

## Foot and mouth disease in sub-Saharan Africa moves over short distances, wild buffalo are a problem

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New research shows that in sub-Saharan Africa the virus responsible for foot and mouth disease (FMD) moves over relatively short distances and the African buffalo are important natural reservoirs for the infection. The study, published in *mBio*, the online open-access journal of the American Society for Microbiology, sheds light on how the type of FMD virus called SAT 2 emerged in sub-Saharan Africa and identifies patterns of spread in countries where SAT 2 is endemic.

"The data suggest that the common ancestor of all SAT 2 was in [African] buffalo. It's very clear that historically infections have moved from buffalo to cattle," says corresponding author Matthew Hall of the University of Edinburgh in Scotland.

Foot and mouth disease (FMD) is devastating to livestock all over the world, but it's a particular problem in Africa, where wildlife that harbor the virus are thought to pass it on to their domesticated cousins.

FMD strikes cloven-hoofed animals, presenting as a high fever, blistering in the mouth and feet, decline in milk production in females, and weight loss. Although most animals recover over the course of months, some die of complications from the disease. In wild buffalo, the disease is very rarely symptomatic and animals can be persistently infected for a period of several years. The SAT 2 serotype of the virus is endemic in sub-Saharan Africa, but it has crossed the Sahara and caused



outbreaks in North Africa and the Middle East between 1990 and 2012.

In the hopes they could eventually predict future outbreaks, Hall and his colleagues wanted a better picture of the diversity of SAT 2 <u>viruses</u> in sub-Saharan Africa and how they move around from one location to another. They used 250 genetic sequences of the VP1 section of the genome from SAT 2 isolates taken from all over sub-Saharan Africa and tracked the appearance of the various unique 'topotypes' over the region.

Hall says the patterns in which the topotypes appear in different places gives strong support to the idea that the virus is spread by infected hosts in land movements over relatively short distances. What's more, African buffalo are an important "maintenance host", meaning they maintain a reservoir of the virus that can re-infect domesticated animals after time and culling has ended an outbreak among livestock. The relationships between the 250 sequences also indicate that it's possible the original source of the SAT 2 viruses that are now found in wild and <u>domesticated animals</u> was African buffalo.

To Hall, these results indicate that genetic tracking of viruses has a lot of potential for making inferences about viral spread and heading off future outbreaks.

"We showed that we can demonstrate [virus movement] using genetic data. It's a tool that can be used for that kind of inference. In cases where less is known, this is a valid way of going about answering the questions," says Hall.

Going forward, Hall says he plans to apply a similar approach to studying serotype O FMD viruses in Africa, Asia, and South America to identify links between different animal populations. "It's good to know the reason it spreads," says Hall. "It could be quite a contribution to eradication or control efforts."



## Provided by American Society for Microbiology

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