REVIEW ARTICLE

Epidemiological Patterns of Foot-and-Mouth Disease Worldwide

M. Rweyemamu[1], P. Roeder[2], D. Mackay[3], K. Sumption[2], J. Brownlie[4], Y. Leforban[5], J.-F. Valarcher[3]*, N. J. Knowles[3]* and V. Saraiva[6]

[1] Royal Veterinary College, University of London and 6 Robins Dale Woking, Surrey GU21 2LQ, UK
[2] Food and Agriculture Organization of the United Nations, Rome, Italy
[3] World Reference Laboratory for FMD, IAH, Pirbright, UK
[4] Royal Veterinary College, Department of Pathology and Infectious Diseases, University of London, Hawkshead Lane, North Mymms, Hatfield Herts AL9 7TA UK
[5] Ministère de l'agriculture et de la pêche. 251, rue de Vaugirard. 75732 Paris Cedex 15. France
[6] Centro Panamericano de Fiebre Aftosa (PANAFTOSA), Rio de Janeiro, RJ Cep: 25040-000, Brazil

Keywords:
Epidemiology, foot-and-mouth-disease, globalisation

Correspondence:
Mark Rweyemamu. 6 Robins Dale Woking, Surrey GU21 2LQ, UK.
Tel.: 0044-(0)1483-473774; E-mail: mark.rweyemamu@btinternet.com

Present addresses:
Taurus Animal Health, Hollyhedge Cottage, Spats Lane, Headly Down, Bordon, Hampshire GU35 8SY, UK
D. Mackay, European Medicines Agency (EMEA), London E14 4HB, UK
J.-F. Valarcher, IVI – Animal Health, Uppsala, Sweden

*Supported by EU CAFMD/CSF FP6-513755.

Received for publication May 29, 2007

doi:10.1111/j.1865-1682.2007.01013.x

Summary

Foot-and-Mouth Disease (FMD) is a clinical syndrome in animals due to FMD virus that exists in seven serotypes, whereby recovery from one sero-type does not confer immunity against the other six. So when considering intervention strategies in endemic settings, it is important to take account of the characteristics of the different serotypes in different ecological systems. FMD serotypes are not uniformly distributed in the regions of the world where the disease still occurs. For example, the cumulative incidence of FMD serotypes show that six of the seven serotypes of FMD (O, A, C, SAT-1, SAT-2, SAT-3) have occurred in Africa, while Asia contends with four sero-types (O, A, C, Asia-1), and South America with only three (O, A, C). Periodically there have been incursions of Types SAT-1 and SAT-2 from Africa into the Middle East.

This paper describes the global dynamics for the seven sero-types and attempts to define FMD epidemiological clusters in the different regions of the world. These have been described on a continent by continent basis.

The review has reaffirmed that the movement of infected animals is the most important factor in the spread of FMD within the endemically infected regions. It also shows that the eco-system based approach for defining the epidemiological patterns of FMD in endemic, which was originally described in South America, can apply readily to other parts of the world.

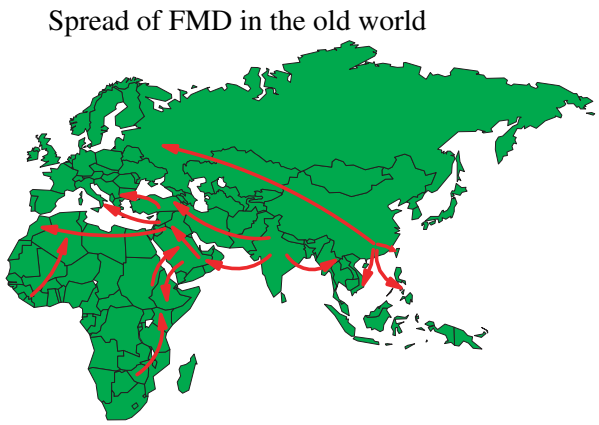
It is proposed that any coordinated regional or global strategy for FMD control should be based on a sound epidemiological assessment of the incidence and distribution of FMD, identifying risk sources as either primary or secondary endemic eco-systems.

An Overview of the Global Prevalence of Foot-and-Mouth Disease

This review forms part of a study by a Working Group appointed in 2004 by the European Food Safety Agency to assess three broad issues, namely:

1 The risk of foot-and-mouth disease (FMD) introduction into the EU from developing countries,
2 The reduction of this risk through interventions in developing countries/regions aiming at controlling/eradicating the disease and.
3 Tools for the control of a foot-and-mouth disease outbreak: update on diagnostics and vaccines.

This assessment was completed in 2005 and adopted in February 2006 by the European Commission (EFSA, 2006). Accordingly, the epidemiological patterns described in this



Source: WRL at IAH, Pirbright, UK

Fig. 1. Spread of FMD in the Old World (WRL at IAH, Pirbright, UK).

paper relate, primarily to the pre-2005 period. It is considered, however, that the underlying issues have not altered substantially since then. The risk-based interpretation of the worldwide prevalence of FMD is described in an accompanying paper by Sumption et al. (2008). The overall likely pattern of FMD spread in the 'Old World' has been summarized by the World Reference Laboratory for FMD in Fig. 1, which shows that in general terms, the overall risk of FMD for Europe is likely to originate from either Asia or Africa, with Asia posing a greater risk than Africa, based on historical experience. Although this summation is useful in conceptualizing global trends in spread, it must be realized that trade and other livestock movement patterns are ephemeral, following the changing economic fortunes of countries and are thus subject to change, sometimes rapidly.

The global incidence and distribution of FMD for the period 2005–2006 have been reviewed by FAO (2006). The present review does not attempt to present a current global incidence and distribution of FMD. Such data can be obtained from the OIE website at http://www.oie.int/wahid, or the website of the World Reference Laboratory for FMD at http://www.wrlfmd.org/, or the Pan-American FMD Centre (PANAFTOSA) at http://www.panaftosa.org.br/ for South America or the website of the South-East Asian FMD Campaign at http://www.seafmd-rcu.oie.int/index.php.

Foot-and-mouth disease virus as seven serotypes and these were, for the most part, aggregated in the import risk analysis (EFSA, 2006) as it was considered that entry into the EU of any serotype of FMD virus was equally unwanted. However, when considering intervention strategies, the specific characteristics of the different serotypes take a more prominent role. Therefore, in this paper, we describe the global dynamics for the different serotypes leading to the description of epidemiological clustering patterns in the different regions of the world. It is hoped that this information will provide the basis for designing programmes for the progressive control of FMD worldwide as presented in the accompanying paper by Rweyemamu et al. (2008). Accordingly, this paper has not considered such unnatural factors as bio-terrorism or virus escapes from laboratories, which might result in FMD outbreaks even of epidemic proportion.

FMD Epidemiological Clusters by Serotype and Topotype in FMD Endemic Areas

Foot-and-mouth disease serotypes are not uniformly distributed in the regions of the world where the disease still occurs. As shown in Fig. 2, the cumulative incidence of FMD serotypes show that six of the seven serotypes of FMD (O, A, C, SAT-1, SAT-2, SAT-3) have occurred in Africa, while Asia contends with four serotypes (O, A, C, Asia-1), and South America with only three (O, A, C). Periodically, there have been incursions of types SAT-1 and SAT-2 from Africa into the Middle East (Donaldson, 1999; Valarcher et al., 2004; FMD Homepage – Maps, 2006).

The advent of molecular biology technology has enabled the genetic characterization of virus strains and thereby the tracing of strains isolated from outbreaks can be carried out with far greater accuracy than was possible hitherto with serological techniques (Knowles and Samuel, 2003). As a result, it is now possible to group countries into epidemiological clusters according to the topotypes within each serotype that occur there. It should be noted that as a result of globalization, the spread of FMD epidemics can change from local and regional spread to wide international spread, even to distant areas as happened with the type O Pan-Asian lineage (Knowles et al., 2005; Cottam et al., 2006).

As type O is the most widely prevalent serotype in the world, the topotype distribution of this serotype gives an indication of possible epidemiological clustering (Fig. 3). It is apparent that South America has had a genetically stable type O virus not only for the 10 years under study, but also for nearly 50 years. Five different type O topotypes could be identified in Africa. Here, the Sudan-Sahel strain in West Africa appears to have been responsible for the type O outbreak in the Mahgreb in 1999. A topotype that is still confined to IGAD[1] countries has been identified in Sudan. There seems to be a strain that is common between Uganda and Kenya while the topotype that was identified in Tanzania in 1998 seems to have spread on

[1]IGAD, Inter-governmental Authority on Development (IGAD) coordinating development in the Horn of Africa. IGAD Member States are: Djibouti, Eritrea, Ethiopia, Kenya, Somalia, Sudan and Uganda.

