Chapter 10

Virus Topotypes and the Role of Wildlife in Foot and Mouth Disease in Africa[1]

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Introduction

The epidemiology of foot and mouth disease (FMD) on the African continent is influenced by two different patterns, viz, a cycle in which wildlife plays a role in maintaining and spreading the disease to other susceptible domestic animals and wild ungulates and a cycle that is maintained within domestic animals and that is independent of wildlife. In southern Africa, the former cycle predominates due to the presence of African buffalo (*Syncerus caffer*), the only wildlife species for which long-term maintenance of FMD has been described (Hedger 1972, Hedger *et al*. 1972, Hedger 1976, Condy *et al*. 1985, Thomson 1994, Thomson *et al*. 2001, Thomson *et al*. 2003). In East Africa, both cycles probably occur, while in West Africa, due to the absence of significant numbers of wildlife hosts, FMD is believed to be maintained primarily within the domestic animal cycle.

The disease is endemic in most countries in sub-Saharan Africa (Vosloo, Bastos *et al*. 2002). In southern Africa, where a number of countries have been able to control FMD by separating infected buffalo from livestock and by limited use of vaccination (control policies in South Africa have been described by Brückner *et al*. 2002 and Thomson *et al*. 2003), disease-free areas are recognised. FMD cannot be eradicated from southern and East Africa unless all infected buffalo are removed, which is untenable from both ecological and ethical points of view. Lack of movement control within countries and across international borders for both wildlife and domestic animals aggravates the problem, and gives credence to the fact that FMD will remain a problem on the subcontinent for the foreseeable future.

The role of different species in the epidemiology of FMD

African buffalo

The manner in which FMD is maintained within African buffalo populations is equivocal, as it is not clear how disease is transmitted from carrier buffalo to susceptible animals in the herd (Thomson 1996). FMD is probably transmitted in one of two ways: contact transmission between acutely infected and susceptible individuals, which is likely to account for the majority of infections, and occasional transmission between carrier buffalo and susceptible individuals. In Kruger National Park (KNP) in South Africa, most buffalo calves become infected by all three SAT serotypes prevalent in this region of the continent by the time they reach 1 year of age (Hedger 1972, Thomson *et al*. 1992, Thomson 1994). Calves are protected against infection by maternal antibodies, which can persist for 2–7 months (Condy and Hedger 1978), although antibodies have been detected in calves for up to 17 months (W. Vosloo and R.G. Bengis, unpublished results). Protection of calves from infection may not persist beyond 3–4 months, presumably because high antibody levels are required to maintain protection (Condy and Hedger 1978). Calves are not necessarily infected by their mothers and, in KNP at least, infection with SAT-1 usually precedes that with SAT-2 and SAT-3 (Condy and Hedger 1974, Thomson *et al*. 1992, Thomson *et al*. 2003). It seems therefore that infection of most calves in breeding herds probably occurs as a result of "childhood" epidemics, i.e., horizontal transmission between calves less than one year old (Thomson *et al*. 1992). Another possibility for transmission of disease, for which the evidence remains tenuous, is sexual transmission (Bastos *et al*. 1999, Thomson *et al*. 2003, Vosloo and Thomson, 2004).

Following the acute stage of infection, which lasts less than two weeks, detectable virus disappears from all secretions and excretions of individual animals except for those of the pharynx, where low-level viral replication persists in 60% or less of individuals (Hedger 1972, Hedger 1976, Anderson *et al*. 1979, Thomson 1996). Individual animals may retain the virus for at least five years while in an isolated herd; the infection was maintained for over 24 years (Condy *et al*. 1985). It is probable that a significant number of animals do not maintain infection for a prolonged period of time because the proportion of persistently infected animals falls after reaching a peak in the 1- to 3-year age group (Hedger 1976, E.C. Anderson and N.J. Knowles, personal communication 1994).

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More than one type of SAT virus may be maintained by individual buffalo (Hedger 1972, Anderson *et al*. 1979).

However, during the acute phase of infection, routes of virus excretion in buffalo are similar to those in cattle, although of a lower order, and viral excretion appears to persist longer in buffalo than in acutely infected cattle (Gainaru *et al*. 1986, Thomson 1994). Most transmission to cohorts and other species is believed to occur during acute infection. It has been shown unequivocally that carrier buffalo are able to transmit the infection not only to other buffalo (Condy and Hedger 1974) but also to cattle (Dawe, Flanagan *et al*. 1994, Dawe, Sorenson *et al*. 1994, Vosloo *et al*. 1996). More information is needed about the maintenance of various serotypes of FMD in buffalo populations outside southern Africa, and whether serotypes other than the SAT types have become established in those populations.

