Annual OIE/FAO FMD Reference Laboratory Network Report

January – December 2007

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1. Summary report on FMD outbreaks during period in question from surveillance region covered by reference laboratory

1.1. The conjectured status of FMDV in 2007.

The WAHID Interface provides access to all data held within OIE's new World Animal Health Information System (WAHIS):
http://www.oie.int/wahid-prod/public.php?page=home

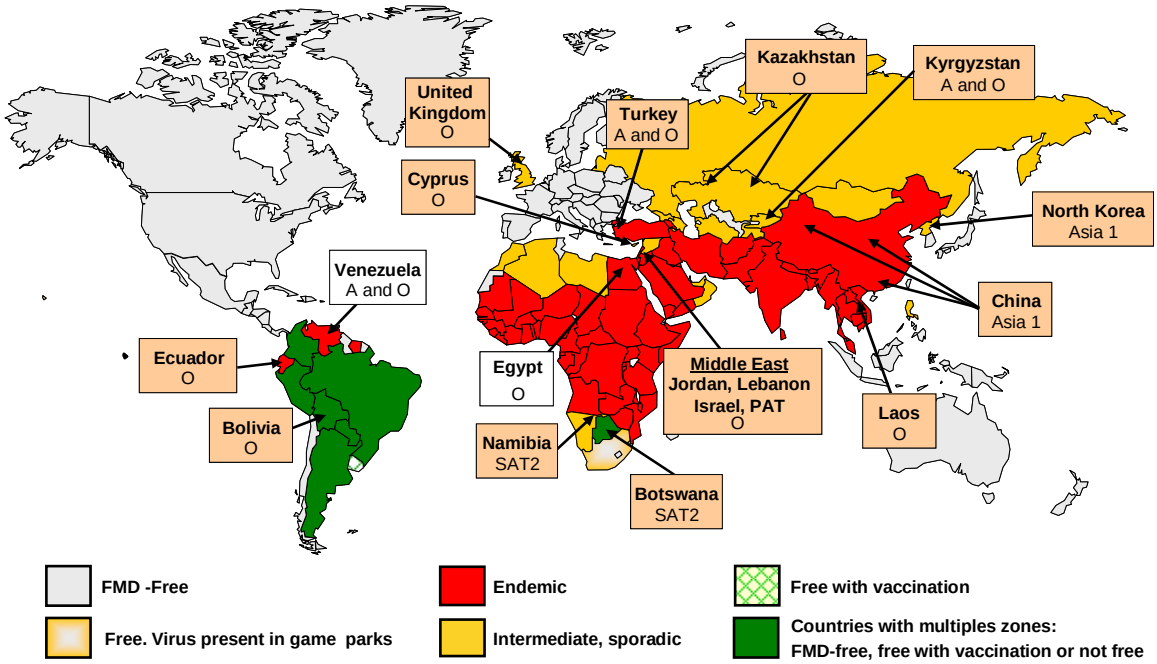
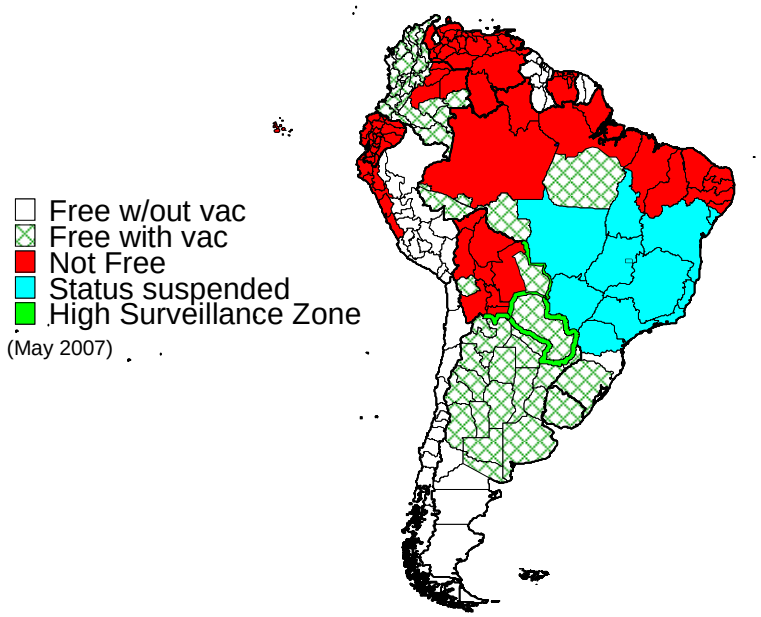