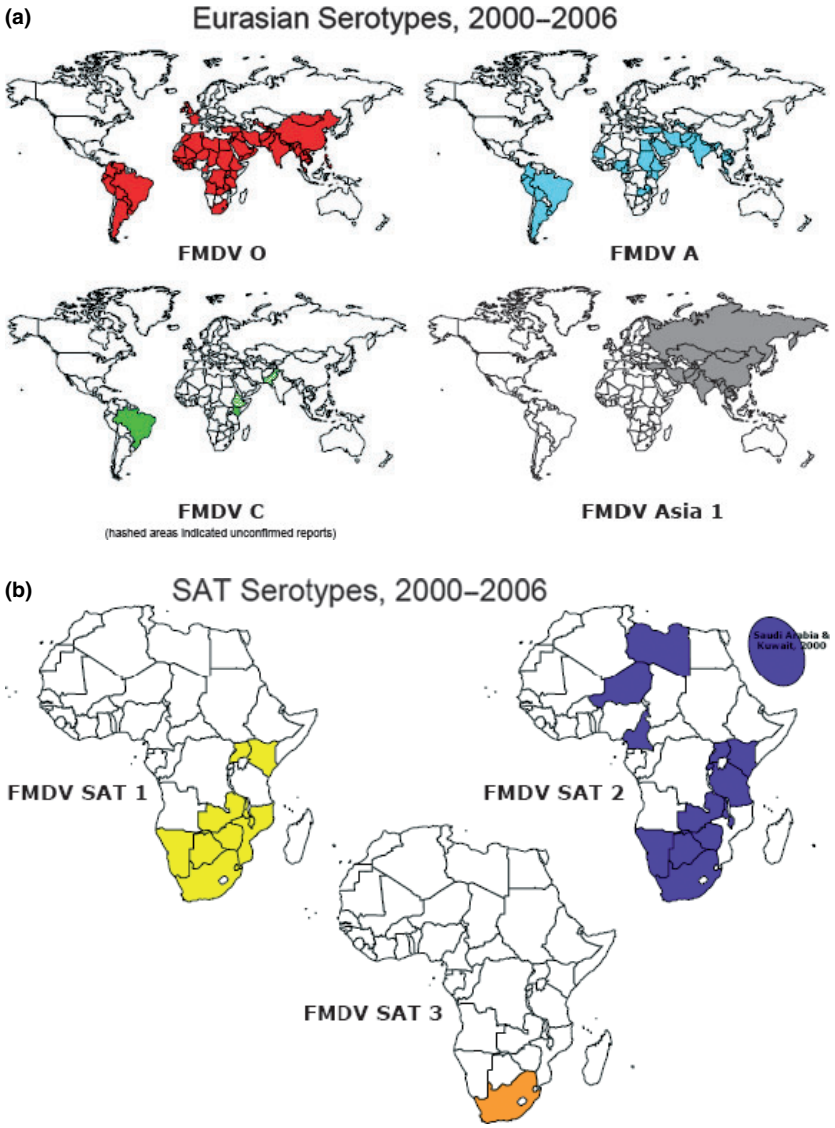


Fig. 2. World distribution of FMD serotypes 2000–2006 (World Reference Laboratory for FMD, http://www.wrlfmd.org/maps/fmd_maps.htm).

one hand to Rwanda, Burundi, Kenya and Uganda and on the other to Malawi and Zambia (Knowles et al., 2004).

In Asia, several sublineages are circulating; the dominant topotypes seem to have been the ME-SA topotype and more particularly the Pan-Asia strain that originated from South Asia (Knowles et al., 2005).

However, other topotypes are still present in East Asia such as the Cathay and the SEA topotypes.

Epidemiological Patterns in Europe

The status of FMD in Europe has been reviewed by Leforban and Gerbier (2002) and in the accompanying paper by Valarcher et al. (2007). Two categories of countries can be distinguished in the European region.

The countries recognized by the World Animal Health Organization (OIE) as free of FMD without vaccination include almost all European countries west of the Russian Federation plus the Balkan countries of Bosnia-Herzegovia, Macedonia and Serbia-Montenegro (including the territory of Kosovo administered by the United Nations).

Countries not recognized by OIE as free of FMD without vaccination either on account of not having successfully submitted their application to the OIE (Moldovia) or because of being at risk from incursion of FMD from neighbouring regions.

Trans-Caucasus countries are countries which have been mainly FMD free but are bordering endemically affected parts of neighbouring countries (Turkey and Iran). Trans-Caucasus countries will effectively be maintained free of FMD through improved regional control of FMD in north east Turkey and western Iran, and with improved measures in their border regions. They might

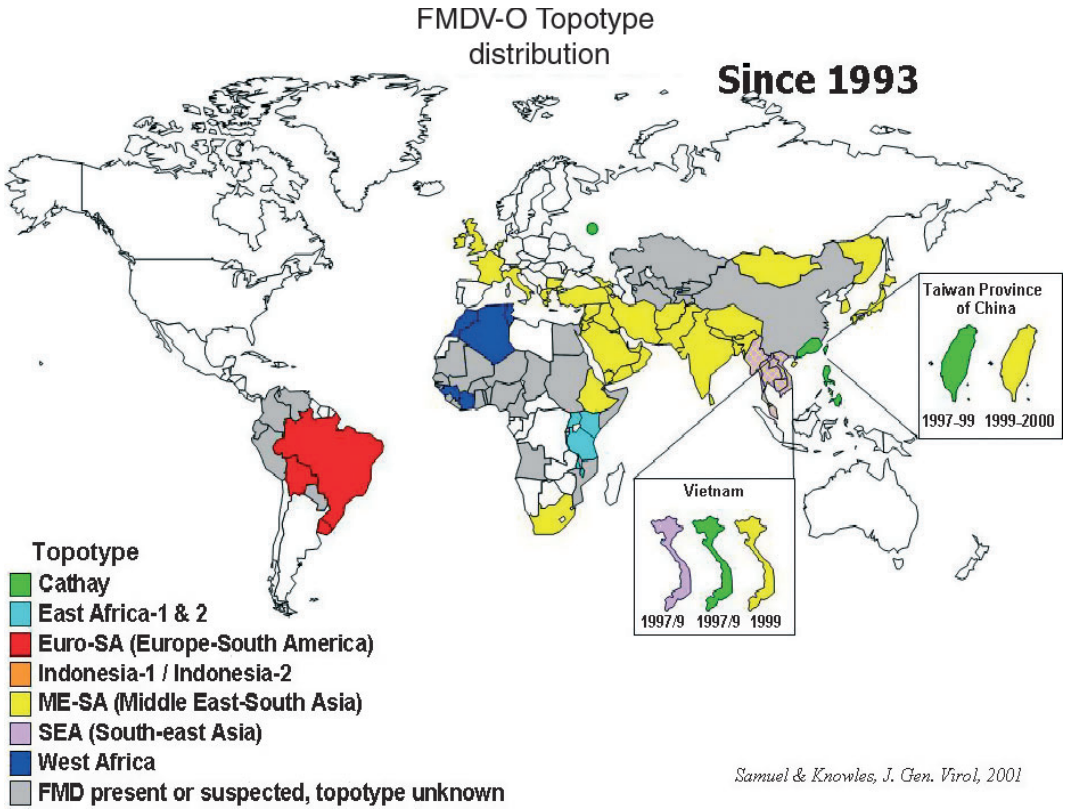


Fig. 3. FMDV-O topotype distribution worldwide 1993–2004 [World Reference Laboratory (WRL) for FMD at IAH, Pirbright, UK].

seek official recognition for FMD freedom with and without vaccination for parts of their territories.

Turkey is a country with areas that have a true endemic status, i.e. disease is being reported through the year, in the east and south-east of Anatolia. Western Anataolia and even more so Thrace only experience periodic incursions of disease, generally as a result of animal movement from the east and south-eastern parts of the country.

The Russian Federation, where outbreaks reported are very few, attributed to preventive measures along the borders with countries in the south, centre and east, which are not free of FMD and in which true prevalence is difficult to establish.

Epidemiological Patterns in Africa

The epidemiology of FMD in Africa has been reviewed by Vosloo et al. (2002, 2004). Batho (2003) conducted a FMD emergency audit on Southern Africa. As already remarked, Africa has the greatest diversity of FMD serotypes.

Based on the prevalence data, serotype and topotype distribution (Table 1), expert evaluation of factors such as animal movement patterns, impact of wildlife and farming systems, the following epidemiological clusters are proposed for Africa (Fig. 4).

The epidemiological clusters have the following characteristics:

Indian Ocean Island Countries Madagascar, Mauritius and Seychelles are free of FMD, with a recognized status of FMD freedom without vaccination.

The commercial (large and small) livestock sectors of South SADC countries, i.e. Swaziland, Lesotho, South Africa, Botswana and Namibia, are free from FMD and meet the conditions of the OIE for zonal or country freedom from FMD without vaccination. In some of these countries, however, there are segregated wildlife areas that harbour African/Cape buffaloes known to be infected, asymptomatically, with FMD virus serotypes SAT-1, SAT-2 and SAT-3. These wildlife parks are segregated from livestock through a system of game-proof fencing and vigorous surveillance. In these countries, game ranching or other wildlife conservation activities with FMD-infected African buffaloes are not allowed within FMD-free zones.