Other wildlife species

Many species of wild animals have been reported as having been infected with FMD virus (Macaulay 1963, Hedger 1981) and a wide range of species in southern Africa have been shown to have antibodies (Lees May and Condy 1965, Condy *et al*. 1969). Essentially all cloven-hoofed animals and Camelidae (i.e., members of the order Artiodactyla) are susceptible to infection with FMD viruses. FMD infection depends on the species and even breed of animals, the strain and dose of virus causing infection, and the level of immunity of the animals (Thomson 1994). The susceptibility of most wildlife species is unknown, as are the levels of virus excretion during infection. However, the bulk of evidence suggests that wildlife species other than buffalo play only a minor role in the maintenance and spread of FMD viruses in southern Africa. This is corroborated by the fact that only kudu (*Tragelaphus strepsiceros*) have been shown to maintain FMD virus in a carrier state for significant periods of time (Table 1). (Carriers are defined as animals from which virus can be isolated from the oropharyngeal area more than 28 days after infection [Salt 1993].) Impala (*Aepyceros melampus*) seem to be the most susceptible species in South Africa and are considered an indicator host for the presence of SAT viruses because infection in impala in the past often presaged the occurrence of FMD in livestock (Meeser 1962). In Zimbabwe, however, kudu have been associated with clinical FMD more frequently than impala (C. Foggin, personal communication 2003). In the Serengeti, where wildebeest (*Connochaetes taurinus*) are by far the most numerous large mammal species, FMD is infrequently reported, although a severe outbreak caused by SAT-2 was recorded in wildebeest in 1999. Evidence indicated that FMD had spread from domestic animals to the wildebeest, and at least 20% of the migratory herd of wildebeest was affected (T. Mlengeya, personal communication 2003).

Outbreaks of FMD among impala within KNP occur regularly although, strangely, other species are rarely affected. FMD in impala appears generally in areas of dense impala populations. Also, because impala depend on water, infection frequently has spread along watercourses in KNP; i.e., it is assumed that the virus is not transmitted via the water itself but by contact between animals congregated along rivers and streams. During times of low rainfall, buffalo and impala come into close contact because they congregate at watering points. The available evidence, based on genome sequencing of appropriate viruses, indicates that impala in KNP usually, if not always, become infected with SAT viruses derived from buffalo in the vicinity (Keet *et al*. 1996, Bastos *et al*. 2000, Bastos *et al*. 2003b).

Persistent infection in impala has not been demonstrated (Hedger *et al*. 1972, Anderson *et al*. 1975, C. de W. van Vuuren, personal communication 1997) and a serologic survey investigating three localities in KNP confirmed this finding (Vosloo and Thomson 2004). However, FMD epidemics caused by identical viruses have recurred in impala 6–18 months after the original outbreak (Vosloo *et al.* 1992, Keet *et al*. 1996), indicating that the virus may have been maintained within the impala population. If that were so, the mechanism whereby the viruses survived in interepidemic periods remains to be explained. An alternative explanation is that the same virus has been transmitted on more than one occasion from buffalo to impala in the same vicinity.

However, any acutely infected animal could potentially spread FMD regardless of whether it is of a known carrier species. Because antelope such as impala and kudu can jump fences up to 2.4m high, this poses a severe problem for disease control where such fences are used to separate wildlife from susceptible domestic animals; in Zimbabwe, this could explain outbreaks on cattle farms adjoining wildlife conservancies (Hargreaves *et al.* 2004).

Domestic animals

The role of domestic animals in the maintenance and spread of FMD in sub-Saharan Africa has not been studied in detail. However, it is accepted that domestic animals play a significant role in the epidemiology of FMD in East and West Africa due to uncontrolled domestic animal movement within and between countries, lack of vaccination strategies to prevent disease transmission, and the fact that cattle, sheep, and goats can become FMD carriers (Table 1). In Zimbabwe, in southern Africa, for example, FMD seems to have been perpetuated by domestic animal populations since the initial possible spread from buffalo in September 2001 (W. Vosloo, R.M. Dwarka, and C.I. Boshoff, unpublished data).

Molecular epidemiology of FMD in Africa

A better understanding of the epidemiology of FMD could greatly assist in planning control strategies. Molecular epidemiologic studies have contributed in this regard by elucidating historical and current disease transmission patterns within and between countries. Additionally, such studies have demonstrated the presence of viral topotypes in both wildlife and domestic animals, information that should be

Table 1. Duration of viral persistence in selected domestic animals and wildlife species

