Tuesday 12 October, 2010

Theme for the second edition: The FMD problem in relation to wildlife conservation

(1) We need more accurate and complete sample submission history/recording as well as integration of data from different laboratories to make progress with understanding FMD in southern Africa;

(2) More regional co-ordination of data and its interpretation is needed to take account of FMD’s transboundary nature;

(3) There are insufficient data on the distribution of SAT topotypes in buffalo populations to be able to understand the pattern of FMD outbreaks in cattle in the Region (because they ultimately derive from buffalo populations).

Background: As explained in the 1st edition of the Bulletin, (Foot-and-mouth disease: southern Africa [FMD Bulletin]), cattle outbreaks of FMD in the SADC Region caused by SAT2 particularly appear to have increased in frequency since 2003/4. This edition of the FMD Bulletin will attempt to provide more insight and discuss the implications.

It is well established that SAT serotype viruses are maintained by healthy, free-living African buffalo populations although, once established in cattle, SAT viruses appear to be capable of persistence in cattle populations without the need for further contact with infected buffalo. Therefore, the approach of most of southern Africa is, as far as possible, to prevent contact between buffalo and cattle and to eliminate outbreaks as soon as they occur. This has historically been achieved through a combination of animal movement control, often aided by fences, and vaccination of at-risk cattle populations. The 1st edition of the FMD Bulletin pointed out some of the reasons why recent vaccination programmes have been less successful than expected. In this edition we concentrate on the origin of outbreaks in and close to the recently created Kavango-Zambesi Transfrontier Conservation Area (KAZA TFCA) in the context of interaction between wildlife conservation and FMD management.

Fencing as a means of managing FMD in southern Africa and the environmental effects that FMD-control fences have had and continue to have is an on-going point of dispute between conservationists and livestock farming interests. The problem is that the benefits as well as the environmental consequences of fences are difficult to measure and are therefore subject to conjecture. However, with escalating environmental awareness globally and the growing income derived from eco-tourism for countries of the SADC Region (foreign exchange earnings from tourism now exceed those of livestock, forestry and fisheries combined!),

OIE Collaborating Centre
Since May 2009, the World Organization for Animal Health (OIE) has recognized the Department of Veterinary Tropical Diseases (DVTD) and its consortium partners as a Collaborating Centre for Training in Integrated Livestock and Wildlife Health and Management.

One of the major roles of the Collaborating Centre is to assist the OIE in developing and offering training in the management and health of livestock and wildlife with particular reference to sub-Saharan Africa.

The overall objectives of the Collaborating Centre are to support quality livelihoods, optimal animal health and production, rural development, ecosystem health, biodiversity, food security and sustainability.

Other Consortium partners:
University of Pretoria, SA (Centre for Veterinary Wildlife Studies, Department of Animal and Wildlife Sciences, Department of Agricultural Economics, Extension and Rural Development);
Onderstepoort Veterinary Institute, SA;
Animal Health Department of the Institute of Tropical Medicine, Antwerp, Belgium;
National Institute for Communicable Diseases, SA;
Department of Agriculture, Fisheries and Forestry, SA.
the need for and alignment of animal disease control fences are increasingly under scrutiny. A review dealing with this subject has recently been published by the Mammal Research Institute, University of Pretoria and can be accessed on-line (http://www.wcs-ahead.org/gltfca_grants/grants.html). Much information is contained in the collection of papers edited by Ken Ferguson and John Hanks.

Perhaps the most far-reaching and imaginative conservation initiative for many decades – the transfrontier conservation area (TFCA) or Peace Parks movement – is evolving rapidly in southern Africa. The idea is to conserve unique bio-diversity and wilderness areas. There are, of course, many obstacles to the realization of the vision of "a network of protected areas that link ecosystems across international borders and create wildlife dispersal routes between them or, in some circumstances, link them". This vision is clearly incompatible with the perceived need for fences to control movement of wild and domestic animals in order to manage animal diseases. Currently, 13 terrestrial TFCAs are foreseen for the Region covering approximately 1.2 million km² (Figure 1). The largest of these is the Kavango-Zambesi (KAZA) TFCA which extends across 5 countries and covers an area larger than Italy. It includes major wetlands such as the Okavango Delta and most of Africa’s charismatic wildlife species including about 250 000 elephants; the largest population in the world. What is often overlooked is that it is also home to more than a million people, mostly poor, and their livestock. Livestock are socially and economically important to these people as well as others living in the vicinity of the KAZA TFCA. In fact, a number of southern African countries plan to expand cattle production in this general area and export beef as an important element of future rural development. At present this requires creation of so-called FMD-free zones that are clearly separated from areas where wild or domestic FMD-infected animal populations occur. Fencing, impermeable to both livestock and cloven-hoofed wildlife, is usually necessary to achieve this.