The north SADC cluster comprises Zimbabwe, Zambia, Mozambique, Malawi and southern Tanzania. In these countries, FMD was brought under control in livestock during the 1970s and 1980s through intensive vaccination and livestock movement control. In the case of Zimbabwe, the livestock remained largely unaffected and the country was able to export beef to the international market,

Table 1. Summary of the topotype distribution of FMD serotypes in sub-Saharan Africa (Vosloo et al., 2002)

Serotype	Topotype	Representative country/countries
SAT-1	I	South Africa, Southern Zimbabwe, Mozambique
	II	Botswana, Namibia, Zambia, Western Zimbabwe
	III	Zambia, Malawi, Tanzania, Kenya, Northern Zimbabwe
	IV	Uganda
	V	Uganda
	VI	Uganda
	VII	Nigeria, Sudan
	VIII	Nigeria, Niger
SAT-2	I	South Africa, Mozambique, Southern Zimbabwe
	II	Namibia, Botswana, Northern & Western Zimbabwe
	III	Botswana, Zambia, Zimbabwe
	IV	Burundi, Malawi, Kenya, Tanzania, Ethiopia
	V	Nigeria, Senegal, Liberia, Ghana, Mali, Cote d'Ivoire
	VI	Gambia, Senegal
	VII	Eritrea
	VIII	Rwanda
	IX	Kenya, Uganda
	X	Democratic Republic of the Congo, Uganda
	XI	Angola
	XII	Uganda
	XIII	Sudan
	XIV	Ethiopia
SAT-3	I	South Africa, Southern Zimbabwe
	II	Namibia, Botswana, Western Zimbabwe
	III	Malawi and Northern Zimbabwe
	IV	Zambia
	V	Uganda
	VI	Uganda
O	I	Ethiopia, Eritrea, Kenya, Somalia
	II	Côte d'Ivoire, Guinea, Morocco, Niger, Ghana, Burkina Faso, Sudan
	III	Uganda, Kenya, Sudan
	IV	Uganda
	V	Uganda
	VI	Tanzania, Uganda
	VII	South Africa
	VIII	Angola
A	I	Mauritania, Mali, Côte d'Ivoire, Ghana, Niger, Nigeria, Cameroon, Chad, Senegal, Gambia, Sudan
	II	Angola, Algeria, Morocco, Libya, Tunisia, Malawi
	III	Tanzania, Burundi, Kenya, Somalia, Malawi
	IV	Ethiopia
	V	Sudan, Eritrea
	VI	Uganda, Kenya, Ethiopia
C	I	Kenya
	II	Ethiopia, Kenya
	III	Angola

including the EU, until 2000 when the maintenance of game fencing deteriorated allowing cattle and buffalo to mix and set up outbreaks at a time when the veterinary services were too inadequately resourced to be able to contain such outbreaks. Consequently, the disease spread within the country and to neighbouring countries. SAT-1 and/or SAT-2 outbreaks in Mozambique, Malawi and Zambia between 2002 and 2004 were either because of outbreaks spreading from neighbouring countries or to internal buffalo-cattle contact. Northern Malawi and Northern Zambia are under constant threat of FMD spread from southern Tanzania.

For this epidemiological cluster, the primary source of FMD seems to be the risk posed by the wildlife buffalo herds (Sutmoller et al., 2000; Hargreaves et al., 2004). Several studies in Southern Africa have shown that the Cape/Africa buffalo is capable of maintaining silent infection of serotypes SAT-1, SAT-2 and SAT-3 for a long time, independently of circulation in livestock (Vosloo and Thomson, 2004). Under circumstances that are ill understood, the carrier buffalo can transmit infection to other buffalo or to impala or cattle although South African workers have shown experimental transmission of virus from buffalo to contact cattle. Overt disease in buffalo is a rare event. There have been only two documented outbreaks in South Africa, one involving type SAT-2 in 1970 (Young et al., 1972) and the other type SAT-1 in 2001 (Vosloo et al., 2007).

The Angola (and probably western Democratic Republic of Congo) cluster is a subregion of endemic CBPP and possible FMD, which threatens to spread into northern Namibia and south-western Zambia. However, there is little known about the true incidence of FMD in this cluster. Official data indicate that FMD has not been recorded in Angola since 1974 (F. Vissesse, personal communication).

The Great Lakes cluster comprise the countries of the East African Community (EAC) (i.e. Tanzania, Uganda, Kenya, Rwanda and Burundi) plus the eastern part of the Democratic Republic of Congo (DRC) not only have large livestock populations but also the highest concentration of wildlife in the world. Farming is dominated by agro-pastoral and pastoral communities and is characterized by communal grazing and migrations. Eastern DRC is heavily dependent on trade livestock from Uganda, Tanzania, Rwanda and Burundi. This Great Lakes cluster probably contains the most complicated FMD situation in the world. The cluster probably contains several FMD primary endemic foci. Five serotypes (O, A, C, SAT-1 and SAT-2) are endemic in this cluster and a sixth serotype (SAT-3) was isolated in wildlife (African buffalo) in Uganda in 1970 (Hedger et al., 1973) although it has never been isolated from livestock in the Great Lakes cluster. As discussed above, there are also wide genetic

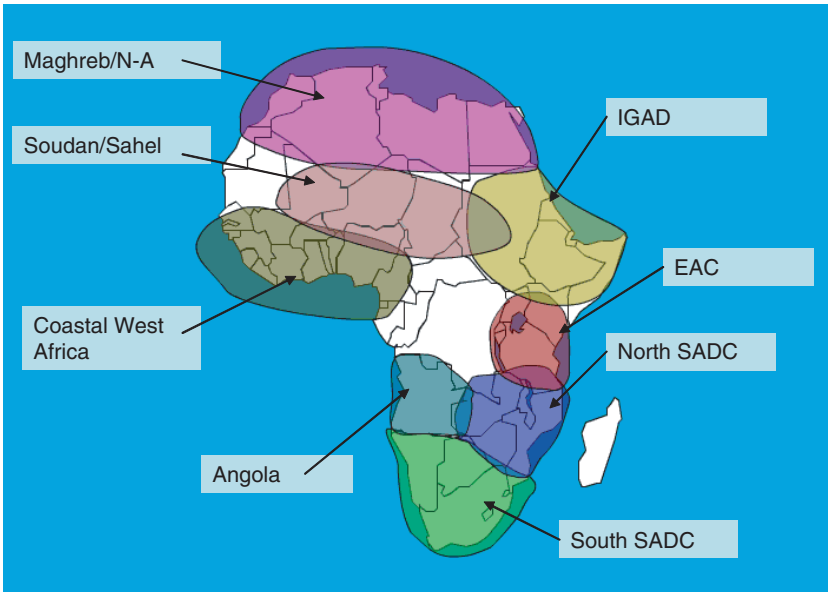


Fig. 4. FMD epidemiological clustering in Africa.

variations in the virus strains in this epidemiological cluster. The role of the African buffalo in the maintenance and transmission of FMD serotypes that occur in this cluster has not been systematically studied.

The Horn of Africa/IGAD Cluster, comprising Sudan, Eritrea, Ethiopia, Djibouti, Somalia, Northern Kenya and Northern Uganda, is another cluster which probably harbours major FMD primary endemic foci. Ethiopia and Sudan have the highest cattle populations in Africa. This region has also major ambitions for export of cattle and small ruminants, especially to the Middle East. The WRL for FMD has identified a type O topotype in Sudan that seems to be peculiar for this cluster.

The Soudan/Sahel Cluster comprises Western Sudan, Niger, Chad, Burkina Faso, Mali, Northern Nigeria, Senegal and Mauritania. The farming system in this ecosystem is predominantly pastoral, characterized by long distance movement of livestock due to either transhumance or trade. This cluster probably also contains important FMD primary endemic areas. Furthermore, it may be an important disease corridor cluster, linking the IGAD cluster with West Africa and probably West Africa with North Africa. The 1999 FMD strain in Algeria was found to be related to the West African type O topotype. In the past, transhumance and trade were important vehicles for spreading rinderpest in this region (Roeder et al., 2005).

Although the epidemiology of FMD in the Coastal belt countries of West and Central Africa has not been deeply studied, it seems that this cluster probably gets infected from the Soudan/Sahel cluster. It could be described as secondary endemic.

North Africa/Maghreb Cluster Morocco, Algeria (last infected by type O) and Tunisia have not reported FMD since 1999, through routine preventive vaccination and other measures. Libya and Egypt have sporadic FMD, and take routine preventive vaccination; Libya reported SAT-2 infection in 2003, probably as a result of live animal introductions from neighbouring countries to the south, breaching the Sahara barrier. Egypt experienced a type A outbreak in 2006 after many years of freedom from this serotype. This virus was shown to be genetically related to type A strains previously isolated from Eastern Africa (Wadsworth et al., 2006). Thus, North African countries will remain at risk from the south and east, but across the majority of their territories and at risk populations should effectively maintain FMD freedom.

Epidemiological Patterns in Asia

The situation of FMD in the Middle East and North Africa has been reviewed by Aidaros (2002) and by FAO (2006).