Species/animal	Duration of viral persistence	Reference
Domestic animals		
Cattle	2.5–3.5 years	Hedger 1976 Hargreaves 1994
Sheep	9–12 months	Burrows 1968 McVicar and Sutmoller 1968
Goats	2–3 months	Singh 1979 Anderson *et al*. 1976
Wildlife		
Wildebeest (*Connochaetes taurinus*)	28 days	Anderson *et al*. 1975
Sable *(Hippotragus niger)*	28 days	Ferris *et al*. 1989
Eland (*Taurotragus oryx*)	32 days	Anderson 1980
Fallow deer (*Dama dama*)	63 days	Forman *et al*. 1974
Kudu (*Tragelaphus strepsiceros*)	104–160 days	Hedger 1972
Water buffalo (*Bubalis bubalis*)	2–24 months	Moussa *et al*. 1979
African buffalo (*Syncerus caffer*)	5 years	Condy *et al*. 1985

heeded when planning FMD vaccination strategies (Vosloo *et al.* 1992, Vosloo *et al.* 1995, Bastos 1998, Bastos *et al.* 2001, Bastos *et al.* 2003a, Bastos *et al.* 2003b, Sangare *et al.* 2003, Sangare *et al.* 2004).

SAT-type viruses are constantly evolving in buffalo populations in southern Africa (Vosloo *et al.* 1996, Bastos *et al.* 2001, Bastos *et al.* 2003b). Therefore, different buffalo populations can be differentiated on the basis of SAT-type viruses recovered from carrier animals representative of those populations (Vosloo *et al.* 2001). Even within the buffalo population of the KNP, which numbers less than 27,000 individuals, clear intratypic differences in the genomes of SAT-1, -2, and -3 viruses from different regions of KNP have been shown (Vosloo *et al.* 1995, Bastos *et al.* 2000, Bastos 2001, Bastos *et al.* 2001, Bastos *et al.* 2003b, R.M. Dwarka, unpublished results).

Buffalo populations in southern Africa have not been completely free ranging for at least 70 years and have been concentrated mainly in conservancies and game parks where migratory routes have been disrupted by fences. This may partially explain the locality-specific distribution of viral topotypes apparent today. High mutation rates (Vosloo *et al.* 1996) and continuous, independent virus cycling within discrete buffalo populations (Condy *et al.* 1985) probably account for the current, extensive intratypic variation. However, little information is available on the buffalo populations in East Africa; possibly because of the free-ranging nature of buffalo in that region, discrete topotypes may not be found.

Based on nucleotide sequence analysis of a portion of the viral genomes obtained from buffalo and domestic animals in sub-Saharan Africa, eight independently evolving viral topotypes were identified for SAT-1 (Table 2). These topotypes originated from eight correspondingly separate geographic localities, with three different topotypes found in Uganda alone. For SAT-2 isolates, 14 topotypes have so far been identified within the sub-Saharan African region, while 6 topotypes have been identified for SAT-3. For serotypes O, A, and C- 8, 6, and 3 topotypes were identified respectively and could be related to geographic regions (Table 2).

For all FMD serotypes, the genetic differences between viruses from different topotypes is such that outbreaks should be traceable to specific countries, specific game parks, and even to specific regions within game parks, as has been described for the SAT serotypes in southern Africa (Bastos 2001, Bastos *et al*. 2001, Vosloo *et al.* 2001, Vosloo, Bastos *et al.* 2002, Vosloo, Boshoff *et al.* 2002, Bastos *et al.* 2003b). However, if uncontrolled movement of buffalo occurs in countries that have more than one topotype within their borders (such as Botswana and Zimbabwe), these viral topotypes will become commingled (as has already happened in Zimbabwe). Consequently, a single region could have high levels of viral genetic diversity that will most likely be reflected in antigenic differences. This poses challenges for vaccination schemes because for vaccines to be effective, the viruses incorporated into vaccines must be antigenically related to viruses circulating in the field (Hunter *et al.* 1996, Hunter 1998); this means that several topotypes would have to be incorporated into a single vaccine. Therefore, the uncontrolled movement of buffalo within the sub-Saharan African region could have serious implications for the control of FMD.

Based on distribution patterns of SAT virus lineages and topotypes in buffalo populations, we can clearly conclude that SAT viruses from buffalo are transmitted to other species (Bastos *et al*. 2000, Brückner *et al.* 2002, Vosloo, Boshoff *et al.* 2002, Thomson *et al*. 2003). This confirms early observa-

Table 2. Topotype distribution of FMD serotypes O, A, C, and SAT types 1–3 in Africa

