Molecular epidemiology of foot-and-mouth disease viruses 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
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 (+ topotype/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
<table>
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<tr>
<th>Serotype</th>
<th>Years detected</th>
<th>Countries in the region</th>
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Phylogenetic trees

Serotype “A”

Serotype “O”

Kasanga et al., 2015 - TBED
Phylogenetic trees

Serotype “SAT1”

Serotype “SAT2”

Kasanga et al., 2015 - TBED
**Phylogenetic tree: serotype SAT 1-3 from buffalo**

**SAT 1**
- SAT1/RV/11/37 kudu (AY593839)
- SAT1/AM/5/66 (AY593846)
- SAT1/ROO/5/66 (AY593846)
- SAT1/MOZ/P13/2010 buffalo B16 (KF219693)
- SAT1/T15/71 (HQ267519)
- SAT1/BEC/1/48 (AY593838)
- SAT1/BOT/1/68 (AY593845)
- SAT1/BOT/1/77 (KF219686)
- SAT1/UGA BUFF/21/70 buffalo (KF219682)
- SAT1/UGA/1/97 buffalo (AY442012)
- SAT1/ETH/3/2007 (FJ798154)
- SAT1/NIG/11/75 (AF431711)
- SAT1/UGA/13/74 (AY442010)
- SAT1/ISR/4/62 (AY593844)
- SAT1/SUD/3/76 (DQ009725)

**SAT 2**
- SAT2/CAR/8/2005 (JK570616)
- SAT2/SAU/6/2000 (AF367135)
- SAT2/RWA/1/2000 (AF367134)
- SAT2/ZAI/1/74 (DQ009737)
- SAT2/UGA/51/75 (AY343963)
- SAT2/KEN/3/57 (AJ251473)
- SAT2/KEN/2/84 (AF343941)
- SAT2/UGA/19/98 (AY343969)
- SAT2/ZAI/1/82 (AV367100)
- SAT2/GHA/2/90 (AF479415)
- SAT2/GNI/2/75 (AF367139)
- SAT2/ANG/4/74 (AF479417)
- SAT2/ZAM/5/81 (EF134951)
- SAT2/ZAM/7/83 (AF367100)
- SAT2/UGA/19/98 (AY343969)
- SAT2/ZAI/1/82 (AV367100)

**SAT 3**
- SAT3/SA/57/59 (AY593850)
- SAT3/KNP/10/90 buffalo (AF286347)
- SAT3/BEC/20/61 (AY593851)
- SAT3/BEC/1/65 (AY593853)
- SAT3/ZIM/25/91 UR-5 buffalo (DQ009740)
- SAT3/ZAM/2/96 MUL-4 buffalo (DQ009741)
- SAT3/UGA/27/70 buffalo (KF219685)
- SAT3/UGA/2/97 buffalo (DQ009742)

**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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