Iran, Iraq and Syria can be currently considered to have endemic FMD. However, it is unclear whether this cluster constitutes a primary or secondary endemic cluster. However, increased capacity for early reaction and regional co-operation might reduce the penetration and duration of persistence by exotic type A and Asia-1 viruses, and routine vaccination may affect persistence of type A types so that the complexity is reduced. Thus, improved FMD surveillance, better co-ordinated mass vaccination as a tool and targeting of control measures, should reduce the outbreak frequency over time and reduce the risk of catastrophic exotic FMD extension from their eastern and southern borders. Nevertheless, it is likely that the situation will continue to be unstable, and further exotic virus incursions can be forecast.

Thanks to support through the European Commission for the Control of FMD and the molecular analytical work of the World Reference Laboratory for FMD, there is now considerable information about the genetic characterization of FMD virus strains isolated from Iran, as for Turkey (FAO, 2006; Wadsworth et al., 2006). Results from such analyses indicate a link between virus strains from Afghanistan, Pakistan, Saudi Arabia, Iran and Turkey, suggesting that FMD probably spreads from South-Central Asia westward along what has been termed the 'Ruminant Street'. Accordingly sustainable FMD control in Asia Minor may depend on the success of control programmes farther east in Central and South Asia.

The countries of the 'Persian Gulf and Arabian Peninsula' (Middle East Cluster) are at high risk through trade in live ruminants from both Asia and Africa. From Asia, Pakistan and Iran are the main suppliers. Viruses of type Asia 1 are now constantly present, together with those of types O and A. From Africa, demand is met primarily by trade from Ethiopia, Somalia, Djibouti and Sudan. Both SAT-1 and SAT-2 serotypes have invaded from the Greater Horn of Africa. Genetic analyses of FMD virus strains in Yemen show these to be closely related to those known to circulate in Eastern Africa (Knowles unpublished data). The cattle enter marketing chains which permeate the country; FMD viruses are distributed along with the cattle. In Saudi Arabia and Kuwait, where FMD outbreaks cause major economic losses in large, intensive dairy production units, even systematic short interval application of multivalent vaccines fails to give full protection (Hutber et al., 1999). One of the reasons for this is that the ultra-modern high-technology dairy units are immersed in a system of traditional, nomadic sheep husbandry in which FMD is rife and uncontrolled. Imported livestock seed FMD viruses into the small ruminant flocks, which then disseminate them. Bio-security is insufficient to give protection.

As regards the Far East and South-East Asia Cluster, the status of FMD in South-East Asia has been reviewed by Donaldson (1997), Gleeson (2002) and Sakamoto and Yoshida (2002). FMD is endemic in seven countries (Cambodia, Laos, Malaysia, Myanmar, the Philippines, Thailand and Vietnam) and three are recognized by the OIE as free of the disease without vaccination (Brunei, Indonesia and Singapore). Part of the 'Philippines' (i.e. Mindanao, Visayas, Palawan and Masbate) and part of 'Malaysia' (i.e. zones of Sabah and Sarawak) are also recognized internationally as being free of FMD without vaccination. Large parts of the archipelago are also recognized by the OIE as being free from infection without vaccination. However, until 2005, the virus used to circulate in swine in the south of Luzon Island and thereby complicating the elimination of FMD from the archipelago. 'Indonesia' has sustained its freedom for more than two decades. In East Asia, 'Japan and the Republic of Korea' are recognized as countries free without vaccination while Taiwan Province of China is recognized as free with vaccination.

Even though there is a dire lack of phylogenetic data, patterns are evident within what is superficially an amorphous pattern of occurrence. The present account provides some insight into previously unpublished observations.

The Cathay topotype of FMD-type O appears to be endemic in swine production systems of 'southern China' and there is some evidence that in Yunnan Province there is a type A virus superimposed on this. There seems to be a pattern of widespread dissemination of different viruses after their introduction. This is illustrated by the dramatic events leading up to the Eurasian pandemic of the type O Pan-Asia topotype during the decade leading up to the incursion into the UK in 2001. Now in 2005, spread of an Asia 1 virus seems to be recapitulating the spread of the Pan-Asian type O virus which phylogenetic evidence suggests also had its origin in South Asia (Valarcher et al., 2005). However, the epidemiology of FMD in China remains enigmatic even to the Chinese authorities. For example, there appears to be no clear answer to the question: How does a FMD virus move from Tibet to the east coast of China when all trade in animals and meat is reported to take place in the opposite direction. Evidently, without more detailed information, it is difficult to exclude the possibility (however remote) of some trade in animals and meat from west to east along the Yellow and Yangtse rivers.

FMD viruses, which originate in South China, for example the Cathay 'O' and the Pan-Asia 'O' topotypes, possibly to be joined by the Asia 1 topotype evolving in 2005 (Valarcher et al., 2005), cross into South-East Asia across the border into Vietnam. The vibrant two-way trade across the river separating China from 'Vietnam' is in fact a common route for exchange of FMD viruses, which then tend to spread westwards into Cambodia, Laos and eventually Thailand. Periods have been known when ruminants have featured in this cross-border movement. For example, in the early 1990s, there was a significant movement of buffaloes out of China into South-East Asia as mechanization made buffaloes redundant for the preparation of paddies. However, by the end of the decade, buffalo and cattle were moving in the opposite direction into China to supply the increasing demand for meat created by rising prosperity.

FMD viruses of types O and Asia 1 are maintained in the rice farming systems along the Mekong River in 'Vietnam, Cambodia and Laos'. Farmers here still use buffaloes for paddy preparation and, in addition, keep small numbers of cattle and swine for consumption and sale at peak times of demand. Flooding of the Mekong River, increasing in frequency in recent years and now occurring every 2–3 years, displaces farming families and their live-

stock to seek temporary refuge on higher land where they aggregate at high density. Rapid transmission of FMD at such times is common and, when livestock return to their villages as the flooding recedes, FMD viruses are seeded out into the communities and generate slowly moving epidemics spreading from village to village. In Laos, and to some extent in the other countries, where farmers have very limited access to services of any sort and where there is no organized marketing system, farmers are preyed on by traders who offer low prices for affected animals, which farmers are keen to sell to cut their losses. These traders move livestock between villages, slaughtering them to sell meat and adding to the spread of disease. FMD viruses from southern Vietnam can spread easily to Cambodia, to which piglets are sent for fattening, and may then spread eventually into 'Thailand'.

FMD viruses regularly move into China from 'Myanmar and Laos' from which there is a thriving cattle trade into Yunnan. Fattening units have even been established within China close to the border. Historically the FMD viruses concerned have belonged primarily to the O and Asia 1 types but type A was also encountered. These viruses are likely to be derived originally from South Asia. FMD virus of type A seems to have been maintained in northern Laos and Yunnan Province of China. Viruses of this type were not visible in South-east Asia for some years but have now returned in 2005. Little is known about this virus system nor is it known if the large population of feral swamp buffalo inhabiting this area from which people are excluded by massive amounts of unexploded ordinance, could be involved in virus maintenance. This virus also finds its way into 'Thailand' following trade.

Outbreaks of FMD in Xingjian Province in the 'extreme west of China' could suggest FMD endemicity within the large ruminant herds pastured there, but there is also a possibility that the virus could have spread from Kyrgyzstan now that the FMD status of the Central Asian states has deteriorated from the former free status that these states enjoyed until the 1990s.

Events of the last decade have clearly indicated the vulnerability of the 'island states' with both Taiwan and the Philippines having received virus through illegal importation of pig meat. In the case of 'Japan', importation of fodder was blamed as the source.

FMD viruses of types A, O and Asia 1 which originate in South Asia but spread into South-East Asia, presumably through movement of livestock from Bangladesh into Myanmar. How these viruses move from South Asia to South-East Asia is debatable as most of the border is thought to be inaccessible for trade because it is very mountainous. However, there is an accessible area and it is known that Indian cattle from West Bengal have on occasion found their way into the Myanmar cattle trade. Virus may also move in small numbers of animals, which are more frequently traded across the border. Whether or not cattle from South Asia can reach Malaysia is not known but what is certain is that South Asian FMD viruses can end up causing outbreaks in 'Myanmar, Thailand and Malaysia'. Another possible source for Malaysia could conceivably have been buffalo meat imported from India. Type C FMD virus used also to follow this route from a reservoir, which seems to have existed in the past in north-east India and possibly Bangladesh.

Faced with such an inflow of FMD viruses from both sides, 'Thailand' has little prospect of improving its control in a sustainable manner until the origins of these viruses is addressed. As the areas of origin, Myanmar, Laos, Cambodia and Vietnam, are the least developed areas in which FMD also has its severest impact on rural livelihoods, it is doubly important that these areas should be a prime focus of attention for regional FMD control programmes.

Type C FMD virus has not been detected in South, South-East or East Asia for a number of years and this leads to optimism that the virus might no longer be present in Asia. However, this conclusion must be reached with care. Type C FMD virus was present in the Philippines for many years but from 1991 onwards it appeared that FMD, including type C, had been eliminated from the archipelago. Yet, in 1994, when the Cathay type O topotype was introduced to Manila, a single-farm outbreak caused by a Type C FMD virus was also detected. All subsequent outbreaks checked by laboratory examination (and these numbered thousands) were caused by type O except for one outbreak a year later to the north of Manila. The type C virus has not now been detected in the Philippines since 1995. Molecular characterization demonstrates very clearly that the type C identified in 1994 fits into the evolving topotype, which had been referred to as the 'Philippines C' virus, originally introduced probably from South America in the 1970s. It must, therefore, have been present in some occult manner for several years in the early 1990s and it could still be present in other countries in the region.