Figure 1. Southern African Peace Parks
An inevitable consequence of the development of TFCAs generally and the KAZA TFCA in particular is that numbers and distribution of FMD-infected buffalo will increase, resulting in more frequent contact between buffalo and cattle and therefore potentially more frequent FMD outbreaks in cattle. As it is, most FMD outbreaks that occurred in southern Africa in the period 2005-present were located in or near the KAZA TFCA (Figure 2). Even more important is that, based on the ability to compare virus isolates accurately by genome sequencing (i.e. by comparison of the nucleotide sequences of their RNAs), we now know that the occurrence of cattle outbreaks is sometimes unexpected and not deducible without this technology. Therefore, effective management of endemic FMD in this setting is dependent on the availability of effective vaccines and the ability to follow viral transmission using modern molecular epidemiological methods.

While genome sequencing has added an important element to FMD management worldwide, recent experience in southern Africa has shown that its application needs to be better coordinated. The OIE/FAO FMD Reference Laboratories Network offers potential in this regard. The accounts below illustrate this point.

**Figure 2. KAZA-TFCA showing FMD outbreaks 2005-August 2010**

![Map of FMD outbreaks in southern Africa 2005-2010](image)

**SAT outbreaks in cattle recorded between 2005 and August 2010**

Table 1 summarises the 13 SAT outbreaks in cattle recorded in the KAZA TFCA area over the last 5 years. This list is certainly an underestimate because it is evident that some outbreaks have not been reported to the World Organisation for Animal Health (OIE). Some data additional to that available from WAHIS on the OIE website has become available from the FMD reference laboratories website (ReLaIS) to which diagnostic material was submitted. WAHID and ReLaIS data have been used in drafting the account of events that follow.

The first interesting point to note from Table 1 is the preponderance of SAT2 viruses associated with cattle outbreaks. Historically in this part of southern Africa, SAT2 has accounted for approximately half of FMD outbreaks, with SAT1 and SAT3 jointly accounting for the other 50% (outbreaks due to other serotypes are rare except in the northern regions of the sub-continent). This apparent increase in SAT2 activity could be due to the SAT2 component of the FMD vaccine in current use being less efficacious than the other components (i.e. SAT1 & SAT3).
Table 1. SAT FMD outbreaks in the area of the Kavango-Zambesi TFCA: 2005-August 2010

