

Molecular epidemiology of foot-and-mouth disease viruses in Southern Africa

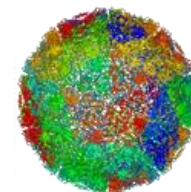
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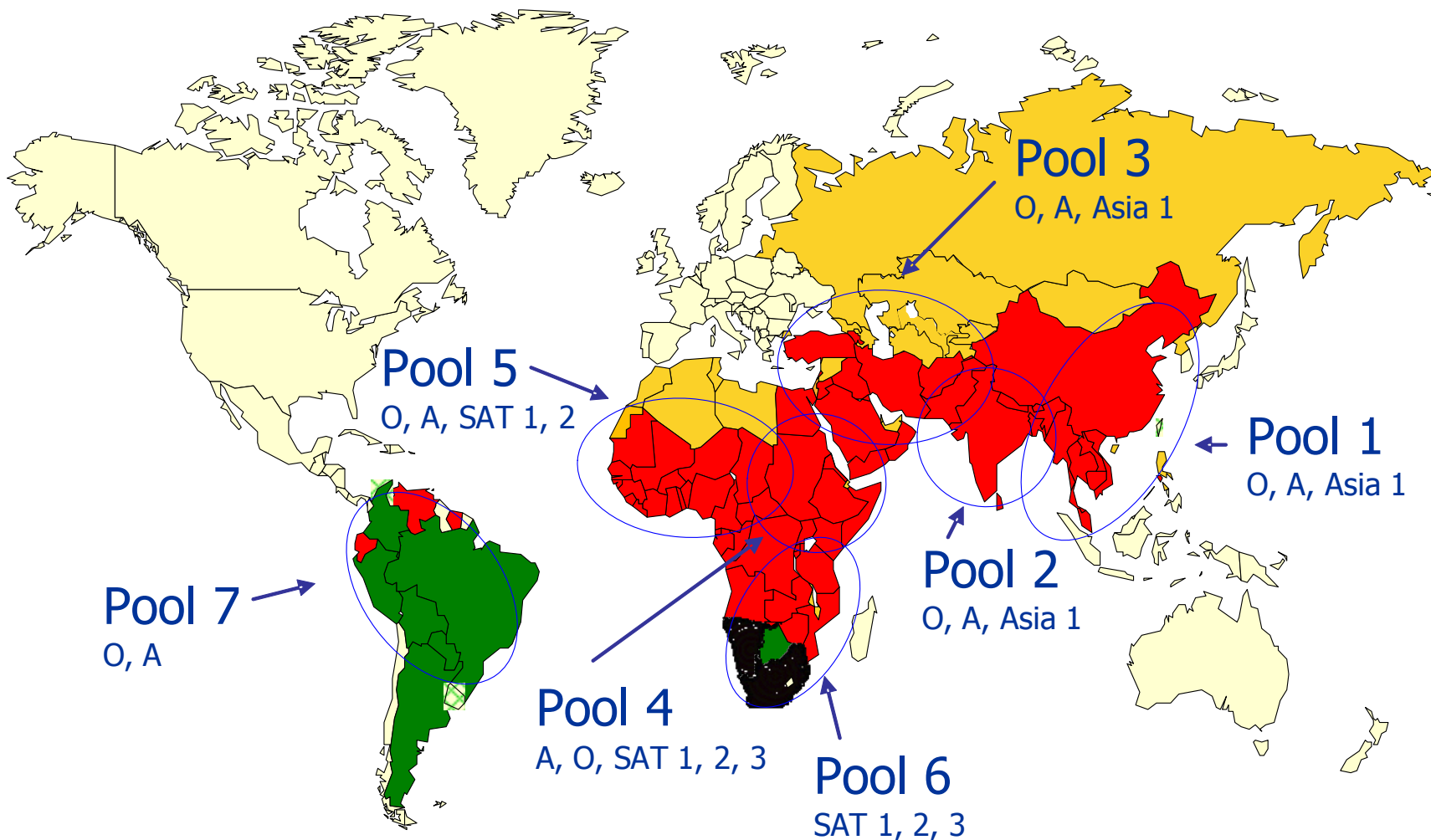
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FMD in Southern Africa

