Foot-and-Mouth disease serotypes SAT1 and SAT2 Epidemiology in East Africa

Abraham K Sangula

Foot-and-Mouth Disease Laboratory, Embakasi
P.O. Box 18021, 00500 Enterprise Road
Nairobi, Kenya.

Abstract:

Foot-and-Mouth Disease (FMD) is endemic in East Africa with six of the seven serotypes occurring thus complicating the epidemiology and control of the disease in the region. During the period 2004-2006, circulating FMD serotypes in Kenya have included types A, C, O, SAT1 and SAT2. In this period, an upsurge of SAT1 and SAT2 outbreaks was recorded. With the support of the Food and Agricultural Organization of the United Nations (FAO) and the Pan African-Programme for the Control of Epizootics (PACE) project, several isolates from Kenya were submitted by the Embakasi FMD laboratory to the World Reference Laboratory, Pirbright, for molecular epidemiology analysis. Results of the sequence analysis indicate the identification of some new genotypes of SAT1 and SAT2 as causing these epidemics and are discussed in this report.

Introduction:

Foot-and-Mouth Disease (FMD) is endemic in East Africa with six of the seven serotypes namely; O, A, C, SAT types 1, 2, and 3 reported to occur thus complicating the epidemiology and control of the disease in the region. Serotype SAT3 has been recorded only in Uganda (Vosloo et al. 2002). It has been suggested that the pastoralist livestock keeping areas in the East African region form ecosystems in which FMD is maintained (FAO/AU-IBAR/PACE FMD workshop, 2006). These ecosystems also play an important wildlife-livestock interface hosting large populations of FMD susceptible wildlife.

In Kenya, the FMD control measures which include vaccinations and animal movement controls have not been applied at an intensity that could curtail the transmission and maintenance of the disease. The multiplicity of serotypes and the low levels of vaccination coverage only serve to complicate the control efforts. Control measures in the country are being enhanced with the focus on improving the diagnostic and surveillance capacities as well as the improvement of the efficiency of vaccinations through better quality and relevant strain vaccines. The goal of these measures is to establish FMD free Zones in parts of the country to promote livestock export trade and production earnings for livestock farmers.

During the period 2004-2006, circulating FMD serotypes in Kenya have included types O, A, C, SAT1 and SAT2 (Figure 1). In the recent past, the majority of the outbreaks in Kenya have been caused by serotypes O and SAT2. Serotype A occurs on a lesser frequency while serotype C has been rare with only one outbreak last reported in 2004. Recently, an upsurge of SAT1 and SAT2 outbreaks was recorded. In the year 2004, one outbreak of SAT1 and nineteen of SAT2 were recorded while three of SAT1 and ten of SAT2 occurred in 2005. At the end of September 2006, seven outbreaks of SAT1 and four of SAT2 have been reported. The upsurge of these outbreaks particularly SAT1 after a long absence, needed further examination on the possible sources of the virus.

Materials and Methods:

With the support of the Food and Agricultural Organization of the United Nations (FAO) and the Pan African-Programme for the Control of Epizootics (PACE) project, fifty three FMD suspect samples from Kenya were submitted by the Embakasi FMD laboratory to the World Reference Laboratory, Pirbright, for serotype confirmation and molecular epidemiology analysis. Of the initial fifteen samples sent, one was confirmed as SAT1 while seven were SAT2. These isolates were all subsequently sequenced. The summary of the Kenyan SAT1 and SAT2 virus isolates sequenced by the World Reference Laboratory are as shown in Table1.
This report considers whether the sequence results provide evidence of wildlife as possible sources of the recent epidemics of the SAT1 and SAT2 in Kenya and also whether the virus distributions support the suggestions that FMD is maintained in the pastoralist ecosystems of the East African region.

Results and Discussion:

Results of the sequence analysis indicate the identification of some new genotypes of SAT1 and SAT2 as causing these epidemics. These viruses could also be from non-livestock sources as suggested by their inability to cause persistent outbreaks in livestock.

Serotype SAT2.

Sequences of the SAT2 isolates indicate that the viruses fall into distinct groups (Figure 2). A group of 2004/2005 viruses from the Central (KEN/10/2004, and KEN/13/2004), Eastern (KEN/17/04) and Rift Valley (KEN/5/2004, KEN/8/2004, KEN/22/2004 and KEN/8/2005) provinces are closely related to viruses isolated from outbreaks of FMD in Tanzania and Malawi in 2004 (98.44 to 99.23% nucleotide identity) suggesting a sweeping regional epidemic. Rwanda 2000-2004 isolates are distinct suggesting a different source for the outbreaks in Rwanda. Similarly the identification of additional genetic types in Kenya represented by 1999 isolates and SAT2/KEN/7/2005 also suggests additional sources of outbreaks such as wildlife.

Two genetic lineages of SAT2 have been identified in East Africa with one group involving Kenya, Rwanda and Uganda while the other involves Kenya and Tanzania (Bastos et al. 2003). These viruses are also suggested to evolve independently. The existence of multiple lineages in Kenya is suggestive of introductions from the cross-border animal movements prevalent in the country (Ndiritu, 1984).

Serotype SAT 1.

Isolate SAT1/KEN/1/2005 from Nyeri District in Central province which was sequenced was not closely related to any other SAT1 viruses in the database. The closest relationship was with the Kenyan vaccine strain T155/71 (88.39%) originally isolated from Northern Tanzania (Figure 3). It is also different from those causing outbreaks in Zambia in 2004. Although the other isolates from the Eastern and Rift valley provinces during the outbreak are yet to be sequenced, field reports suggest spread from this outbreak.