Serotype	Topotype	Representative country(ies)	Reference
SAT-1	I	South Africa, southern Zimbabwe, Mozambique	Vosloo *et al.* 1995
	II	Botswana, Namibia, Zambia, western Zimbabwe	
	III	Zambia, Malawi, Tanzania, Kenya, northern Zimbabwe	Bastos *et al.* 2001
	IV	Uganda	Reid *et al.* 2001
	V	Uganda	
	VI	Uganda	Sahle 2003
	VII	Nigeria, Sudan	
	VIII	Nigeria, Niger	Sangare *et al.* 2003
SAT-2	I	South Africa, Mozambique, southern Zimbabwe	
	II	Namibia, Botswana, northern and western Zimbabwe	Bastos *et al.* 2003b
	III	Botswana, Zambia, Zimbabwe	Vosloo *et al.* 1995
	IV	Burundi, Malawi, Kenya, Tanzania, Ethiopia	
	V	Nigeria, Senegal, Liberia, Ghana, Mali, Cote d'Ivoire	
	VI	Gambia, Senegal	Sangare 2002
	VII	Eritrea	
	VIII	Rwanda	Sahle 2003
	IX	Kenya, Uganda	
	X	Democratic Republic of the Congo, Uganda	Sangare *et al.* 2004
	XI	Angola	
	XII	Uganda	
	XIII	Sudan	
	XIV	Ethiopia	
SAT-3	I	South Africa, southern Zimbabwe	
	II	Namibia, Botswana, western Zimbabwe	Vosloo *et al.* 1995
	III	Malawi and northern Zimbabwe	
	IV	Zambia	Bastos *et al.* 2003a
	V	Uganda	
	VI	Uganda	Reid *et al.* 2001
O	I	Ethiopia, Eritrea, Kenya, Somalia, Sudan, Tunisia, Egypt	
	II	Algeria, Côte d'Ivoire, Guinea, Morocco, Niger, Ghana, Burkina Faso, Tunisia, Sudan	Samuel and Knowles 2001
	III	Uganda, Kenya, Sudan	
	IV	Uganda	Sangare 2002
	V	Uganda	
	VI	Tanzania, Uganda	Sahle 2003
	VII	South Africa	
	VIII	Angola	Sangare *et al.* 2001
A	I	Mauritania, Mali, Côte d'Ivoire, Ghana, Niger, Nigeria, Cameroon, Chad, Senegal, Gambia, Sudan	
	II	Angola, Algeria, Morocco, Libya, Tunisia, Malawi	Knowles and Samuel 2003
	III	Tanzania, Burundi, Kenya, Somalia, Malawi	
	IV	Ethiopia	Knowles *et al.* 1998
	V	Sudan, Eritrea	
	VI	Uganda, Kenya, Ethiopia	
C	I	Kenya	Reid *et al.* 2001
	II	Ethiopia, Kenya	
	III	Angola	Knowles and Samuel 2003

tions made by J.B. Condy and R.S. Hedger that led them to hypothesize a link between the occurrence of FMD in cattle and the distribution and behaviour of buffalo harbouring SAT-type viruses (Condy *et al.* 1969, Hedger *et al*. 1969, Condy 1971, Hedger 1972, Hedger *et al.* 1972, Condy and Hedger 1974, Hedger 1976, Condy 1979, Hedger and Condy 1985).

Studies conducted in East and West Africa were based mostly on historical isolates obtained from previous outbreaks in domestic animals. Due to the endemicity of the disease, few outbreaks are investigated to determine the serotype and to ensure that isolates are available for further studies. The topotypes from those regions may be extinct if the disease was successfully controlled. Interestingly, it was also found that long-term maintenance of certain topotypes occurred for periods of up to 24 years and appeared in more than one country (Sangare *et al*. 2004, Sahle 2003).

Conclusions

Protecting sub-Saharan Africa's wildlife heritage is a priority, while maintaining a harmonious interaction between agriculture and wildlife conservation is also imperative. Transboundary diseases such as FMD that can be transmitted between wildlife and livestock are obstacles to livestock development and conservation. Undoubtedly, this problem will merit even greater scrutiny with the increasing drive towards the creation of export zones for livestock and animal products in order to access lucrative markets elsewhere.

The epidemiology of FMD in sub-Saharan Africa is not fully understood. The role of wildlife in East and possibly West Africa in the maintenance and spread of the disease remains to be clarified. It is not known whether isolates from serotypes A and O have become established in buffalo populations in East Africa, which is a possibility, because numerous outbreaks due to these serotypes have occurred in domestic animals in the past. The role of small stock should also be investigated to ensure that control policies are designed to exclude possible spread of FMD by sheep and goats. Current outbreaks of FMD should be researched to ensure that vaccine strains will be appropriately matched against the strains currently in the field.

Fences to separate infected wildlife from susceptible domestic animals have been used with success in southern Africa to ensure that FMD does not spread and adversely affect livestock and livestock producers. However, these fences and their impacts on the economically critical wildlife sector have been severely criticised, highlighting the need to explore alternative, ecologically sensitive ways of controlling FMD. Additionally, because FMD is only one of many transboundary diseases that can negatively affect livestock farming in the region, efforts to design novel control policies should attempt to address all important diseases.

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