- FMD is endemic in nearly all countries of sub-Saharan Africa
- First FMD outbreak reports ~ 1950s (in many Southern African countries)
- Animal affected: Cattle, Pigs, small ruminants, wild animals
- Six (A, O, C, SAT1, SAT2 & SAT3) of seven FMDV serotypes have been reported in the region
- Outbreaks occur in different geographic regions
- Factors associated with outbreaks are not clearly known
- Epidemiology of FMD is complicated by involvement of wildlife

The 7 regional FMD virus pools



- Each pool has specific viral lineages
- Tailored vaccines/diagnostics may be appropriate

Hypotheses and justification

Key research Qn: What factors contribute to FMD endemicity in Southern Africa, and what options exist for its risk management?

Hypotheses:

- ✓ Molecular characteristics of FMD virus (FMDV) are determinants of FMD endemicity
- ✓ Molecular approaches contribute to better options for FMD control strategies

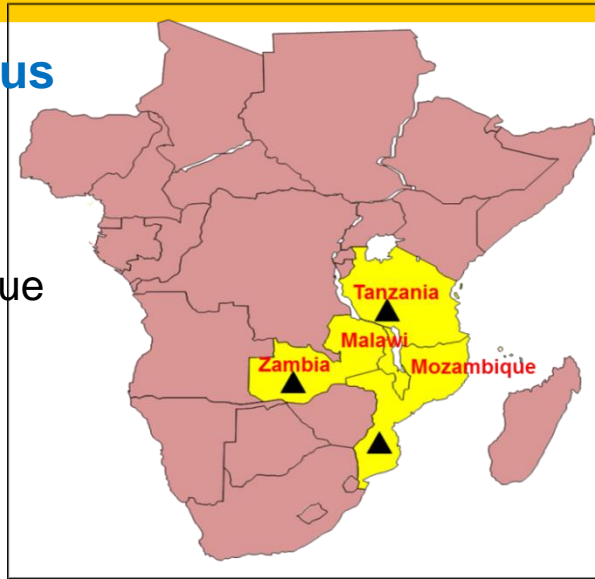
Justification and importance:

Factors for endemicity, serotype (+ toptype/genotype) distribution & rational control options have not been clearly investigated

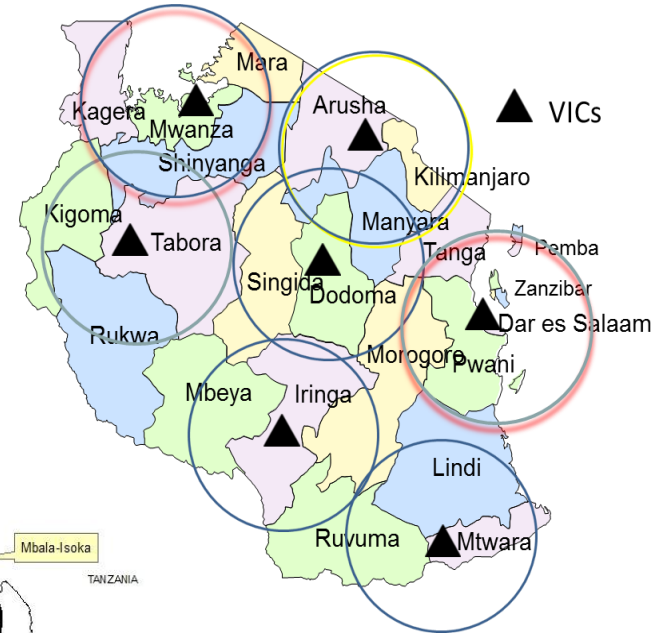
FMD study areas in Southern Africa

Current focus countries:

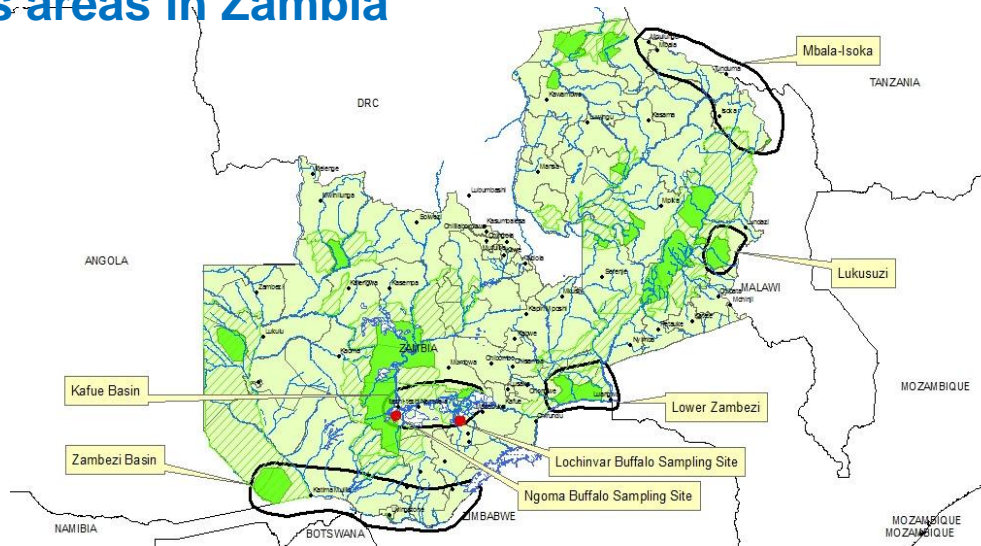
- Tanzania
- Zambia
- Mozambique
- Malawi



