

Molecular Epidemiology of Foot-and-Mouth Disease Virus in Tanzania

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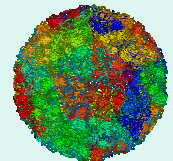
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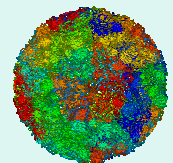
FMD in Tanzania

- Foot-and-mouth disease (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



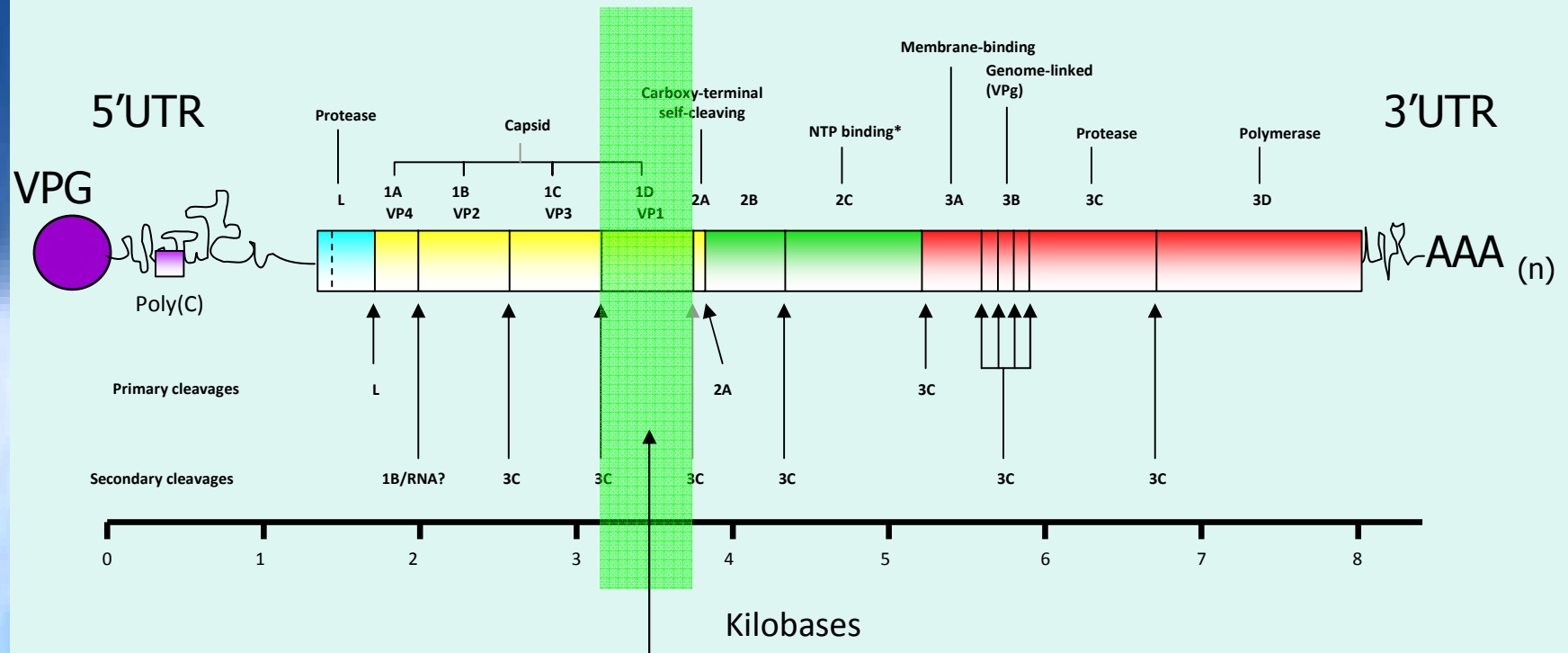
FMD virus (FMDV)

- *Aphthovirus* of the family *picornaviridae*
- Non-enveloped, icosahedral virus, 26 nm in diameter
- +ve sense ss RNA virus
- Seven serotypes exist: A, O, C, Asia 1 and SAT1-3)
- Displays high genetic and antigenic variation

