Overview of FMD epidemiology in East Africa with focus on Kenya/Uganda

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Abraham K Sangula
FMD Lab, Embakasi/Makerere University
Status of FMD in EA

- **Endemic**
- **Recorded serotypes**
  - SAT2: Kenya (1956-2010), Uganda (1956-2007), Tanzania (1954-?)
FMD recorded outbreaks in Kenya: 1954-2006
From: Sangula et al., 2009, unpublished
Highlights of results from the livestock wildlife diseases project studies at Makerere

• Serological studies in Uganda
  - Domestic small ruminants
    • Seropositive for: O, A, SAT1, SAT2 & SAT3? (Balinda et al., 2009: Transboundary Animal Diseases)
  - African buffalo
    • Seropositive for: SATs, O? (Ayebazibwe et al., 2009, unpublished)
  - Non-buffalo wildlife
    • Nil seropositive (Ayebazibwe et al., 2009, unpublished)
  - Cattle at the wildlife livestock interface
    • Seropositive for: O, SAT1, SAT2 & SAT3? (Mwine et al., 2009, unpublished)
Molecular epidemiology studies

- **Uganda**
  - Bufallo isolates
    - SAT1 & SAT2 (Ayebazibwe et al., 2009, BMC Vet Res, in press)
  - Cattle isolates
    - SAT2 (Balinda et al., 2009, Epid & Inf)
    - Type O (Balinda et al., unpublished)

- **Kenya**
  - Cattle isolates (Embakasi collection)
    - O, A, C, SAT1 & SAT2 (Sangula et al., 2009, unpublished)
Current outbreak strains

Evolutionary relationships among serotype O foot-and-mouth disease virus in East Africa
Sangula et al., unpublished
Type O

- Predominant serotype - livestock - major role in epid
  - 4 topotypes
    - EA-1
      - Kenya, Uganda
      - Reduced circulation, K77/78 vaccine strain belongs
    - EA-2
      - Widespread across the region from the 1980s
      - Predominant at the moment
    - EA-3
      - Ethiopia, Kenya, Sudan
    - EA-4
      - Ethiopia, Uganda
Low diversity of foot-and-mouth disease serotype C virus in Kenya Sangula et al., unpublished

Phylogenetic relationships of FMDV type C
Type C

- Disappeared since 2004 when last reported in Kenya, where is it?
- Least genetic diversity i.e. closely related strains
Evolutionary analysis of foot-and-mouth disease virus serotype SAT 1 isolates from East Africa suggests two independent introductions from southern Africa. Sangula et al., unpublished.
SAT1

- Strains common to Kenya and Tanzania
- Uganda has strains not shared with Kenya and Tanzania
- Different introduction events for Uganda and Kenya/Tanzania from southern Africa
- Buffalo role likely to be important (serological evidence and virus isolation in e.g. Uganda)
- Low evolution rate found for the EA SAT1 viruses
Co-circulation of two extremely divergent serotype SAT 2 lineages in Kenya highlights challenges to foot-and-mouth disease control. Sangula et al., unpublished
SAT2

- Most prevalent SAT serotype
- 2 very different lineages co-circulated in Kenya for very long period
- Bufallo role likely to be important in epidemiology (serological and virus isolation evidence e.g. in Uganda)
High genetic diversity of foot-and-mouth disease virus serotype A in Kenya: a challenge to vaccination strategies
Sangula et al., unpublished
Type A

- Wide distribution across the eastern Africa region
- Less prevalent than type O
- In Kenya, type A viruses:
  - Show high genetic diversity
  - Belong to 2 lineages with no spatial structuring (i.e. both have countrywide distribution)
Conclusions

• Type O is the preorminant serotype responsible for most outbreaks in livestock. Current outbreak strains in EA are genetically distant from vaccine strain.

• Type A has a high genetic diversity and is widely distributed across the region whereas type C has the least genetic diversity, and its current status needs survey in Kenya were it was last reported in 2004.

• Among the SATs, SAT2 is most widespread. Wildlife role (Bufallo) is important in epidemiology but Very few isolates are available and there is therefore a need for sampling. SAT3 activity in Uganda needs survey

• Overall, the resolution of circulation patterns of FMDV in EA is undermined by limited number of isolates and there is need for constant sampling.
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