<table>
<thead>
<tr>
<th>No.</th>
<th>Country</th>
<th>Location</th>
<th>Start date</th>
<th>End date</th>
<th>Virus Isolates</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>Botswana</td>
<td>Selibe-Phikwe District</td>
<td>April 2006</td>
<td>Nov 2006</td>
<td>SAT2 WRL, SAT2/BOT/1, 5, 8/2006</td>
<td>Infection suspected to have originated from adjacent Zimbabwe</td>
</tr>
<tr>
<td>3</td>
<td>Botswana</td>
<td>Pandamatenga, Kasane, Kachikau &amp; Satau Districts of Zone 1</td>
<td>June 2006</td>
<td>July 2006</td>
<td>SAT1 WRL, SAT2/BOT/124/2006</td>
<td>Outbreak situated close to the Chobe NP &amp; Caprivi border (Namibia)</td>
</tr>
<tr>
<td>4</td>
<td>Botswana</td>
<td>Habu Extension Area, Ngamiland</td>
<td>Oct 2007</td>
<td>Nov 2009</td>
<td>SAT2 WRL, SAT2/BOT/2, 3, 5, 6/2007 WRL, SAT2/BOT/5-8/2009</td>
<td>Extensive &amp; persistent outbreak that spread widely in Ngamiland in 2008/9; cattle population vaccinated repeatedly during the outbreak. Originally reported as SAT1 – later corrected. Spread to FMD-free area (Ghansi District)</td>
</tr>
<tr>
<td>5</td>
<td>Namibia</td>
<td>Eastern Caprivi</td>
<td>Nov 2007</td>
<td>Nov 2008</td>
<td>SAT2 WRL, SAT2/NMB/1 &amp; 4/2007</td>
<td>Persistent outbreak during which cattle in the area were vaccinated repeatedly</td>
</tr>
<tr>
<td>7</td>
<td>Botswana</td>
<td>Kasane District</td>
<td>July 2008</td>
<td>Sept 2008</td>
<td>SAT2 WRL, SAT2/NMB/1-4/2008</td>
<td>Outbreak location close to the Namibian (Caprivi), Zambian &amp; Zimbabwean borders</td>
</tr>
<tr>
<td>8</td>
<td>Namibia</td>
<td>Mukwe Constituency, Kavango Region</td>
<td>July 2008</td>
<td>Jan 2008</td>
<td>SAT2 WRL, SAT2/NMB/1-4/2008</td>
<td>Location close to western end of the Caprivi</td>
</tr>
<tr>
<td>10</td>
<td>Botswana</td>
<td>Ghansi District</td>
<td>Oct 2008</td>
<td>Dec 2008</td>
<td>SAT2 WRL, SAT2/BOT/6, 7, 8, 9, 10, 11, 16, 18/2008</td>
<td>Outbreak occurred in Botswana’s recognized FMD-free zone. Focus eliminated by stamping out of all infected &amp; in-contact animals</td>
</tr>
<tr>
<td>11</td>
<td>Angola</td>
<td>Luiana, Rivungo, Cunado Cubango</td>
<td>Feb 2009</td>
<td>?</td>
<td>SAT2 WRL, SAT2/BOT/6, 7, 8, 9, 10, 11, 16, 18/2008</td>
<td>Outbreak situated close to the borders of Zambia (Western Province) &amp; Namibia (Eastern Caprivi). FMD not recorded in Angola since 1974. Diagnosis based on serology</td>
</tr>
<tr>
<td>12</td>
<td>Namibia</td>
<td>Impalila Island, Caprivi</td>
<td>April 2010</td>
<td>Aug 2010</td>
<td>SAT1 WRL, SAT2/BOT/12 &amp; 13/2008</td>
<td>Location close to the Zambian, Botswana &amp; Zimbabwean borders</td>
</tr>
<tr>
<td>13</td>
<td>Botswana</td>
<td>Lesoma, Kasane</td>
<td>July 2010</td>
<td>?</td>
<td>SAT2 WRL, SAT2/BOT/6, 7, 8, 9, 10, 11, 16, 18/2008</td>
<td>Location about 20 km east of Kasane town, i.e. close to Zimbabwean border</td>
</tr>
</tbody>
</table>
Interrelationship between SAT2 outbreaks

The occurrence of 11 SAT2 outbreaks out of a total of 13 reported in this 5-year period involving cattle in and around the KAZA TFCA is shown in Table 1. This is a high rate bearing in mind that almost all the cattle in these areas are routinely vaccinated against FMD. Figure 2 shows the close proximity in time and place between many of these SAT2 outbreaks. Some genome sequences for viruses involved from these outbreaks are available but for others they are not which is unfortunate. The data are summarized in Table 1 (viruses associated with individual outbreaks) and in Figures 3 & 4.