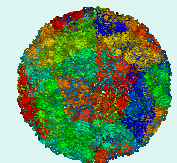


FMDV genome orientation

* putative functions

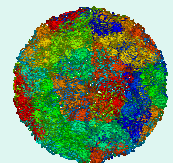


variable **VP1** region
sequences used for isolate characterisation

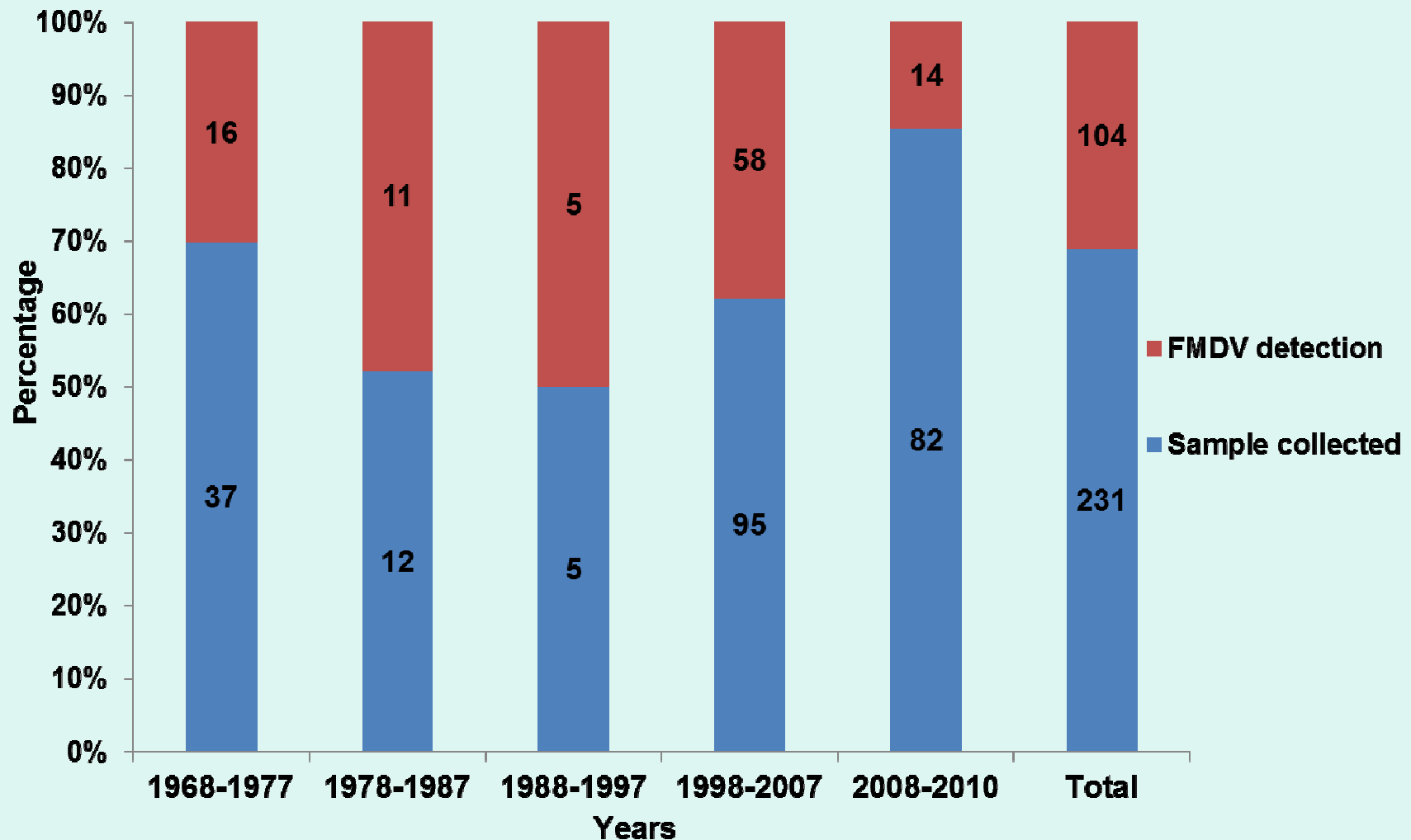


Samples and analysis

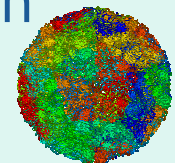
- 231 samples (epithelial tissues, probang samples, and whole blood) were submitted to the WRLFMD from 1967 to 2009 for analysis
- Lab analysis for FMDV was conducted by VI, CF, Antigen ELISA, RT-PCR and sequencing of the VP1 gene
- Phylogenies of VP1 sequences were determined by neighbor-joining method