Focus areas in Tanzania



Focus areas in Zambia



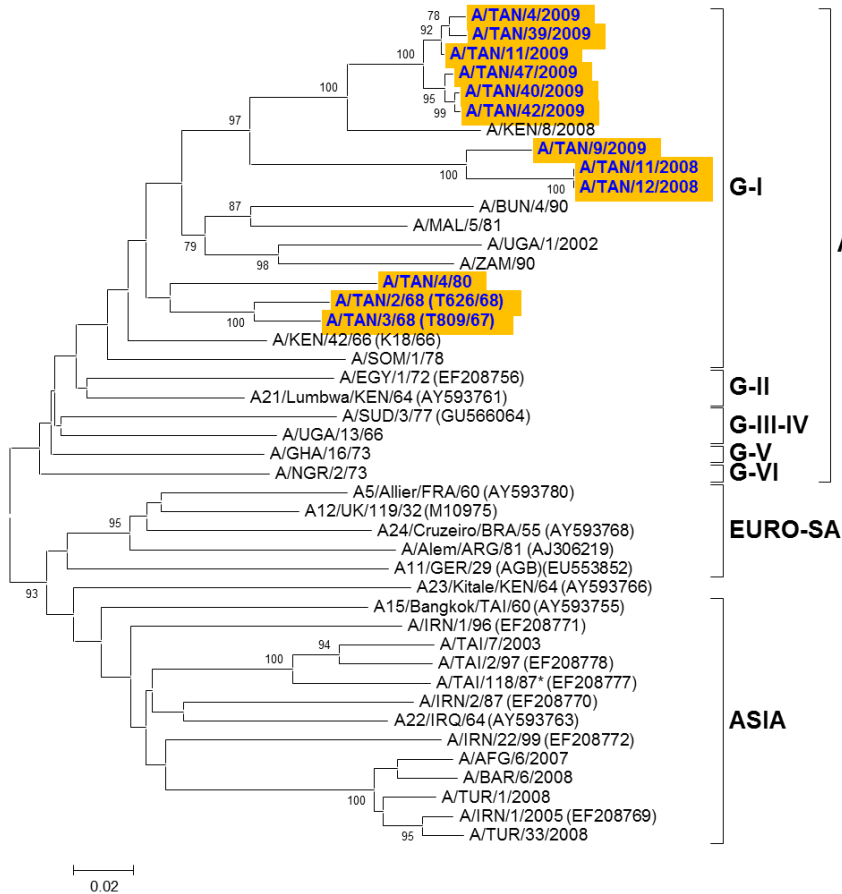
Samples and analysis

- Tissue epithelia and probang samples following FMD outbreaks were collected
- Lab analyses for FMDV were conducted by VI, Antigen ELISA, real-time RT-PCR and sequencing of the VP1 gene
- Descriptive statistics for serotype detection, genotype/topotype and distribution
- Phylogenies of VP1 sequences were determined by Neighbor-joining method

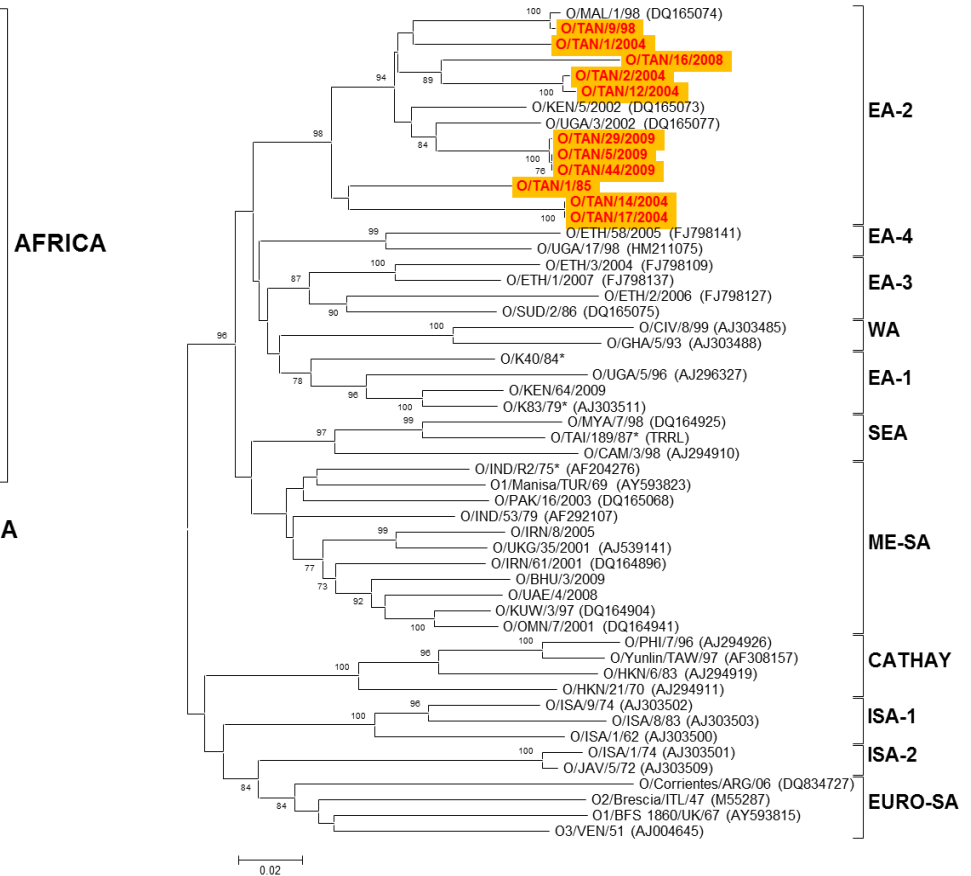
Years and zones of FMDV detection

Serotype	Years detected	Countries in the region
O	1971, 1980, 1984, 1985, 1996, 1998, 2004, 2008, 2009, 2010, 2011, 2013, 2015, 2016	Tanzania, Zambia, Zimbabwe, Malawi, Mozambique
A	2008, 2009, 2014, 2016	Tanzania, Zambia
SAT1	1971, 1972, 1977, 1980, 1996, 1999, 2008, 2012, 2014, 2015	Tanzania, Mozambique, Zambia, Malawi
SAT2	1970, 1972, 1975, 1986, 1999, 2004, 2009, 2010, 2012, 2014, 2015, 2016	Tanzania, Mozambique, Zambia, Malawi