While serotype C has shown no genetic variation in Kenya, the other serotypes occurring in the country namely serotypes O and A have significant variation genetically indicating long and persistent circulation with evidence of geographical/epidemiologic clustering (Mesfin, 2004).

At a recent FAO/AU-IBAR/PACE meeting held in August 2006 in Nairobi, Kenya, it has been suggested that FMD in the East African region exists and spreads in specific pastoralist ecosystems such as the Kagera Basin ecosystem on the Uganda/Rwanda/Tanzania border, the Maasai ecosystem on the Kenya-Tanzania border, and the Somali ecosystem on the Kenya-Somalia border (Figure 4). This suggestion could be supported by these genetic results. For example, the SAT1 genetic relationships suggest circulation and persistence in the Maasai ecosystem. The existence of distinct genotypes of SAT2 with close relationships within the genotype covering different regions may also be an indicator in support of the ecosystem existence of the viruses. Evidence of geographical/epidemiologic clustering of serotypes O and A is also in line with this observation. However, no isolates have been received from the Somali ecosystem and it would be necessary to get isolates from the region and also to study more isolates from the other ecosystems to determine a more complete phylogenetic picture of the viruses. Evidence from provisional study of the population structure of the tribal Somali cattle in the Somali ecosystem suggest extensive gene-flow between clan areas (Muwanika et al. 2005) with the implication of a fast spread of disease in the entire ecosystem once there is an outbreak. Spread from the Somali ecosystem into Eastern Kenya should be occurring and it is possible the isolates in this region are genetically related to the ones in the Somali ecosystem.
Whereas investigations of foot-and-mouth-disease virus diversity in southern Africa have shown that independently evolved sub-serotypes may exist in discrete African buffalo populations (Vosloo et al. 1996, Bastos et al. 2003; Thomson et al. 2003), in East Africa, little is known about the occurrence and distribution of FMD diversity in wildlife. Evidence of viruses emerging from wildlife into the domestic animal populations is therefore difficult to find. However, in Kenya, most cattle clusters are nested within potential wildlife reservoirs thus increasing the risk of FMD spread from wildlife (Bett et al. 2006). The identification of genetically distinct isolates which do not persist in cattle by causing limited outbreaks e.g. SAT2/KEN/7/2005 suggests most likely a wildlife source. Of the SAT1/2 viruses, some seem to go on to cause regional outbreaks (e.g. Kenya/Tanzania/Malawi SAT2 viruses) suggesting that these are probably cattle selected viruses.

Conclusions and recommendations:
The molecular epidemiology of the recent SAT1 and SAT2 outbreaks in Kenya and the earlier findings indicating the geographic and epidemiologic distribution of the viruses provides evidence in support of the suggested ecosystems for FMD in the East African region. However more isolates from the ecosystems need to be sequenced to be able to conclusively establish these findings. Efforts should be directed at obtaining isolates from the Somali ecosystem where very few if any have been sequenced so far. These gaps in information on the circulating FMD viruses need to be filled by regionally co-ordinated efforts.

Given the close interaction between livestock and wildlife in the suggested ecosystems for FMD in the East African region, the molecular epidemiology has provided a clue that wildlife could be responsible for some of the SAT1 and SAT2 epidemics in Kenya. Antigenic comparison should be made to identify if existing vaccines could provide any protection against these currently circulating SAT1 and SAT 2 viruses.

Virus surveillance and typing in East Africa should be enhanced through improved diagnostic capacities so as to help re-build prospects and confidence in trade in livestock. Good collaborative programmes between the vaccine production and diagnostic laboratories like the Embakasi laboratory, the Veterinary Services in the East African region, the World Reference Laboratory and the FAO could result in a regional surveillance network that will improve the control of FMD.

Table 1. Summary of 2004-2005 SAT1 and SAT2 FMD virus isolates from Kenya sequenced by the WRL-Pirbright.

<table>
<thead>
<tr>
<th>WRL Reference</th>
<th>District/ Province of Origin</th>
<th>Year of Sampling</th>
<th>Species of Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td>SAT2/KEN/5/2004</td>
<td>Nakuru/ Rift Valley</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/6/2004</td>
<td>Nairobi/ Nairobi</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/8/2004</td>
<td>Nakuru/ Rift Valley</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/9/2004</td>
<td>Laikipia/ Rift Valley</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/10/2004</td>
<td>Nyandarua/ Central</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/11/2004</td>
<td>Thika/ Central</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/13/2004</td>
<td>Thika/Central</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/17/2004</td>
<td>Machakos/ Eastern</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/22/2004</td>
<td>Nakuru/ Rift Valley</td>
<td>2004</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT2/KEN/7/2005</td>
<td>Thika/ Central</td>
<td>2005</td>
<td>Cattle</td>
</tr>
<tr>
<td>SAT1/KEN/1/2005</td>
<td>Nyeri/ Central</td>
<td>2005</td>
<td>Cattle</td>
</tr>
</tbody>
</table>
Kenyan Reported FMD Outbreaks: 2004-2006

Figure 1: Map of Kenya showing reported FMD Outbreaks per province: 2004-2006
Figure 2: Phylogenetic tree for FMDV SAT2 (produced by WRL-Pirbright).
Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (663 nt). The tree was outgroup-rooted using the SAT1/ISR/4/62 & SAT1/UGA/47/71 sequences.

*, not a WRLFMD Ref. No.

Figure 4. Phylogenetic tree for FMDV SAT 1

Figure 3: Phylogenetic tree for FMDV SAT1 (produced by WRL-Pirbright)
Figure 4: Map of East Africa Showing the Major Pastoralist ecosystems maintaining Foot-and-Mouth Disease.
Acknowledgements:

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References:


Food and Agricultural Organization/African Union-Interafrican Bureau for Animal Resources FMD Workshop, Nairobi, August, 2006).