As regards the South Asia Cluster, India and Pakistan are the key to the progressive control of FMD in South and Central Asia. Very little is known about the epidemiology of FMD in 'India'. Despite a significant capacity for molecular characterization being used to generate information on many hundreds of viruses per year, there appears to have been no published information on systematic analysis of the spatial and temporal distribution of topotypes. As is the case in China, more attention seems to be focussed on pulsed vaccination campaigns than on epidemiological analysis. India's 12 million swine

are not generally considered to play an important role in the maintenance of FMD even though wild feral pigs are present everywhere and swine raising is an important agricultural enterprise in north-eastern parts of India. India is unusual in having an enormous cattle population (approximating 200 million) used for dairy production and draught purposes; yet generally speaking, their meat is not consumed in India. This situation generates an enormous surplus of cheap cattle, which can be exported from some states.

'Bangladesh' imports up to two million head of cattle per year for slaughter and, as has been noted above, some of these, or the FMD viruses they support, find their way into Myanmar and onwards to Thailand and Malaysia. Large cattle markets in the west of Bangladesh receive these cattle and hold them for sale to traders who then move them to markets near Dhaka in central Bangladesh where they are again held until sold. From these markets, they are distributed all over Bangladesh. It is not uncommon to see cattle with active FMD standing in the market in Rajshahi on the Indian border, for example. Approximately 3000 cattle per day pass through the market and the opportunities for FMD virus transmission are obvious. The other major route by which cattle leave India is to the west through Pakistan and Afghanistan, where some were slaughtered, and then on through the city of Harat into Iran.

In addition, many surplus buffalo (derived from a population of about 100 million) are sold for slaughter in Nepal and others are slaughtered for meat export in several processing plants. The meat is widely distributed in the Middle and Far East. The 1996 type A outbreak, which started in Albania and spread to Macedonia, Bulgaria and Thrace-Turkey is believed to have originated from importation of buffalo meat on-the-bone from South Asia (Leforban and Gerbier, 2002). 'Nepal' suffers severely from FMD it receives by not only importing buffalo and goats from India but also by cattle transiting Nepal en route Bangladesh.

The long-term persistence of FMD in 'Sri Lanka' is of little significance for the rest of the subregion for livestock flow only into Sri Lanka. However, the repeated, virtually annual, slowly moving enzootics which start from the north and slowly track through villages to the south are of considerable significance to rural livelihoods based on milk production. As in the case of Laos, it is not known if the 30 000 or so strong feral swamp buffalo population of a national reserve in the north of the country are involved in FMD maintenance and transmission in the country. It is however, tempting to suggest that they are, for there is close seasonal contact when domestic buffaloes are released into the reserve to fend for themselves after paddies have been planted for rice production. Outbreaks appear to start from this area. Phylogenetic evidence suggests persistence of a particular 'O' topotype supplemented by occasional introductions of Indian 'O' viruses.

'Pakistan' is another country with a massive ruminant population amounting to some 45 million buffalo and cattle and 100 million sheep and goats. As the dairy industry has developed, FMD has become an increasingly severe problem with the major dairy colonies supplying the city of Karachi, for example, suffering several waves of infection per year. With a turnover of hundreds of thousands of buffalo per year, these colonies receive infected animals constantly and also disseminate FMD viruses back into source populations in the Indus River buffalo tract of Sindh and Punjab Provinces and also to other dairy areas in other provinces. Buffalo moving for slaughter in Afghanistan introduce FMD viruses into the intermediate markets of central Pakistan. Elsewhere in Pakistan, FMD is constantly circulating in all ruminant livestock without any concerted control measures; the situation of naturally occurring enzootic FMD is exacerbated by the use of formalized vaccines, which themselves are capable of generating outbreaks (Beck and Strohmaier, 1987). The east of 'Afghanistan' is ecologically a part of Pakistan and is linked to it by transhumance, trade and fattening enterprises. Thus, there is a free flow of viruses between the two countries.

As regards the Central Asia Cluster, the block of five Community of Independent States (CIS) countries, which form the core of Central Asia – Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Uzbekistan – were formerly kept FMD-free by virtue of USSR border disease control procedures and minimal trade beyond the USSR. Since the transition to independence, veterinary services have been unable to cope with an increased cross-border trade at the time of diminished border controls. FMD of types O and Asia 1 are now widespread and reporting is suboptimal. There is little to prevent movement of FMD viruses from Afghanistan, where infection is rife, into Tajikistan through contiguous livestock farming communities spanning the border and through uncontrolled (and uncontrollable) trade in small ruminants through Tajikistan to Kazakhstan where they fetch far higher prices. Kyrgyzstan reported infection in 2004, which could have come from Xingjian in China. Alternatively, it could have been a reflection of spread within Central Asia. In the absence of information and molecular phylogenetic information, little epidemiological information can be deduced from unsystematic reporting.

'Afghanistan' is in many ways ecologically linked to Central Asia as is Iran. Afghanistan has virtually no

official veterinary service; such veterinary services as are provided by donors are conducted through non-governmental organizations focussing on clinical service delivery. Some FMD viruses have been collected by the US military in the last few years and these are known to have belonged to serotypes O and A. However, there is no publicly available data on the molecular characterization of the strains.

Once in 'Iran', Indian cattle used to continue to central Iran or move onwards to Iraq and Turkey. At present, it appears that this trade is in abeyance, but if prices pick up in Iraq and/or Turkey, this could create the demand to start up this marketing chain once more. Even if cattle themselves do not travel the whole route, the viruses they bring from India clearly do. Iran struggles to exert control over FMD by quarantine of livestock on the Iranian border and by vaccination in higher risk areas. The latter seems to have brought some success in the last year and this appears to have had a 'knock-on' effect in Turkey where FMD incidence has also declined in Eastern Anatolia.

Epidemiological Patterns in South America

The evolution of FMD in South America has been reviewed by Correa Melo et al. (2002) and Saraiva (2003, 2004). Briefly, the first record of the disease in South America dates back to *circa* 1870 in the Province of Buenos Aires, Argentina spreading later on to the central region of Chile, to Uruguay and to southern Brazilian States, as a result of importation of livestock from Europe. FMD spread further into central western Brazilian States and was recorded during the first half of the 20th Century in Peru, Bolivia and Paraguay, reaching Venezuela and Colombia in the 1950s, and Ecuador in 1961. Since then, the disease has been endemic in the subcontinent. Currently in September 2007, Chile, Guyana, the Argentinean Patagonia, Southern and Central Western zones in Peru, and the Colombian Urabá are free without vaccination. Other important livestock producing zones of South America are considered FMD free with vaccination. It is therefore most appropriate to consider the epidemiology of FMD in South America according to ecological zones.

Ecosystem approach

In South America, FMD spreads mainly with trade of animals, especially bovines, and the knowledge gathered in the region shows the existence of epidemiological relationships between complementary livestock production systems. Traditional forms of raising, fattening and processing livestock influence the diffusion and maintenance of infection in different areas. Range farming areas, characterized by low rates of productivity but high outputs, produce steers sold for fattening in areas with better productive infrastructure, closer to the centres of processing and consumption. The seasonal flow of animals is responsible for a concentration of susceptible and infected animals in the fattening areas (OPS, 1985; Astudillo et al., 1986). The vulnerability and susceptibility of these areas because of their peculiar livestock structure and varying levels of immunity of animal populations, maintain and spread the FMD virus (Fig. 5). The Hemispheric Foot-and-Mouth Disease Eradication Plan – PHEFA (Correa Melo et al., 2002), was instrumental in the application of this concept.

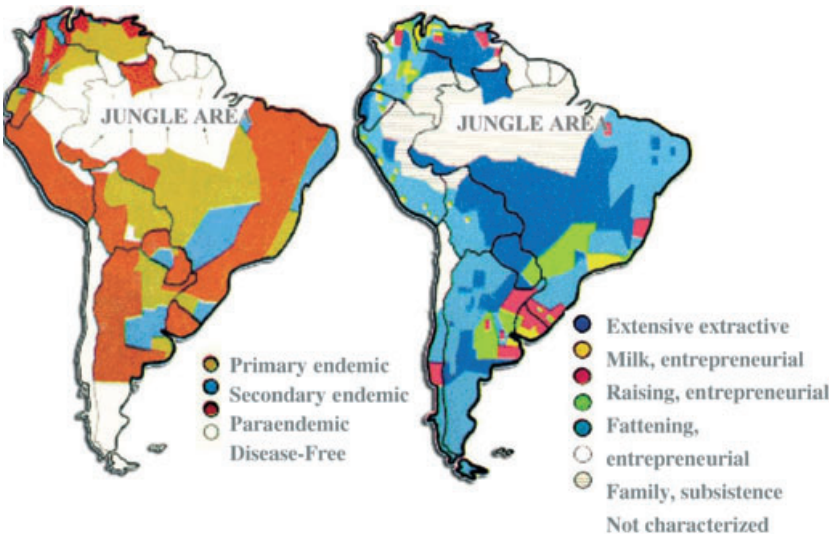


Fig. 5. Forms of production and FMD ecosystems.