Phylogenetic trees

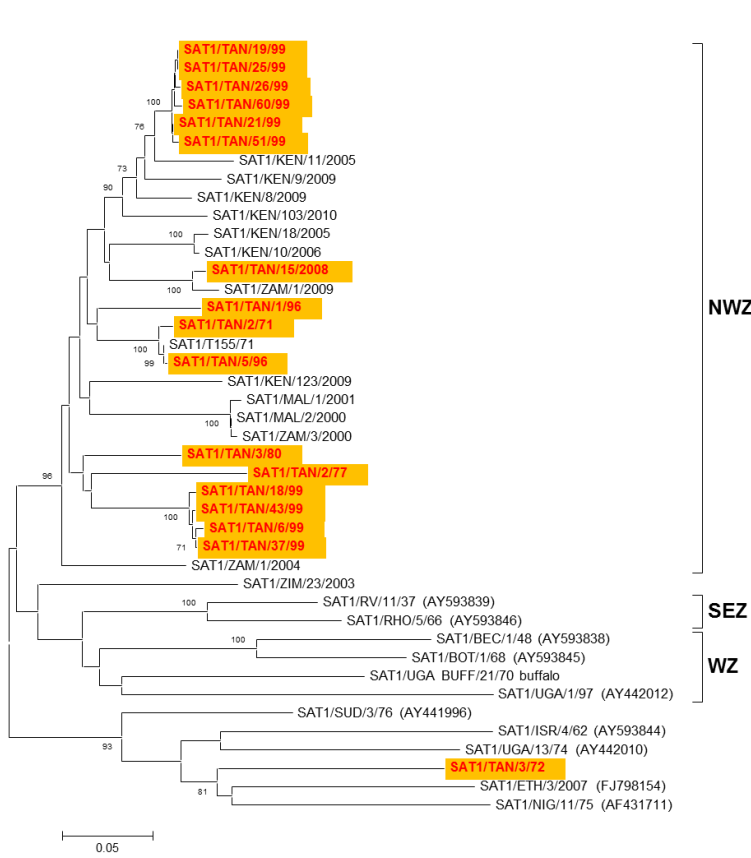


Serotype "A"

