# A review of foot-and-mouth disease viruses collected in Tanzania from 1967 to 2009

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## Summary and conclusion

- The aim of this paper was to review the FMD viruses collected in Tanzania from 1967 to 2009
- Serotypes A, O, SAT1 and SAT2 viruses prevail in different regions of Tanzania, and contribute to FMD outbreaks
- However, the epidemiology and factors associated with outbreaks remain unclear and need to be investigated
- Improved FMD surveillance, genetic and antigenic characterisation of FMDV field strains is recommended to understand endemicity and hence rational control measures of the disease

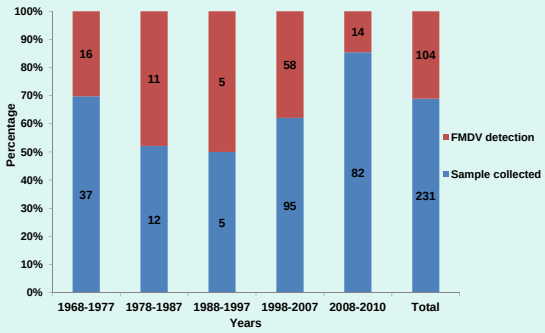
## FMD in Tanzania

- FMD is endemic in Tanzania
- First FMD outbreak reports ~ 1954
- Animal affected: Cattle, Pigs, small ruminants, wild animals
- Outbreaks occur in different geographic regions
- Factors associated with outbreaks are not clearly known

## Samples and analysis

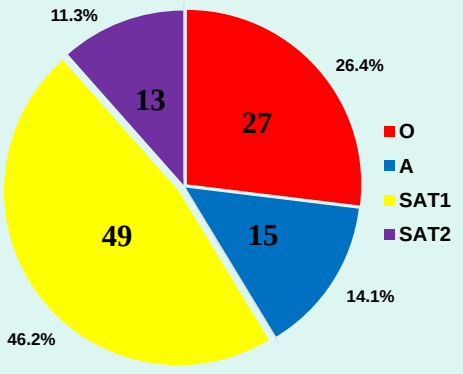
- 231 samples (epithelial tissues, probang samples, and whole blood) were submitted to the WRLFMD from 1967 to 2009 for analysis
- Lab analysis for FMDV was conducted by VI, CF, Antigen ELISA, RT-PCR and sequencing of the VP1 gene
- Phylogenies of VP1 sequences were determined by Neighbor-joining method

## Detection rate of FMDV

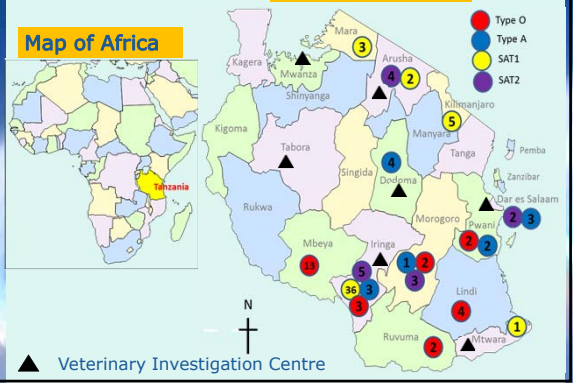



- Detection rate varied with time and geographic location
- Are the correct samples being collected?
- Preservation of the samples?

## Detection frequency of FMDV serotypes



## Geographic distribution of serotypes

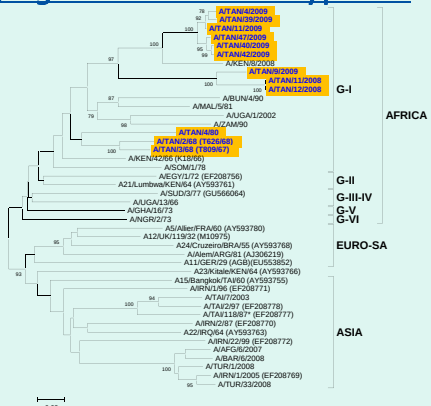



## Years and zones of FMDV detection

| Serotype | Years detected | Zones in Tanzania |
|---|---|---|
| O | 1971, 1980, 1984, 1985, 1996, 1998, 2004, 2008, 2009 | Southern and Eastern-Coastal |
| A | 2008, 2009 | Eastern, Southern, Central and Eastern-Coastal |
| SAT1 | 1971, 1972, 1977, 1980, 1996, 1999, 2008 | Southern, Northern, Northern-lake, Southern-Coastal |
| SAT2 | 1970, 1972, 1975, 1986, 1999, 2004, 2009, 2010 | Southern, Northern, Eastern and Eastern-Coastal |

- No FMDV isolates from Western zone???

## Phylogenetic tree: serotype "A"

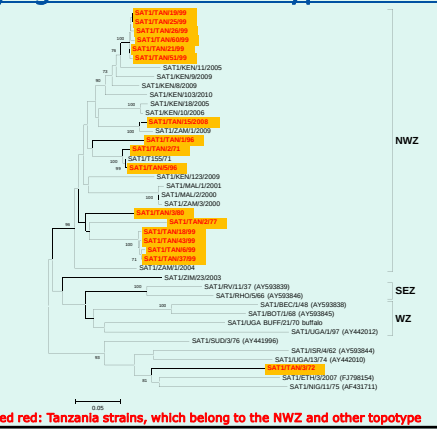



Coloured blue: Tanzania strains, which belong to the Africa G-I

## Phylogenetic tree: serotype "O"

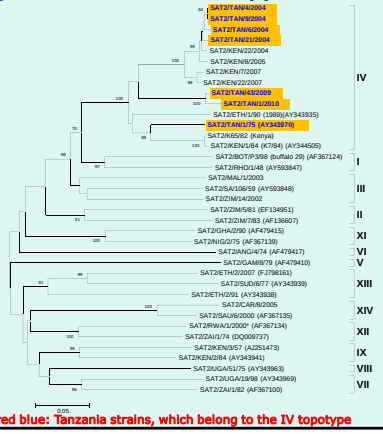

Coloured red: Tanzania strains, which belong to the EA-2 topotype

## Phylogenetic tree: serotype "SAT1"




Coloured red: Tanzania strains, which belong to the NWZ and other topotype

## Phylogenetic tree: serotype "SAT2"




Coloured blue: Tanzania strains, which belong to the IV topotype

## Discussion and conclusion

- Serotypes A, O, SAT1 and SAT2 are the main cause of FMD outbreaks in Tanzania
- FMDV isolates so far detected in Tanzania are genetically related to lineages and topotypes from West and East Africa
- Presence of multiple serotypes and topotypes complicates FMD control in the region
- Understanding the spatio-temporal distribution, epidemiology, genetic and antigenic characteristics of circulating FMDV is a pre-requisite for control of FMD in Tanzania and sub-Saharan region

## Recommendations

- FMD outbreak investigation:
  - More sample collection and appropriate diagnosis is needed
- Research to describe the complex epidemiology and endemicity of FMD in Tanzania and sub-Saharan Africa is needed
- Molecular characterisation and analysis of many FMD samples is needed to elucidate the phylodynamics and evolutionary nature of FMDV
- Cross-protection and vaccine-matching of the field isolates to available vaccines is required

## Future work

- Collaborative research on FMD in Tanzania by SACIDS, BBSRC-CIDLID (UoG and IAH) and SADC-TADs projects will be conducted focusing at:
  - Improving surveillance and diagnostic capacity
  - Molecular, antigenic and evolutionary characteristics of circulating FMDV
  - Understanding livestock-wildlife interface on FMD epidemiology
  - Developing appropriate control strategies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