Table 2. Foot-and-mouth disease diagnosis by type of virus, country and year. South America, 1995–2006

Count/year	Virus	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
Argentina	O	0	0	0	0	0	0	0	0	0	0	0	1
	A	0	0	0	0	0	0	2.126	1	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Bolivia	O	17	7	4	1	2	7	7	8	0	0	0	0
	A	19	1	4	6	18	18	81	1	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Brazil	O	83	9	19	5	13	12	0	0	1	1	34	0
	A	99	18	5	1	2	6	15	0	0	0	0	0
	C	3	0	0	0	0	0	0	0	4	4	0	0
Chile	O	0	0	0	0	0	0	0	0	0	0	0	0
	A	0	0	0	0	0	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Colombia	O	144	25	19	92	49	37	5	8	0	0	0	0
	A	79	81	17	11	8	1	0	0	2	2	1	0
	C	0	0	0	0		0	0	0	0	0	0	0
Ecuador	O	32	17	30	67	17	11	15	104	42	42	22	15
	A	0	5	34	14	2	8	8	4	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Guyana	O	0	0	0	0	0	0	0	0	0	0	0	0
	A	0	0	0	0	0	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Paraguay	O	0	0	0	0	0	0	0	1	0	0	0	0
	A	0	0	0	0	0	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Peru	O	3	10	4	0	0	0	0	0	20	20	0	0
	A	0	15	0	0	15	48	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Uruguay	O	0	0	0	0	0	3	0	0	0	0	0	0
	A	0	0	0	0	0	0	2.057	0	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	0	0	0
Venezuela	O	1	0	2	0	0	0	0	0	5	5	3	11
	A	3	1	1	17	4	4	4	9	29	29	10	25
	C	0	0	0	0	0	0	0	0	0	0	0	0

XXXIV Meeting of COSALFA (2007).

Distribution by type of virus

Only types A, O and C of the FMDV have been recorded in South America. Type C has been diagnosed in the Andean countries only on three occasions. The first outbreak was in Leticia, Colombia in 1967 and again in 1970. The third was in the Huascaran region of Peru in 1980. This outbreak was attributed to vaccine containing incompletely inactivated virus by formalin and released before the full testing regimen had been completed. Type C was prevalent in Argentina, Bolivia, Brazil, Paraguay, Peru, Uruguay between 1972 and 1995 (last outbreak in Brazil), and in Chile between 1976 and 1977 (Saraiva and Lopez, 2001). Even with the improvement of surveillance in these countries, the virus was not detected for 9 years, until it was diagnosed in 2004 in seven premises in the Carreiro da Várzea Island in the Amazon River. This occurrence was instrumental to improve FMD control strategies in that region of Brazil (PANAFTOSA, 2004). Table 2 shows the distribution of diagnoses by virus type in the period 1995–2006, in which type C virus has been diagnosed in 14–25% of the total positive diagnoses.

While type C has been rare in the Andean region, types O and A have been quite common. For example, since 2003, type O has occurred relatively frequently in Ecuador. In Venezuela, though type 'O' virus is also present, type 'A' is the more widespread in the country, especially close to the border with Colombia, posing a risk to the latter.

The prevalence of subtypes and strains follows a geographical pattern in which families of viruses are concentrated in specific areas of the subcontinent as if they were contained within these administrative/programming divisions. The epidemiological findings indicate that FMD types, subtypes and strains are fairly separated into 'families' of viruses, as seen in characterization studies carried out in field strains obtained from emergencies in the Southern Cone region.

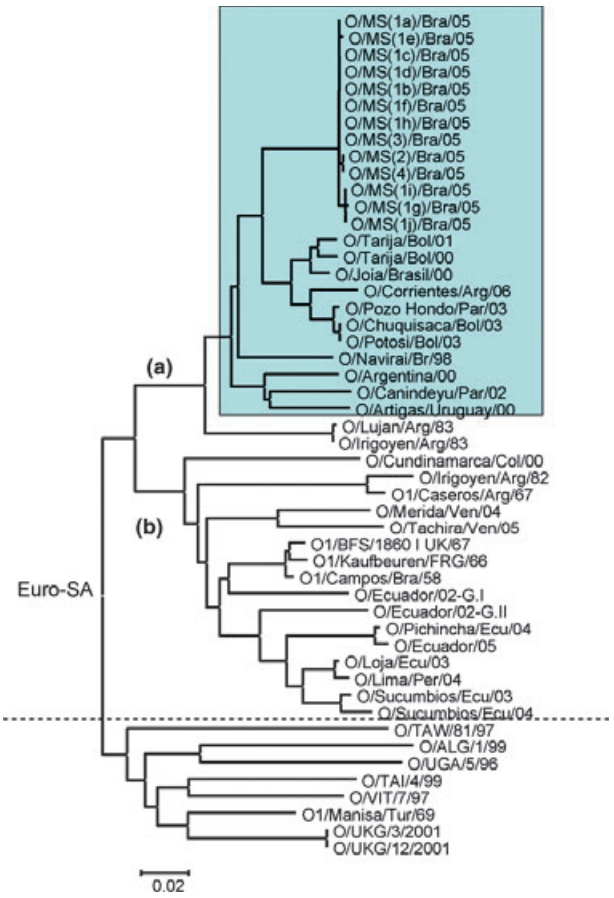


Fig. 6. Dendograms showing the distribution of FMDV-type O strains in South America.

The investigation of the molecular epidemiology of FMDV-type O strains helped in the epidemiological studies of the disease and to assist in the planning of control strategies (Correa Melo et al., 2002). The phylogenetic analysis carried out by the reference laboratory showed that all emergency/sporadic viruses collected between 2000 and 2006 are indigenous to South America and showed a clustering profile with considerable genetic relationships among viruses in countries with common boundaries (Malirat et al., 2007). This genetic relationship found for the isolates from these five countries suggests that, besides being endogenous, cross-border movement is a major cause for disease dissemination (Fig. 6.). Characterization studies for FMDV type A were also developed (Bergmann et al., 2005). These too showed a similar tendency for geographical clustering within South America as for type O.

Importance of other species in the epidemiology of FMD

FMD programmes in South America only routinely vaccinate bovines and buffalo. Sheep, goats and pigs might only be vaccinated during emergencies. Several studies have detailed the participation of susceptible species in the maintenance and diffusion of FMDV in South America, and cattle were considered to be the species that determines disease diffusion and presentation, because of the interactions between the forms of production already described. Even though sheep used to be important in numbers, especially in the Southern Cone, almost on a par with cattle in southern Brazil, twice that of bovines in Uruguay and a sizeable population in Patagonia, the role of this species in the maintenance of infection was not considered important, possibly due to the way the species are reared (Dora and Petry, 1984).

The importance of camelids in the maintenance of FMD in the Andean region (Lubroth et al., 1990) is also limited to small ranges and persistence of infection is short-lived in those species. The role of wildlife in the epidemiology of the disease needs to be determined in South America, where it is accepted that it is mostly affected during outbreaks in domestic species, as a spin-off. At least experimentally, capybaras (*Hydrochoerus hydrochoeris hydrochoeris*) that had been experimentally infected showed clinical signs and infected other susceptible species, although the role of this species in the maintenance of infection in nature is not clear (Gomes and Rosenberg, 1984). Buffaloes (*Bubalus bubalis*) were at least in one case implicated in the spread of the disease in Brazil, when the introduction of this species to a controlled farm caused subclinical FMD cases of virus serotype A, spreading afterwards to other farms (Melo, 1990).

FMD risk epidemiological clustering in South America

In 2004, the Inter-American Group for the Eradication of FMD (GIEFA) fine-tuned the Hemispheric FMD control strategy, taking into account the sanitary situation recognized at that time. The countries were clustered into five risk zones, namely:

1 free without vaccination - according to OIE criteria;
2 free with vaccination – according to OIE criteria;
3 level 1: areas of low risk;
4 level 2: areas of intermediate risk and
5 level 3: areas of high risk and unknown factors.