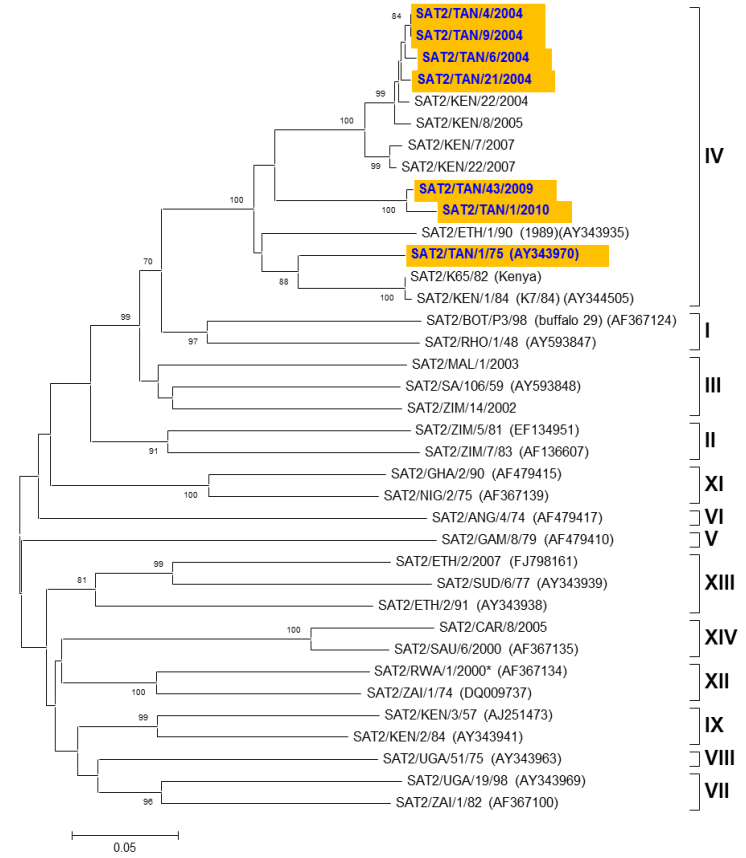


Serotype "O"

Phylogenetic trees



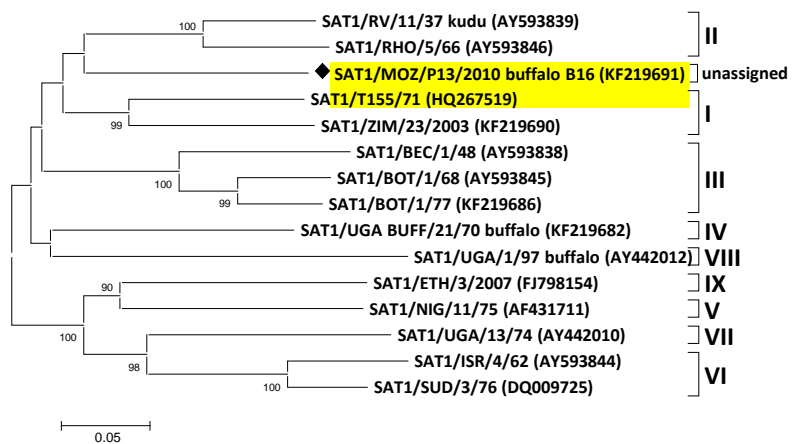
Serotype "SAT1"



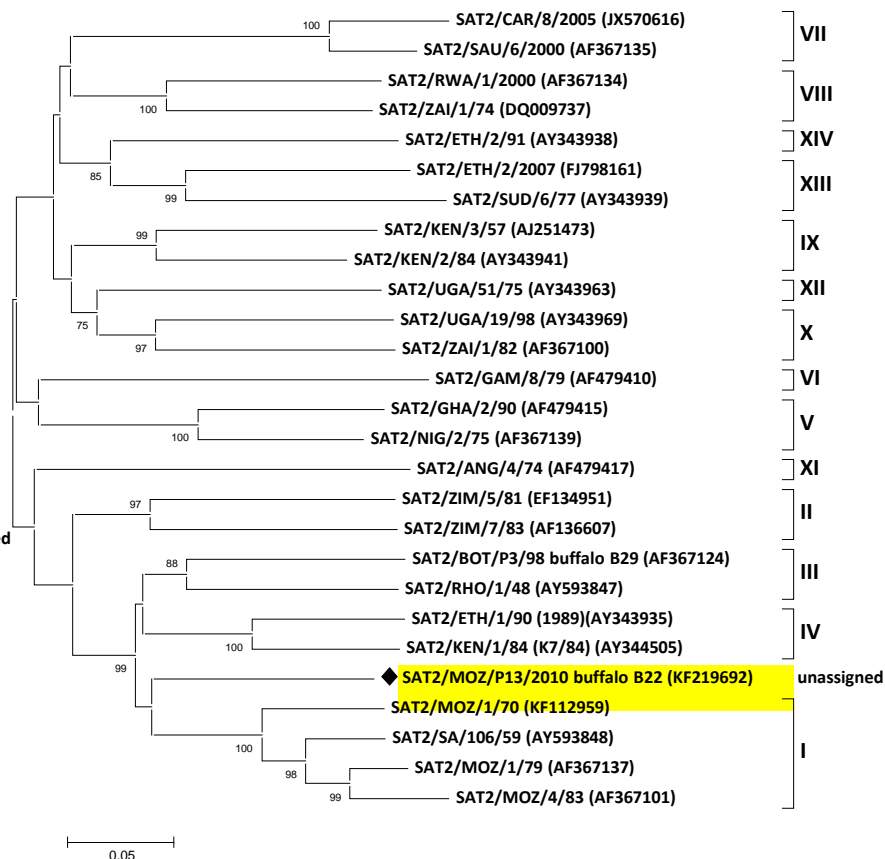
Serotype "SAT2"