Figure 3. Genetic relationships of FMDV SAT2 topotype II isolated from southern Africa

Figure 4. Genetic relationships of FMDV SAT2 topotype III isolated from southern Africa
These figures show, firstly, that not all the SAT2 outbreaks were derived from a single source. However, determining individual relationships is complicated by a number of factors that need to be addressed if more precise understanding of the epidemiology of FMD is to be achieved. Two examples are used to illustrate this complex situation:

1. **Relationships of SAT2 viruses derived from cattle outbreaks in southern Zambia, eastern Caprivi (Namibia) and north-western Botswana**

In November 2007 a SAT2 outbreak in cattle occurred in the extreme east of Caprivi, close to the borders of Zambia, Zimbabwe and Botswana (outbreak no. 5, Table 1; Figure 2). Phylogenetic analysis, based on genome sequencing of the viruses recovered from that outbreak by the Pirbright Laboratory of the Institute for Animal Health (UK – Pirbright), showed it to be unrelated to previous SAT2 outbreaks in the Region (i.e. outbreaks 1, 2 & 4, Table 1) but to be closely related to SAT2 viruses from Zambia derived from an apparently unreported outbreak in 2007 (viruses SAT2/ZAM/1-3/2007) and outbreak No 6 in 2008 (SAT2/Zam/08,14,15/2008), as well as to viruses associated with another apparently unreported outbreak in 2009 (SAT2/ZAM/12-14,16/09). All these viruses grouped within topotype III (Figure 3). In July 2008 a further cattle outbreak occurred in the Kasane District of Botswana, i.e. in the north-east of the country (outbreak No 7; Figure 2), adjacent to the eastern Caprivi. However, no record of virus isolates or sequences from that outbreak are available and for that reason the possible link to outbreaks 5 & 6 is a matter of speculation.

In summary, these data show a close relationship between SAT2 viruses from different countries in or near to the Eastern Caprivi. Whether these were all epidemiologically related through cattle movements or represent successive emergence from a possible common buffalo source is unknown.

2. **SAT2 viruses from cattle outbreaks in Kavango/western Caprivi (Namibia) and north-western Ngamiland (Botswana)**

In July 2008, a SAT2 cattle outbreak occurred at the western (i.e. opposite) end of the Caprivi (Mukwe Constituency, Kavango Region – outbreak no. 8, Table 1; viruses SAT2/NMB/1-4/2008). The following month (August 2008) FMD in cattle was diagnosed just across the border at Mahembo West in the north-west of Botswana (outbreak No. 9, Table 1; SAT2/BOT/12-13/2008). Later still, in February 2009, an outbreak occurred in nearby south-eastern Angola (outbreak no 11, Table 1; Figure 2) but no viruses from that outbreak are recorded.

The question therefore arose has to (1) how these viruses were related to those further south that caused the extensive outbreak first identified at Habu in Ngamiland (Outbreak No 4, Table 1); (2) whether the apparently geographically (the border area between the two countries in this region is open) and temporally overlapping outbreaks in Kavango/western Caprivi and in Mahembo West (Botswana) were caused by the same virus or not and (3) how closely the SAT2 viruses recovered from the general area of the eastern Caprivi (i.e. including Zambia & Botswana) were related to viruses from the general area of the western Caprivi. Sequencing results from Pirbright Laborarory provided surprising results:

1. Outbreak Nos 4, 8 & 9 were all caused by different SAT2 viruses. The Mahembo West viruses were SAT2 topotype II while the Habu (and Ghansi) viruses were topotype III (Figures 3 & 4);
2. The two geographically and temporally overlapping outbreaks (Mukwe Constituency/Mahembo West), although both caused by topotype III viruses, were clearly different (Figure 3); and,
3. Most surprisingly, the data showed that the eastern and western Caprivi viruses were closely related, i.e. suggesting that the Kavango outbreak was derived from eastern Caprivi. Namibia’s official veterinary services had been at great pains to prevent this occurring.

Some of the above results provided by Pirbright are rendered even more puzzling because they differ from those produced by the ARC-Onderstepoort Veterinary Institute (ARC-OVI). The ARC-OVI phylogenetic trees (not shown here) clearly indicate that the Eastern Caprivi viruses they worked with belong to a different SAT2 topotype than the Kavango/Western Caprivi viruses. This shows that the eastern and western Caprivi outbreaks were definitely unrelated.

