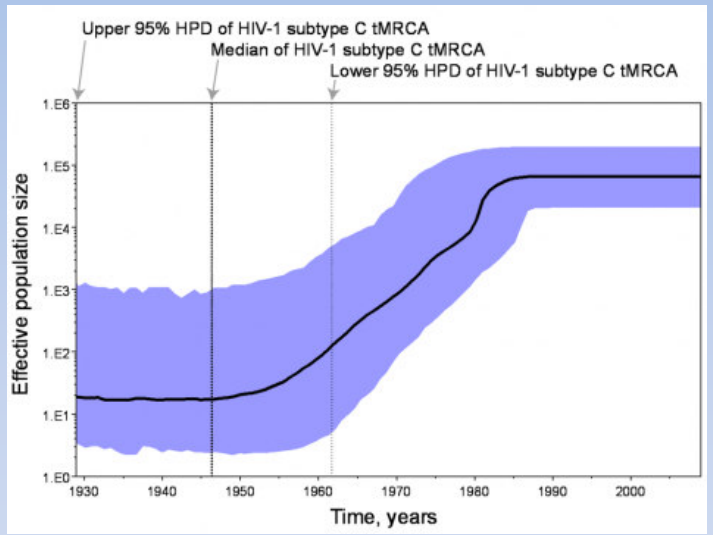


Example: preliminary SAT2 time tree, branches are gradient colored by substitution rate (<blue, >red). Node bars represent uncertainty

Phylogenetic analysis- population diversity over time

Evolutionary dynamics of FMDV SAT viruses using Bayesian Coalescent Approach (Drummond et al. 2002, 2006),

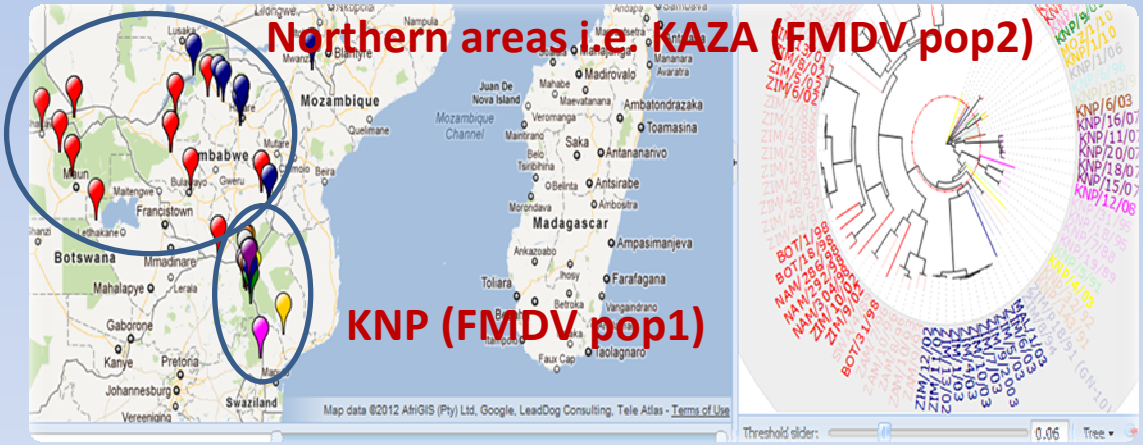
- Use of serially sampled data to estimate evolutionary parameters
- Estimate viral population diversity over time- a Bayesian skyline plot make it possible to interpret if there have been years or period in which the virus population show increase variability- Important to determine historical dynamics (i.e. cyclical trends or specific situations related to virus phylodinamics)
- Null hypothesis: population diversity is constant in time
- Comparison between serotypes

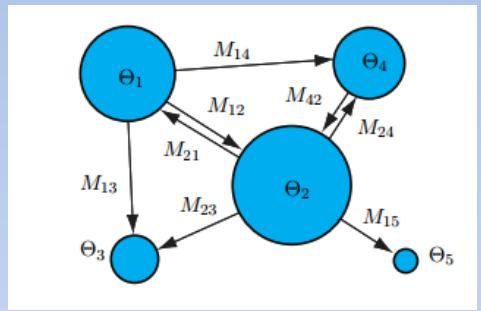


Example: Bayesian skyline plot of HIV-1 subtype C. In Novitsky et al. HIV-1 Subtype C Phylodynamics in the Global epidemic. Viruses 2010, 2(1), 33-54.

Phylogenetic analysis- population size and migration parameters

- Discuss different **virus populations** corresponding to geographically different buffalo populations and estimate exchange of virus migrants within the populations.

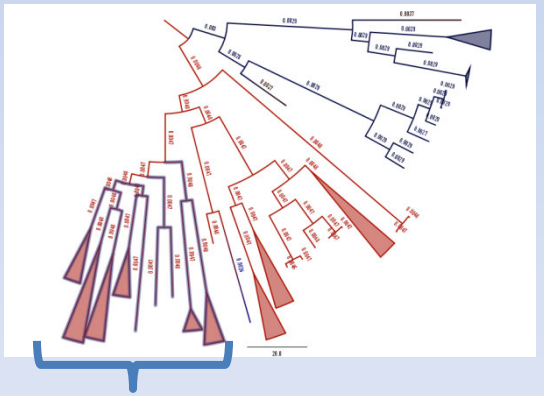




From: Migrate v 3.2documentation Beerli, 2010.

- Population size and migration are scaled by mutation rate (sequence data per site per generation) and geographic distance (to detect if there is an environmental barrier within the population)

- Null hypothesis: in populations without a barrier the intra-population rates should be similar.



KNP (FMDV pop1)

Thank you