# The changing landscape of the molecular epidemiology of foot-and-mouth disease virus in southern Africa north of Limpopo and east Africa

**Author:**
Christopher J. Kasanga[1]

**Affiliation:**
[1]Southern African Centre for Infectious Disease Surveillance, Sokoine University of Agriculture, Tanzania

**Correspondence to:**
Christopher Kasanga

**Email:**
christopher.kasanga@sacids.org

**Postal address:**
PO Box 3019, Chuo Kikuu, Morogoro, Tanzania

**How to cite this article:**
Kasanga, C.J., 2014, 'The changing landscape of the molecular epidemiology of foot-and-mouth disease virus in southern Africa north of Limpopo and east Africa', *Onderstepoort Journal of Veterinary Research* 81(2) Art. #730, 1 page. http://dx.doi.org/10.4102/ojvr.v81i2.730

**Note:**
Proceedings of the 2nd One Health Conference in Africa. Jointly organised by the Southern African Centre for Infectious Disease Surveillance and the Tanzania National Institute for Medical Research, held at the Snow Crest Hotel in Arusha, Tanzania from 16th to 19th April 2013: http://www.sacids.org/kms/frontend/index.php?m=119.





Foot-and-mouth disease (FMD) is endemic in most countries of southern and eastern Africa. It affects cloven-hoofed animals that include livestock and wildlife. FMD is caused by FMD virus (FMDV), the single stranded positive sense RNA virus, with a high rate of genetic mutation(s). southern and eastern Africa relies profoundly on livestock production as a source of economic growth and livelihoods. Despite the importance of FMD in Africa, the epidemiology of FMDV and factors contributing to the endemicity of FMD in susceptible animal populations are not clearly known in the region. In this study, molecular characteristics of FMD virus detected in southern Africa north of Limpopo and eastern Africa were determined using methods such as VI, antigen-ELISA, RT-LAMP, real-time RT-PCR, sequencing of the VP1 and phylogenetic analysis. The findings of this study indicate that serotypes A, O, SAT 1, SAT 2 and SAT 3 predominate in both the African buffalo (*Syncerus caffer*) and cattle in the region. Furthermore, the performance of RT-LAMP discloses its superiority to real time RT-PCR with high potential for the specific detection and surveillance of infectious diseases of humans and animals in the region. In-depth phylogenetic analysis of VP1 sequences reveals the existence unassigned topotype(s) among serotype SAT 1 viruses detected from buffalo in Mozambique. Whole genome sequencing of the virus within the unassigned topotype unravels close genetic relationship to viruses detected in southern Africa with 94% closest nucleotide homology to SAT1rhod5/66 strain isolated from cattle in Zimbabwe in 1966. The presence of multiple serotypes and topotypes, uncontrolled animal movements and the presence of several risk factors for disease occurrence complicate control of FMD in the region. The RT-PCR and whole genome sequencing strategy established in the current study could be deployed to study the evolutionary characteristics of viruses sampled from cattle and buffalo at different locations in time and space. It is suggested that in-depth genome analysis should be conducted to uncover sequence-based evidence for FMDV endemicity in the region. This information is necessary for FMD control strategies in most countries in Africa. The genome sequencing approach allows for targeted and cost-effective FMD control strategies in the endemic settings of southern and eastern Africa rather than application of blanket and expensive interventions – an important consideration for resource constrained countries in the region.

## Acknowledgements

This work was supported by the Wellcome Trust Grant WT087546MA to the Southern African Centre for Infectious Diseases & Surveillance (SACIDS).