

Molecular Biological Characteristics of Foot-and-Mouth Disease Virus in the African Buffaloes in Southern Africa

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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



FMDV genome orientation

* putative functions

The diagram illustrates the FMDV genome orientation from 5' UTR to 3' UTR. The genome is represented as a horizontal bar divided into colored segments corresponding to different proteins or protein regions. Above the bar, labels indicate various functional domains: Protease (L), Capsid (1A VP4, 1B VP2, 1C VP3, 10 VP1), Carboxy-terminal self-cleaving (2A, 2B), NTP binding*, Membrane-binding (3A), Genome-linked (VPg) (3B), and Polymerase (3D). Below the bar, arrows indicate primary and secondary cleavage sites. A scale at the bottom shows kilobases from 0 to 8. A green vertical box highlights the variable VP1 region, which is noted as being used for isolate characterisation.

5' UTR

VPG

Poly(C)

Protease

Capsid

Carboxy-terminal self-cleaving

NTP binding*

Membrane-binding

Genome-linked (VPg)

Protease

Polymerase

3' UTR

AAA_(n)

Primary cleavages

Secondary cleavages

Kilobases

variable VP1 region
sequences used for isolate characterisation

Aim of the study

- The aim of this paper was to determine the genetic relationship of FMDV serotypes recovered from animals in 3 National Parks within Southern Africa
- The results of this study were used to infer the molecular epidemiology of FMD in the region



Samples and analysis



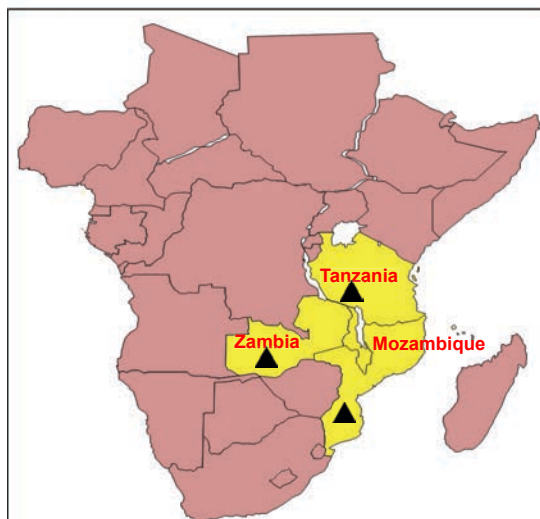
- 150 probang samples collected in 2010 were submitted to OVI and the WRLFMD for analysis
- Lab analysis for FMDV was conducted by VI, Antigen ELISA, real-time RT-PCR and sequencing of the VP1 gene
- Descriptive statistics for serotype detection, genotype/topotype and distribution
- Phylogenies of VP1 sequences were determined by Neighbor-joining method



Study areas in Southern Africa



- Selected areas in Tanzania (Katavi), Zambia (Lochinvar) and Mozambique (Morromeu) were used for FMDV surveillance in both domestic and wild animals



Note:

Yellow colour indicates countries investigated in Southern Africa



Geographic location of National Parks in countries





FMDV genome detection by qRT-PCR



Location	Spp	Number Tested	Number Positive	% Positive
Tanzania - Katavi	Buffalo cattle	25 25	23 3	93 10
Zambia -Lochinvar	Buffalo cattle	25 25	0 1	0 4
Mozambique - Morromeu	Buffalo cattle	25 25	17 2	68 8
Total		150	46	30.7

Note: The Ct values ranged from 26.20 – 40.25

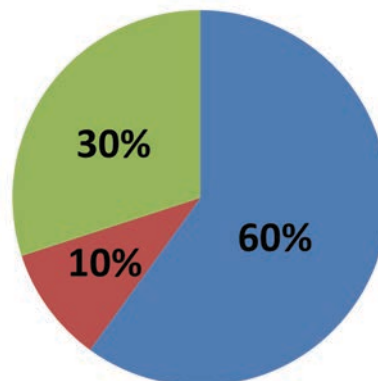
FMD viruses were isolated in **21.7%** (10 out of 46 FMDV GD), and subsequently sequenced for VP1 gene



Detection frequency of FMDV serotypes



■ SAT1 ■ SAT2 ■ SAT3



Phylogenetic tree: serotype SAT 1

Katavi NP (Tanzania)

Phylogenetic tree showing SAT serotypes for Katavi NP (Tanzania). The tree is rooted on the left and branches out to the right. A scale bar at the bottom indicates 0.02 substitutions per site. A legend at the bottom right shows Roman numerals I through VIII. A small globe icon is at the bottom right.