**Discussion on laboratory results**

The most likely explanation for the above discrepancy in laboratory results is that different samples were received by the laboratories from different sources from the field. The difficulties in reconciling the results of the reference laboratories are compounded by the fact that diagnostic samples are often submitted for analysis with no or incomplete information on the locality and epidemiological situation relating to suspected cases. The problem is further exacerbated by the different nomenclature systems used by each of the laboratories. However, the FMD Reference Laboratories Network is addressing the harmonization of nomenclature. Furthermore, the lack of accurate and detailed information on disease outbreaks poses a significant risk to the Region because inadequately managed FMD can have devastating effects on rural economies and the well-being of livestock owners.

**What is known about SAT virus populations maintained by buffalo in the KAZA TFCA?**

A data-base of all SAT viruses in storage in the FMD reference laboratories in Botswana (Botswana Vaccine Institute - BVI), South Africa (ARC-Onderstepoort Veterinary Institute – OVI) and United Kingdom (Institute for Animal Health Pirbright Laboratory – IAH) was developed by the OVI in 2009 (funded by the European Union’s SADC FMD Project). This data-base includes >1500 viruses recovered from wildlife, buffalo mainly, in southern African countries. Some countries (e.g. Botswana, South Africa & Zimbabwe) conducted extensive surveys in the past (1970s-1990s) but recently there have been few additions although it is known that planning is in progress to correct this problem. The result is that, with the exception of the Kruger National Park in South Africa, there is little consolidated information on the distribution of SAT viral genotypes in buffalo populations, including those of the KAZA TFCA. For that reason it is presently impossible to determine the relationships between viruses recovered from cattle outbreaks with those maintained by buffalo populations in different locations.

Nevertheless, this data-base is a valuable regional asset that needs to be maintained and expanded. It will soon be placed on the ReLaIS website.

**What lessons can be learned from recent FMD occurrence in and around the KAZA TFCA?**

Perhaps the most important immediate lesson is the need for the FMD reference laboratories of the Region to communicate more effectively than hitherto and the formation of the FMD Reference Laboratories Network where both reference laboratories in the Region are core members is a step towards this. If this does not happen and important conclusions are not communicated to those in the field required to manage FMD, the expenditure in modern technology becomes irrelevant. The FMD Reference Laboratories network is potentially valuable in this respect but needs to be more proactive.
Secondly, a more detailed understanding of the distribution of SAT viral genotypes in buffalo populations in southern Africa generally and in the KAZA TFCA especially is vital. Steps in this direction are in progress but it is doubtful whether they will be adequate without further investment. This is far from a trivial undertaking.

It is also clear that in deep rural areas such as the KAZA TFCA intersected by complex and artificial country borders which are not fenced, attempts to differentiate the animal disease status of individual countries with respect to transboundary animal diseases like FMD is pointless. This is because the effective control of livestock and wildlife movement is impossible even were the development of the KAZA TFCA to end. Conversely, any attempt to fence these borders effectively would have enormous environmental consequences and derail the whole TFCA movement which is vital for the future of biodiversity conservation and economy in the Region.

In order to accommodate TFCA development together with expansion of livestock productivity and market access for animal products from areas within or associated with TFCA, the TFCA will need to be managed jointly with respect not only to biodiversity conservation but animal diseases as well. The problem is that at the international level such regional approaches to animal disease management are not easily accommodated by present institutional arrangements. So, for example, all SADC countries are individual members of the OIE (World Organisation for Animal Health). However, nothing prevents groups of countries co-operating on a regional basis for their mutual benefit. Perhaps this is an area where SADC could be more pro-active?

**Acknowledgement** We wish to thank the WRLFMD, Pirbright UK, the ARC-Onderstepoort Veterinary Institute and in particular, the Transboundary Animal Diseases Programme and the FAO and National FMD Reference Laboratory for their support and making this data available to us. We also thank Leo Braack, Director, Southern Africa Wilderness Programme, Conservation International for the use of maps.

**Comment/discussion:**

If you have questions and/or comment on this edition of the FMD Bulletin please send them in less than 500 words to foot.and.mouth.bulletin@gmail.com. If of wide enough appeal these may be discussed in future editions.

IN ANY EVENT PLEASE indicate whether you find the Bulletin useful or not - an explanation is not essential although obviously preferred.