Phylogenetic tree: serotype SAT 1-3 from buffalo

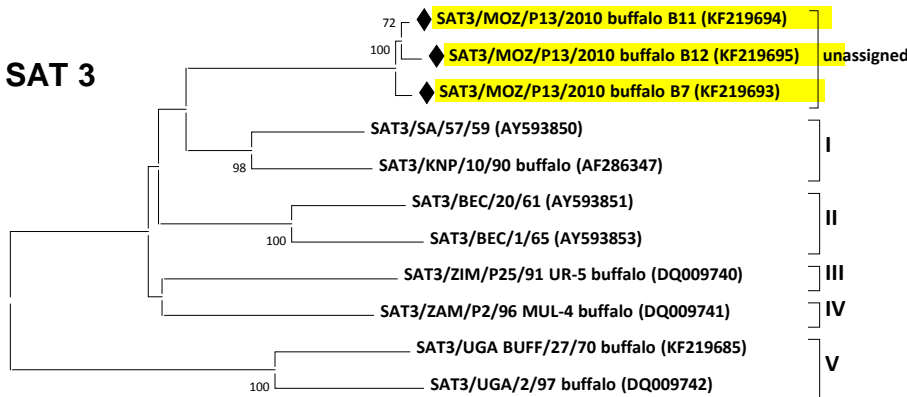
SAT 1



SAT 2



SAT 3



Note: Novel SAT1-3 genotypes detected from buffalo in Mozambique

Discussion/observations

- Serotypes A, O, SAT1 and SAT2 are the main cause of FMD in cattle in Southern Africa
- Serotypes SAT1, SAT2 and SAT3 are the main cause of FMD in livestock-wildlife interface areas of Tanzania, Zambia and Mozambique
- FMDV SATs recently detected in Tanzania and Zambia are genetically related to lineages and topotypes from East and South Africa, with a newly emerged unassigned type SAT1 topotype in Mozambique
- SAT1 outbreaks occur in waves with varied severity in time and space
- Understanding the transmission dynamics, genetic and antigenic characteristics of circulating FMDV is a pre-requisite for control of FMD in sub-Saharan region

Gaps and prioritized research areas

- In-depth genetic and antigenic characterisation of outbreak viruses is required in livestock-wildlife interface and non-interface areas - WGS
 - ✓ vaccination options ~ vaccine matching and selection of candidate strains
- Modelling FMD outbreaks and risk mapping
 - ✓ Spatio-temporal distribution of FMDV serotypes
 - ✓ Animal movements in relation to FMD outbreaks and spread
- Vaccine suitability- matching, purity and potency
- Transmission dynamics of SATs and non-SAT viruses in livestock-wildlife interface areas
 - ✓ role of buffalo (+ other wild animals) in virus transmission
- Rapid, sensitive and field-deployable diagnostic/surveillance systems/methods

On-going and future research

- To use sequence data for designing field-deployable and simple FMDV diagnostic assays
- Whole genome sequencing to investigate FMDV evolutionary characteristics, and clarify molecular determinants for FMDV endemicity in the region
- Modelling of FMD outbreaks in different geographic areas
- Investigation on genetic and antigenic characteristics of circulating FMDV strains in order to define the appropriate control of FMD in the region

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