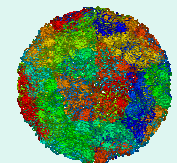
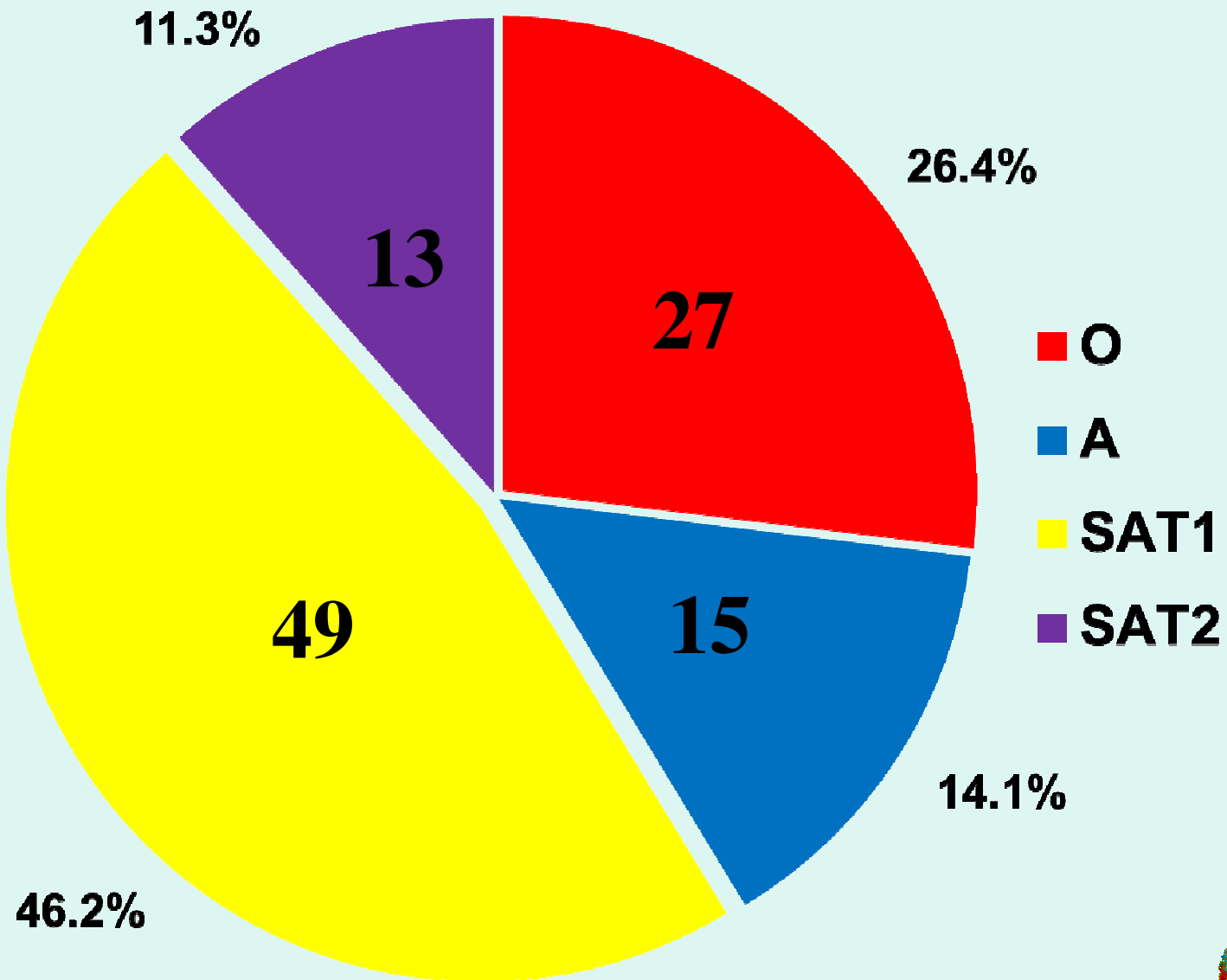
Detection rate of FMDV