Morroemu NP (Mozambique)

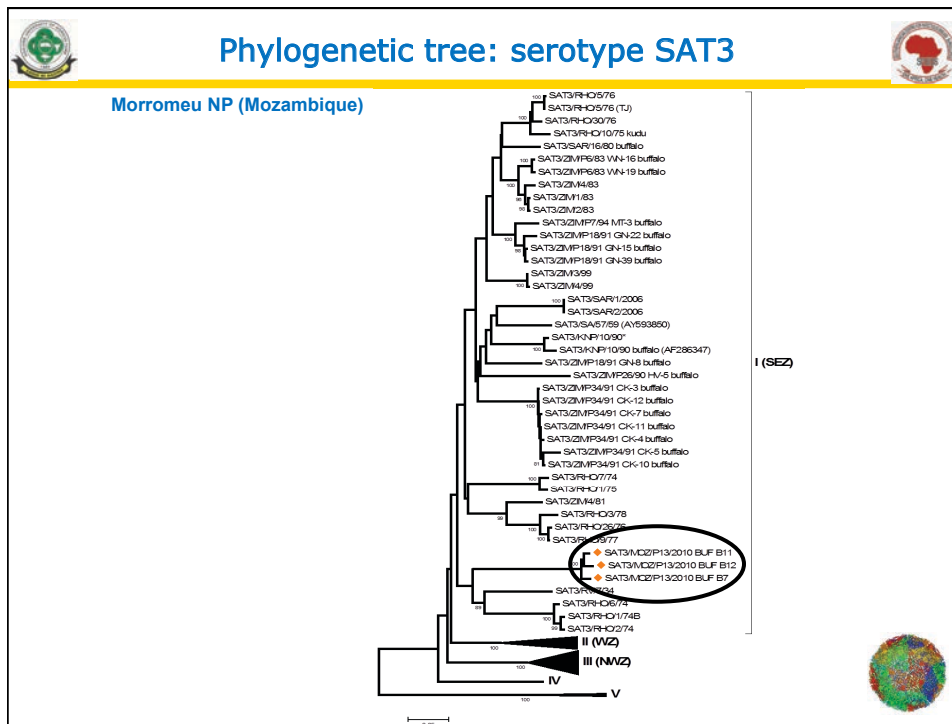
Phylogenetic tree showing SAT serotypes for Morroemu NP (Mozambique). The tree is rooted on the left and branches out to the right. A scale bar at the bottom indicates 0.02 substitutions per site. A legend at the bottom right shows Roman numerals I through VIII. A small globe icon is at the bottom right.

Phylogenetic tree: serotype SAT2

Lochinvar NP (Zambia)

Morromeu NP (Mozambique)

The image displays two phylogenetic trees side-by-side, both rooted at the top. The left tree is labeled 'Lochinvar NP (Zambia)' and the right tree is labeled 'Morromeu NP (Mozambique)'. Both trees show a large cluster of SAT2 serotypes, with a smaller cluster of SAT2 serotypes (SAT2-28A1-100, SAT2-28A1-101, SAT2-28A1-102, SAT2-28A1-103, SAT2-28A1-104, SAT2-28A1-105, SAT2-28A1-106, SAT2-28A1-107, SAT2-28A1-108, SAT2-28A1-109, SAT2-28A1-110, SAT2-28A1-111, SAT2-28A1-112, SAT2-28A1-113, SAT2-28A1-114, SAT2-28A1-115, SAT2-28A1-116, SAT2-28A1-117, SAT2-28A1-118, SAT2-28A1-119, SAT2-28A1-120, SAT2-28A1-121, SAT2-28A1-122, SAT2-28A1-123, SAT2-28A1-124, SAT2-28A1-125, SAT2-28A1-126, SAT2-28A1-127, SAT2-28A1-128, SAT2-28A1-129, SAT2-28A1-130, SAT2-28A1-131, SAT2-28A1-132, SAT2-28A1-133, SAT2-28A1-134, SAT2-28A1-135, SAT2-28A1-136, SAT2-28A1-137, SAT2-28A1-138, SAT2-28A1-139, SAT2-28A1-140, SAT2-28A1-141, SAT2-28A1-142, SAT2-28A1-143, SAT2-28A1-144, SAT2-28A1-145, SAT2-28A1-146, SAT2-28A1-147, SAT2-28A1-148, SAT2-28A1-149, SAT2-28A1-150, SAT2-28A1-151, SAT2-28A1-152, SAT2-28A1-153, SAT2-28A1-154, SAT2-28A1-155, SAT2-28A1-156, SAT2-28A1-157, SAT2-28A1-158, SAT2-28A1-159, 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SAT2-28A1-424, SAT2-28A1-425, SAT2-28A1-426, SAT2-28A1-427, SAT2-28A



- Discussion**
- 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
 - Presence of multiple serotypes and topotypes complicates FMD control in the region
 - Understanding the epidemiology, transmission dynamics, genetic and antigenic characteristics of circulating FMDV is a pre-requisite for control of FMD in sub-Saharan region



Recommendations



- FMDV surveillance and outbreak investigation:
 - More sample collection and appropriate diagnosis is needed
- Research to describe the complex epidemiology, transmission dynamics and endemicity of FMD in sub-Saharan Africa is needed
- Molecular characterisation and analysis of many FMD samples in livestock-wildlife interface areas is needed to elucidate the transmission-phylogenetics and evolutionary nature of FMDV
- Antigenicity, cross-protection and vaccine-matching of the field isolates to be continuously conducted



Summary and conclusion



- The aim of this paper was to determine the genetic relationship of FMDV serotypes recovered from Southern Africa
- Serotypes SAT1, SAT2 and SAT2 viruses prevail in Katavi (Tanzania), Lochinvar (Zambia) and Morromheu (Mozambique) National Parks areas, and contribute to FMD endemicity in those countries
- However, the epidemiology and factors associated with endemicity and genetic diversity of the virus remains unclear and need to be investigated
- Consistent FMD surveillance, genetic and antigenic characterisation of FMDV in livestock-wildlife interface areas is recommended for understanding endemicity and hence rational control measures of the disease



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