On this basis, GIEFA drew up a risk matrix classification of FMD infected regions for South America as listed in Table 3**.** The five risk zones of South America are depicted in Fig. 7. It is apparent that until the South American countries tackle FMD vigorously in the primary endemic areas, identified as risk levels 2 and 3, the sustainability of FMD freedom will remain threatened. It seems likely that the original goal of the Hemispheric Plan to eliminate FMD from the Americas by 2009 is

Table 3. Proposal of a matrix of classification of the FMD programme level in South America [Anti-American Group for the Eradication of FMD(GIEFA, 2004)]

	Program levels (Risk)		
Parameters of characterization	1 (Low)	2 (Intermediate)	3 (High and unknown)
Sanitation control eradication policy	Eradication	Adequate control	Minimal control (or non-existing)
Characteristics of production	Known and updated	Known	Little known
Epidemic characteristics of the areas	Known and updated	Known and updated	Deficiency in knowledge
Veterinary attention systems	Effective	Good	Deficient
Social participation	Effective	Good	Deficient or absent
Inspection system	Effective	Good	Deficient or absent
Clinical cases	Absence >2 years	Absence <2 years; occasional presence	High presence and/or recurring
Vaccine coverage	More than 90%	More than 80% but <90%	<80%
Control/inspection of movements	Effective	Good	Deficient
Prevention programme	Effective	Good	Deficient

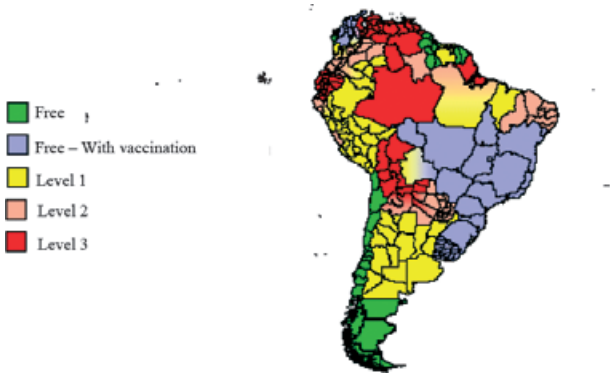


Fig. 7. FMD risk map for South America in 2004(Anti-American Group for the Eradication of FMD, GIEFA, 2004). Inter-American Group for the Eradication of FMD. Level 1, low risk; level 2, intermediate risk and level 3, high risk + unknown factors.

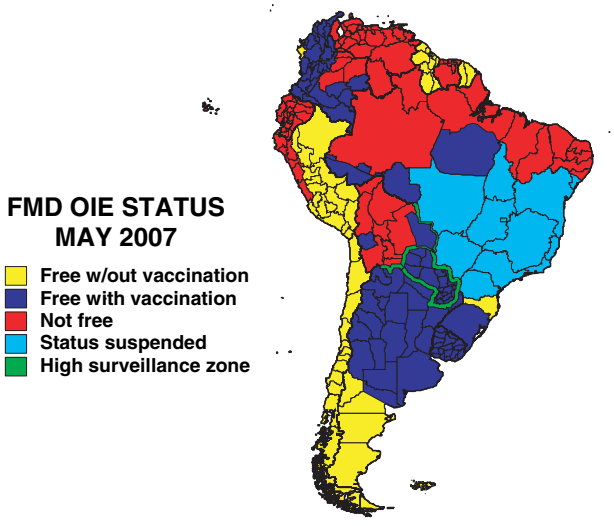


Fig. 8. FMD status recognized by the OIE, May 2007.

unlikely to be realized and, therefore, this timetable may need to be revised.

The risk categorization adopted by GIEFA is a useful approach to guide the disease control strategy. However, it is important to note that such risk maps are accurate only at the time of release; their demarcations will constantly change to reflect the changing epidemiological pattern as disease control programmes evolve. For example, since the map in Fig. 7 was published by GIEFA in 2004, reflecting the risk situation that prevailed then, the epidemiological status in South America has changed as a result of the enlargement of FMD-free zones with vaccination in Argentina, Colombia, Bolivia and Brazil and of FMD-free zones without vaccination in Argentina, Peru and Brazil. The currently OIE recognized FMD-free countries and zones in South America are listed in the OIE website http://www.oie.int/eng/info/en_fmd.htm?e1d6 and the status at May 2007 is summarized in Fig. 8.

Discussion

The above account shows that the movement of infected animals is the most important factor in the spread of FMD within the endemically infected regions of the world. However, the disease is not uniformly spread in these regions. We have shown that the eco-system based approach for defining the epidemiological patterns of FMD in endemic areas that was first described by Astudillo et al. (1986) for South America can apply readily to other parts of the world. These authors described a scheme, which is based on eco-systems and which takes into account the dynamics of FMD, the farming systems and cattle movements to identify primary endemic areas (i.e. virus maintenance areas), secondary endemic areas (i.e. areas of virus propagation) and epidemic areas (i.e. areas of explosive outbreaks). We have described how this

eco-based description of the epidemiology of FMD in South America continues to be the guiding principle for the progressive control of the disease in this continent.

It is proposed that any coordinated regional or global strategy for FMD should be based on a sound epidemiological assessment of the incidence and distribution of FMD, identifying risk sources as either primary or secondary (para-endemic) eco-systems. A sustainable programme for the progressive control of FMD would need to address these areas. This concept forms the basis of the global framework for the progressive control of FMD that is described in the accompanying paper (Rweyemamu et al., 2008). The concept of regional epidemiological clustering as a basis for developing global strategies for FMD control, which were previously described by Rweyemamu and Astudillo (2002) has been more extensively elaborated in the present paper.

Finally, it should be noted that with globalization of trade even areas where FMD is endemic can suffer from introduction of virus strains that are exotic to the region. The most notable example is the incursion of the Pan-Asia topotype, lineage of Type O FMD virus into South Africa in September 2000 (Brückner et al., 2002).

References

Aidaros, H. A., 2002: Regional status and approaches to control and eradication of foot and mouth disease in the Middle East and North Africa. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 451–458.

Astudillo, V. M., F. J. Dora, and A. J. M. Silva, 1986: Ecosistemas y estrategias regionales de control de la fiebre aftosa. Aplicación al caso de Rio Grande do Sul, Brasil. *Bol. Cent. Panam. Fiebre aftosa* 52, 47–61.

Batho, H., 2003. Report to the OIE Following a Request by the Southern African Development Community (SADC) for an Emergency Audit on Foot-and-Mouth Disease (FMD) in Southern Africa. OIE FMD Report SADC – H. Batho. April–May 2003. OIE, Paris.

Beck, E., and K. Strohmaier, 1987: 'Subtyping of European foot-and-mouth disease virus strains by nucleotide sequence determination'. *J. Virol.* 61, 1621–1629.

Bergmann, I. E., V. Malirat, E. Neitzert, and E. Correa Melo, 2005: Evaluation of diagnostic tools for epidemiological purposes – applications to FMD. In: Makkar, H. P. S., and G. J. Villijoen (eds), Applications of Gene-based Technologies for Improving Animal Production and Health in Developing Countries, pp. 335–342. IAEA, the Netherlands.

Brückner, G. K., W. Vosloo, B. J. A. Du Plessis, P. E. L. G. Kloeck, L. Connoway, M. D. Ekron, D. B. Weaver, C. J. Dickason, F. J. Schreuder, T. Marais, and M. E. Mogajane, 2002: Foot and mouth disease: the experience of South Africa. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 751–764.

Correa Melo, E., V. Saraiva, and V. Astudillo, 2002: Review of the status of foot and mouth isease in countries of South America and approaches to control and eradication. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 429–436.

COSALFA, 2007: Report on the sanitary situation of the countries in South America. XXXIV Ordinary Meeting of the South American Commission for the Fight Against Foot-and-Mouth Disease, Caracas, Venezuela, 15–16 May.

Cottam, E. M., D. T. Haydon, D. J. Paton, J. Gloster, J. W. Wilesmith, N. P. Ferris, G. H. Hutchings, and D. P. King, 2006: Molecular epidemiology of the foot-and-mouth disease virus outbreak in the United Kingdom in 2001. *J. Virol.* 80, 11274–11282.

Donaldson, A. I., 1997: Foot-and-mouth disease in Taiwan. *Vet. Rec.* 140, 407.

Donaldson, A. I., 1999: The global status of foot-and-mouth disease and its relevance to control and eradication efforts in South-East Asia. Report of 33rd Session of the European Commission for the Control of Foot-and-Mouth Disease (EUFMD Commission), FAO, Rome, Italy, 7–9 April, Appendix 9. Available at: http://www.fao.org/ag/againfo/commissions/en/eufmd/33report_txt.html.

Dora, J. P. F., and M. C. Petry, 1984: Importância epidemiológica das espécies animais em febre aftosa. *Hora Vet.* 3, 53–60.

EFSA, 2006: Risk assessment on foot and mouth disease. *EFSA J.* 313, 1–34. Available at: http://www.efsa.eu.int/EFSA/Scientific_Opinion/ahaw_op_ej313_fmd_en1,0.pdf (accessed October 2007).

FAO, 2006: Foot-and-mouth disease. Situation worldwide and major epidemiological events in 2005–2006. Prepared by FAO EMPRES and EUFMD Commission Secretariat. Available at: http://www.fao.org/docs/eims/upload//225050/Focus_ON_1_07_en.pdf (accessed October 2007).

FMD Homepage – Maps, 2006: http://www.wrlfmd.org/maps/FMD 2000-2006.pdf.

GIEFA, 2004: GIEFA Action Group Bulletin. Bulletin of the Plan of Action Subgroup. Second Meeting – Bogotá, Colombia, 21–23 July. Inter-American Group for the Eradication of Foot-and-Mouth Disease GIEFA. PANAFTOSA, Rio de Janeiro.

Gleeson, L. J., 2002: A review of the status of foot and mouth disease in South-East Asia and approaches to control and eradication. *Rev. Sci. Tech.* 21, 465–475.