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



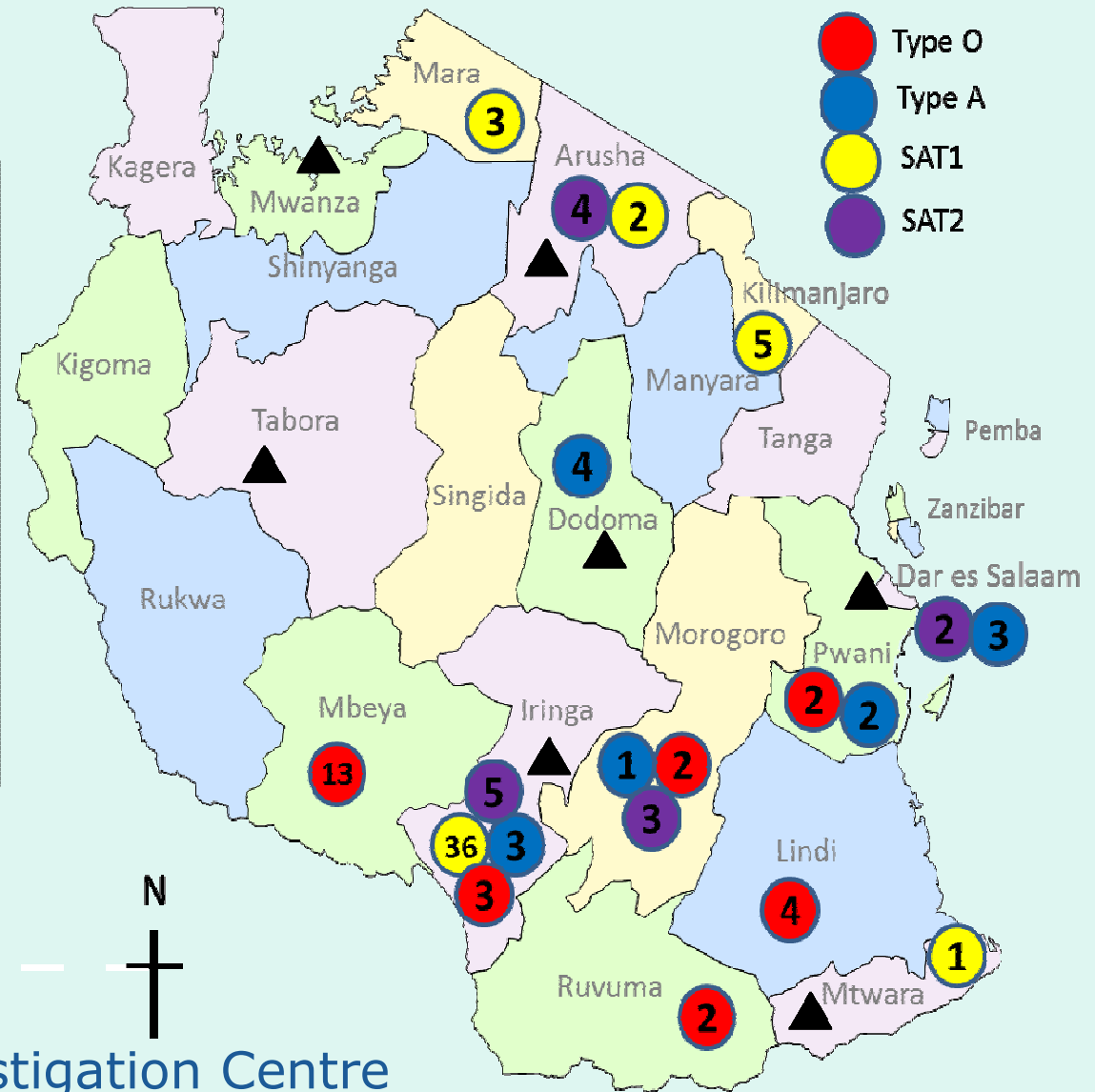
Detection frequency of FMDV serotypes



Geographic distribution of serotypes

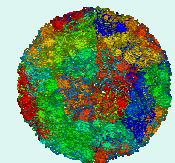
Map of Tanzania

Map of Africa

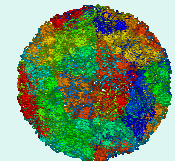


Veterinary Investigation Centre

Phylogenetic tree: serotype "A"



Phylogenetic tree: serotype "O"

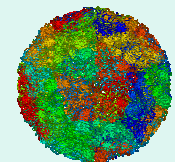


Coloured red: Tanzania strains, which belong to the EA-2 topotype

Phylogenetic tree: serotype "SAT1"

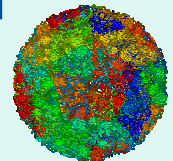


Coloured red: Tanzania strains, which belong to the NWZ and other topotype



Recommendations

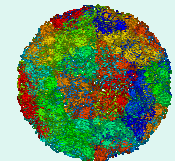
- FMD outbreak investigation:
 - More sample collection and appropriate diagnosis is needed
- Research to describe the complex epidemiology and endemicity of FMD in Tanzania and other parts of Africa is needed
- Molecular characterisation and analysis of many FMD samples is needed to elucidate the phylodynamics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



Phylogenetic tree: serotype "SAT2" (i)

