

Genetic characterisation of foot-and-mouth disease viruses circulating in major cattle production zones in western Uganda

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Background

Foot-and-mouth disease (FMD) is a major trans-boundary animal disease that affects all cloven hoofed animals. FMD is endemic in Sub-Saharan Africa and is generally characterised by lesions on the foot and in the mouth (figures 1 and 2). In Uganda, efforts to control FMD, have registered very minimal success. FMD has persisted and the frequency of outbreaks is on increase (Ayebazibwe *et al.*, 2010).

Little is known about the circulating FMD viral strains in Uganda, yet based on some studies (Kitching *et al.*, 2007) effective control of FMD is based on antigenic specificity of the vaccine. This study therefore was designed to determine the genetic diversity of FMD viruses within the major cattle production zones in Western Uganda.

Materials and methods

The study was conducted in the districts of Rakai, Mbarara and Kasese. A total of 67 samples were collected from cattle and pigs (Table1). Inclusion of the pigs in Rakai was based on farmers' reports that their pigs had FMD. So far 57 samples have been analysed for the first phase. This phase included subjection to RNA extraction, cDNA synthesis and FMDV DNA diagnostic PCR using two primer sets for presence of FMD virus. So far, 17 samples were positive to FMD. These are being prepared for phase two analysis which involves serotype specific PCR, sequencing and phylogenetic analysis.

Table 1: Samples collected from cattle and pigs

Samples	Cattle	Pigs
Oropharyngeal tissue	50	00
Lesion swabs	07	04
Blood samples	00	06
Total	57	10

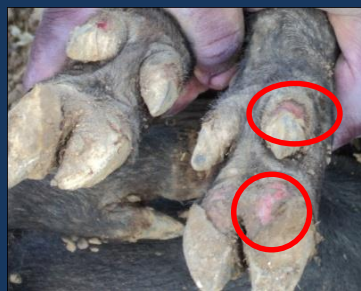


Fig 1: FMD Lesions on pig hoof



Fig 2: FMD lesions in cattle mouth

Preliminary results

Table 2: Distribution of positive samples

Sample	Cattle		Pigs		Total
	O	SAT	O	SAT	
Oropharyngeal tissue	00	00	00	00	00
Lesion swabs	06	01	03	02	12
Blood samples	00	00	03	02	05
Total	06	01	06	04	17

Discussion

Samples from Mbarara and Kasese were negative whereas most of the samples from Rakai showed positivity in the diagnostic PCR since there was an outbreak there at the time of sample collection. Preliminary analysis show that there are mixed infections in the pigs with both serotype O and the SAT serotypes. This finding has implications on the future control since pigs are usually ignored during vaccination and quarantine schemes. It is also important to note that the pig sty and the kraal were often not far apart. This could have triggered the spread of the virus from one location to the other.

Recommendations

MAAIF and farmers should pay more attention to pigs in terms of the vaccinations and the quarantine schemes. Farmers should be sensitized regarding allocation of different resting places for cattle and pigs to avoid spread of infection. Further analysis will be done to ascertain strains of the FMD by amplification and sequencing of the VP1 coding region.

References

Ayebazibwe *et al.*, 2010 *TropAnimal Health Prod.* 42(7): 1547-1559
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