



**SOUTHERN AFRICAN CENTRE
FOR
INFECTIOUS DISEASE SURVEILLANCE**

INVESTIGATION OF FMD OUTBREAKS IN MBALA & KAZUNGULA DISTRICTS IN ZAMBIA

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FMD in Zambia

- Foot-and-mouth disease (FMD) is endemic in Zambia.
- First FMD outbreak reports ~ 1933
- Cattle Pigs, small ruminants, wild animals are affected
- Outbreaks occur in different geographic regions
- Factors associated with outbreaks are not clear
- Spatio-temporal distribution of FMD virus has not been clearly investigated



FMD in Zambia

- The restrictions of livestock and wildlife movement at interface areas and between national borders is limited.
- However the disease is considered as an important TAD in the country
- As government spends huge sums of money on FMD vaccination programs each year

Map of Zambia showing high risk areas of FMD



Objectives

- To investigate and determine the molecular biological characteristics of FMD viruses from 2012 FMD outbreak of Mbala and Kazungula districts of Zambia, focusing on development of rational control methods of FMD.
- To examine FMDV genome in the samples
- To determine the serotype of FMDV detected



Observations

- Animals were carefully examined for presence of characteristic clinical signs of FMD.
- Principal clinical signs were salivation and lameness i.e in both outbreaks
- Most animals showed foot lesions
- Kazungula : mouth lesions consisted of erosions and ulcers on the tongue and dental pad
- Healing mouth lesions observed in Mbala





Sample collection and preservation

- Sampled 60 epithelial tissues / oesophageal–pharyngeal (OP) scrapings
- Mbala (n = 51) & Kazungula (n = 9)
- Epithelial and vesicular tissues were collected from cattle showing oral and foot lesions
- Preserved in equal amounts of glycerol and 0.04 M phosphate buffer, at pH 7.2–7.6
- OP samples – were preserved in L/Nitrogen

Analysis

- Samples were analysed at CVL, Dar es Salam for FMDV.
- Viral RNA was examined by one-step real time reverse transcriptase polymerase chain reaction (qRT-PCR)
- Whilst FMDV serotypes were examined by serotype-specific antigen ELISA(OIE protocol)

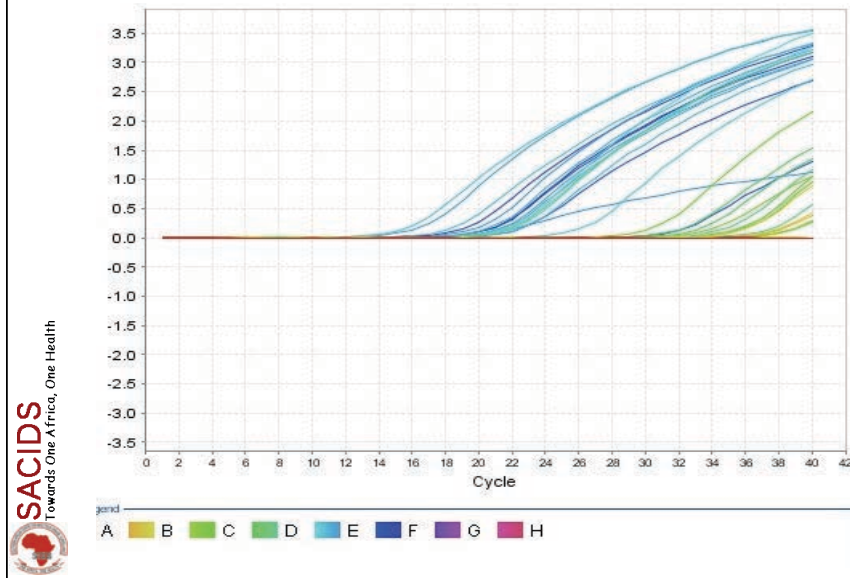


Results

- 22 samples (36.7 %) were positive for FMDV genome by qRT-PCR with Ct values ranging from 13 to 32.
- Epithelial tissue samples showed relatively lower Ct values than those obtained from OP scrapings, irrespective of geographic location.
- Kazungula samples showed lower Ct values than Mbala, values ranged between 13 and 18



Amplification plot for qRT-PCR



Results (Cont)

- Forty percent (40%; $n = 4$) of epithelial tissues from Mbala district were typed by antigen ELISA into serotype SAT 2.
- There was no correlation of Ct values in qRT-PCR with antigen detection in samples collected from Kazungula district.

Discussion and Conclusion

- These findings indicate that the FMD outbreaks that occurred in Mbala and Kazungula were ascribed to at least serotype SAT 2 Viruses.
- The observed high Ct values of samples from both outbreaks, with the clinical signs of FMD also confirm majority of the animals in these herds had been infected by FMDV.

Discussion and Conclusion

- Regular interaction between buffalos from Mosi-o Tunya Park and domestic animals from surrounding areas could be incriminated in the observed regular FMD outbreaks in Kazungula
- Uncontrolled animal movements across borders between Mbala and Sumbawanga in Tanzania might be responsible for disease outbreaks in Mbala.

Recommendations

- Participatory sensitization of wildlife officials and cattle owners grazing their cattle in the national parks about the potential risk of transmission of FMDV from cattle to wildlife or vice versa be carried out.
- Because of the porous borders, a regional FMD control strategy should be developed.



Recommendations

- In-depth molecular biological studies, including sequencing and phylogeny of the viruses, should be conducted.
- This is in order to elucidate the complex epidemiology of FMD in Zambia
- This will provide valuable information needed for a rational control strategy of FMD in Zambia and the neighbouring countries.



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