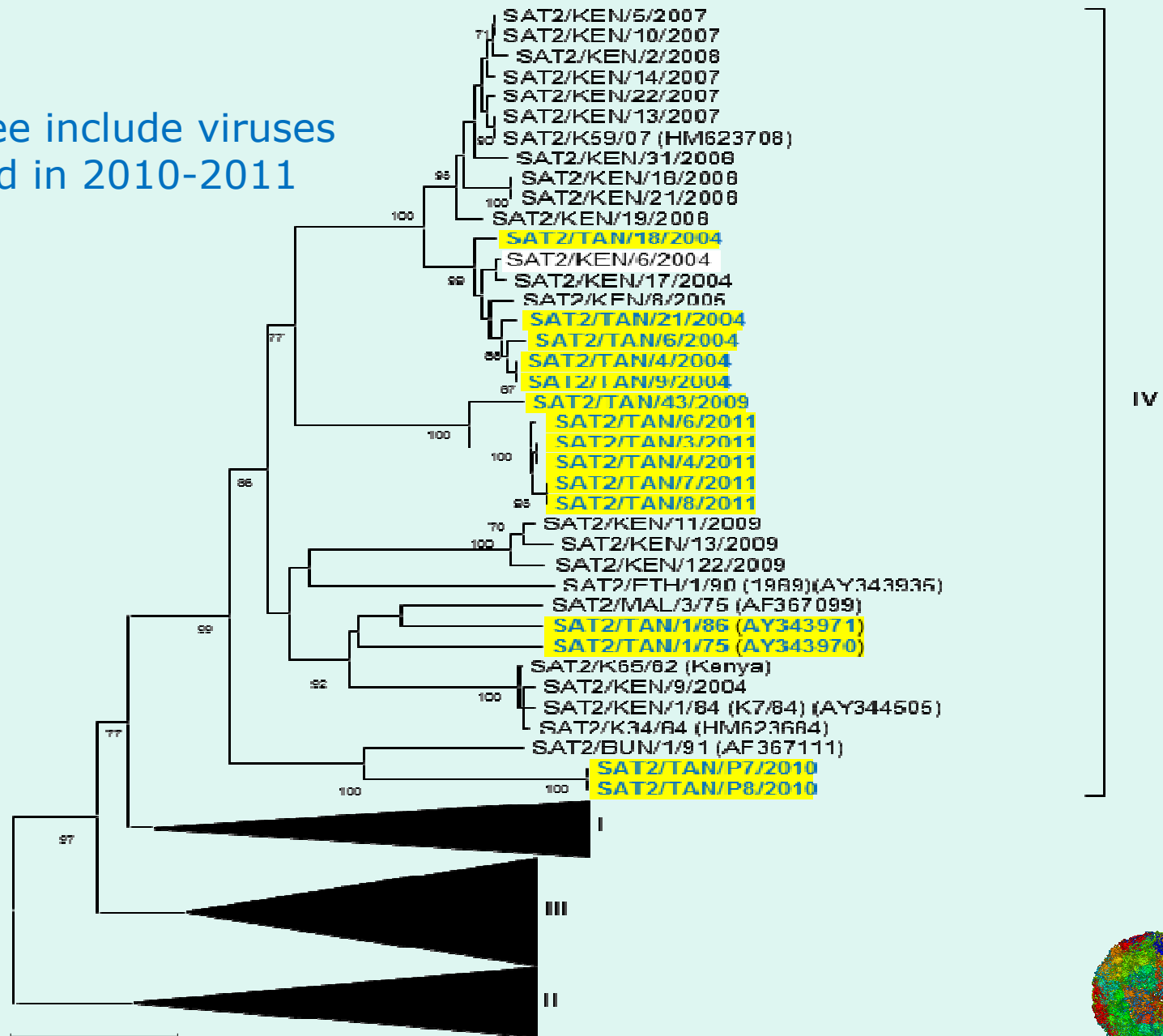


Coloured blue: Tanzania strains, which belong to the IV topotype

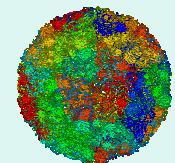


Phylogenetic tree: serotype "SAT2" (ii)

Note:
The tree include viruses
isolated in 2010-2011

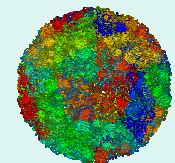


Coloured blue: Tanzania strains, which belong to the IV topotype



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 prerequisite for control of FMD in Tanzania and other parts of Africa



Acknowledgement

wellcometrust



Directors: CVL and DVS in Tanzania