Gomes, I., and J. F. Rosenberg, 1984: Possible role of capybaras (1985). *Hydrochoerus hydrochoeris hydrochoeris* in foot-and-mouth disease (FMD) endemicity. *Prev. Vet. Med.* 3, 197–205.

Hargreaves, S. K., C. M. Foggin, E. C. Anderson, A. D. S. Bastos, G. R. Thomson, N. P. Ferris, and N. J. Knowles, 2004: An investigation into the source and spread of foot and mouth disease virus from a wildlife conservancy in Zimbabwe. *Rev. Sci. Tech. Off. Int. Epizoot.* 23, 783–790.

Hedger, R. S., A. J. Forman, and M. H. Woodford, 1973: Foot-and-mouth disease in East African buffalo. *Bull. Epizoot. Dis. Afr.* 21, 99–101.

Hutber, A. M., R. P. Kitching, and D. A. Conway, 1999: Predicting the level of herd infection for outbreaks of foot-and-mouth disease in vaccinated herds. *Epidemiol. Infect.* 122, 539–544.

Knowles, N. J., and A. R. Samuel, 2003: Molecular epidemiology of foot-and-mouth disease virus. *Virus Res.* 91, 65–80.

Knowles, N. J., P. R. Davies, R. J. Midgley, and J.-F. Valarcher, 2004: Identification of a ninth Foot-and-Mouth disease virus type O topotype and evidence for a recombination event in its evolution. 2004 Session of the Research Group of the Standing Technical Committee of EUFMD, Chania, Crete, Greece, 12–15 October. Available at: http://www.fao.org/ag/againfo/commissions/en/eufmd/crete.html

Knowles, N. J., A. R. Samuel, P. R. Davies, R. J. Midgley, and J.-F. Valarcher, 2005: Evolution and spread of a pandemic strain of foot-and-mouth disease virus serotype O. *Emerg. Infect. Dis.* 11, 1887–1893.

Leforban, Y., and G. Gerbier, 2002: Review of the status of foot and mouth disease and approach to control/eradication in Europe and Central Asia. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 477–492.

Lubroth, J., R. Yedloutschnig, V. Culhane, and P. Mikiciuk, 1990: Foot-and-mouth disease virus in the llama (*Lama glama*): diagnosis, transmission and susceptibility. *J. Vet. Diagn. Invest.* 2, 197–203.

Malirat, V., J. J. Barros, I. E. Bergmann, R. M. Campos, E. Neitzert, E. V. Costa, E. E. da Silva, A. J. Falczuk, D. S. Pinheiro, N. Vergara, J. L. Q. Cirvera, E. Maradei and R. D. Landro, 2007: Phylogenetic analysis of foot-and-mouth disease virus type O re-emerging in free areas of South America. *Virus Res.* 124, 22–28.

Melo, P., 1990: Un episodio subclínico de fiebre aftosa en bovinos probablemente causado por la introducción de búfalos (*Bubalus bubalis*). VI Congresso Fluminense de Medicina Veterinária, Rio de Janeiro, Brazil, pp. 18–22.

OPS, 1985: Organización Panamericana de la Salud. Caracterización de los ecosistemas de la fiebre aftosa, Vol 2: Vigilancia epidemiológica, pp. 533–628. OPS, Washington, DC.

PANAFTOSA 2004: Informe de ocurrencia de casos de fiebre aftosa, virus tipo C, en el Estado de Amazonas, Brasil. PANAFTOSA-OPS/OMS, Río de Janeiro.

Roeder, P. L., W. P. Taylor, and M. M. Rweyemamu, 2005: Rinderpest in the 20th and 21st centuries. In: Barrett, T., and P. P. Pastoret (eds), Rinderpest and Peste des Petits Ruminants: Virus Plagues of Large and Small Ruminants, p. 106. Elsevier, London.

Rweyemamu, M. M., and V. Astudillo, 2002: Global perspective for foot and mouth disease control. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 765–773.

Rweyemamu, M., P. Roeder, D. MacKay, K. Sumption, J. Brownlie, and Y. Leforban, 2008: Planning for the progressive control of foot-and-mouth disease worldwide. *J. Transboundary Emerg. Dis.* 55, 73–87.

Sakamoto, K., and K. Yoshida, 2002: Recent outbreaks of foot and mouth disease in countries of east Asia. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 459–463.

Saraiva, V., 2003: Epidemiology of foot-and-mouth disease in South America. In: Dodet, B., and M. Vicari (eds), Foot and Mouth Disease: Control Strategies, pp. 4. Éditions scientifiques et médicales Elsevier SAS, Paris.

Saraiva, V., 2004: Foot-and-mouth disease in the Americas: epidemiology and ecologic changes affecting distribution. *Ann. N. Y. Acad. Sci.* 1026, 73–78.

Saraiva, V., and A. Lopez, 2001: Análisis descriptivo del riesgo de persistencia del virus "C". VII Seminario Internacional de Control de Vacuna Antiaftosa, Rio de Janeiro, Brazil, 10–14 September.

Sumption, K., M. Rweyemamu, and W. Wint, 2008: Incidence and disribution of foot-and-mouth disease in Asia, Africa and South America; combining expert opinion, official disease information and livestock populations to assist risk assessment. *J. Transboundary Emerg. Dis.* 55, 5–13.

Sutmoller, P., G. R. Thomson, S. K. Hargreaves, C. M. Foggin, and E. C. Anderson, 2000: The foot-and-mouth disease risk posed by African buffalo within wildlife conservancies to the cattle industry of Zimbabwe. *Prev. Vet. Med.* 44, 43–60.

Valarcher, J.-F., N. Knowles, R. Fernandez, P. Davies, R. Midgley, G. Hutchings, B. Newman, N. Ferris, and D. Paton, 2004: Global FMD Situation 2003–2004. Report of the Session of the Research Group of the Standing Technical Committee of EUFMD, Chania, Crete, Greece, 12–15 October. Available at: http://www.fao.org/ag/againfo/commissions/docs/greece04/FINALREPORT.pdf.

Valarcher, J. F., N. J. Knowles, N. P. Ferris, D. J. Paton, V. Zakharov, A. Sherbakov, Y.-J. Shang, Z.-X. Liu, X.-T. Liu, A. Sanyal, D. Hemadri, C. Tosh, and T. J. Rasool, 2005: Recent spread foot-and-mouth disease virus serotype Asia 1. *Vet. Rec.* 157: 30 (Letter).

Valarcher, J.-F., Y. Leforban, M. Rweyemamu, P. L. Roeder, G. Gerbier, D. K. J. Mackay, K. J. Sumption, D. J. Paton, and N. J. Knowles, 2007: Incursions of Foot-and-Mouth Disease Virus into Europe between 1985 and 2006. *J. Transboundary Emerg. Dis.* 55, 14–34.

Vosloo, W., and G. R. Thomson, 2004: Natural habitats in which foot-and-mouth disease viruses are maintained. In: Domingo, E., and F. Sobrino (eds). Foot-and-Mouth Disease: Current Perspectives, pp. 383–410. CRC Press, London.

Vosloo, W., A. D. S. Bastos, O. Sangare, S. K. Hargreaves, and G. R. Thomson, 2002: Review of the status and control of foot and mouth disease in sub-Saharan Africa. *Rev. Sci. Tech. Off. Int. Epizoot.* 21, 437–449.

Vosloo, W., R. M. Dwarka, A. D. S. Bastos, J. J. Esterhuysen, M. Sahle, and O. Sangare, 2004: Molecular epidemiological studies of foot-and-mouth disease virus in sub-Saharan Africa indicate the presence of large numbers of topotypes: implications for local and international control. Report of the session of the research group of the Standing Technical

Committee of EUFMD, Chania, Crete, Greece, 12–15 October. Available at: http://www.fao.org/ag/againfo/commissions/docs/greece04/App22.pdf.

Vosloo, W., L.-M. de Klerkc, C. I. Boshoff, B. Botha, R. M. Dwarka, D. Keete, and D. T. Haydon, 2007: Characterisation of a SAT-1 outbreak of foot-and-mouth disease in captive African buffalo (*Syncerus caffer*): clinical symptoms, genetic characterisation and phylogenetic comparison of outbreak isolates. Available at: http://www.up.ac.za/dspace/bitstream/2263/3115/1/Vosloo_Characterisation(2007).pdf (accessed October 2007).

Wadsworth, J., N. J. Knowles, K. G. Swabey, J. M. Stirling, R. J. Statham, Y. Li, G. H. Hutchings, N. P. Ferris, and D. J. Paton, 2006: Recent spread of new strains of foot-and-mouth disease virus type A in the Middle East and North Africa. 2006 Session of the Research Group of the Standing Technical Committee of EUFMD, Paphos, Cyprus, 15–21 October. Available at: http://www.fao.org/ag/againfo/commissions/en/eufmd/Paphos-epid.html.

Young, E., R. S. Hedger, and P. G. Howell, 1972: Clinical foot-and-mouth disease in the African buffalo (*Syncerus caffer*). *Onderstepoort J. Vet. Res.* 39, 181–184.