Figure 1. The conjectured status of FMDV 2007: This figure also shows a summary of FMD outbreaks reported to the OIE in 2007. Additional outbreaks of interest in Africa and South America are also shown. Note: a number of countries in South America and Southern Africa have multiple FMD zones (see Figure below for further details of recent status in South America).



1.2. Overview and discussion of outbreak information

In 2007, two countries within Europe (previously FMD-free without vaccination) reported outbreaks of FMD. In the **United Kingdom**, FMD was initially confirmed on 3rd August in beef cattle in Surrey, England: the first outbreak in the country since 2001. Subsequently, a total of 8 premises (11 holdings) were found to have animals that were infected by FMDV. These outbreaks occurred in two distinct clusters located around Normandy and Egham in Surrey. Nucleotide sequencing showed that the FMD virus responsible for these outbreaks was derived from O1/BFS 1860; an isolate used as a reference and vaccine strain at the Institute for Animal Health and Merial Animal Health Ltd located on the Pirbright site. Furthermore, analysis of full-genome sequence data was used to demonstrate that outbreaks near Egham (IP3-IP8) were derived from the Normandy cluster (IP1 and IP2), and not through a separate escape from the Pirbright site that reintroduced the virus into the field. Trade restrictions with the EU were lifted in December following 3 months without any subsequent outbreaks of disease. The United Kingdom's status of FMD free-without vaccination was restored by OIE on 19 February 2008.

In **Cyprus**, serological evidence of FMD infection was uncovered in small ruminants. The initial case was identified in October following investigation of a flock of 25 sheep which were exhibiting clinical signs suspicious of bluetongue or contagious ecthyma. FMD testing was carried out as a precaution revealing that 8/25 animals were serologically positive for FMDV non-structural proteins (NSP). In light of these results, movement restrictions and investigations of neighbouring farms were undertaken. Although conclusive evidence of FMDV circulation (antibodies against FMDV structural proteins or FMDV presence in "probangs") was not obtained for this first farm, testing of further samples collected from neighbouring farms (near Larnaca on the south coast of the island) revealed 3 further flocks with serological evidence of FMD infection (including antibodies against FMDV structural proteins of serotype O). Based upon these serological data and clinical evidence of vesicular lesions in some of the animals, an FMD outbreak was declared to the OIE on the 5th November 2007. Control measures to cull the affected sheep and goats were employed on these farms and on some additional flocks which were also found to contain type O seropositive sheep. Subsequent laboratory analyses were unable to detect FMD virus in any of the material collected from the suspect vesicular lesions. Furthermore, despite collection of approximately 250 samples (mainly "probang" samples plus some tissues) from the affected herds, no virus was detected in any samples from these cases. In addition, ongoing circulation of FMDV could not be substantiated using paired serology. Taken together with the age profile of the seropositive animals, the data indicate in-situ infection by FMD virus in the past (approximately 3 years ago). Further surveillance in the affected area and other parts of the island also failed to demonstrate active infection and serologically positive farms were not identified outside of the 10 km surveillance zone surrounding the culled Larnaca flocks. As from 21 February 2008 Cyprus has regained its FMD-free status without vaccination.

Elsewhere in Europe, FMD continues to threaten the FMD-free areas. The issue of greatest concern is the emergence of a highly transmissible lineage of the PanAsia strain of serotype O which has spread from India to the east, north and west causing recent epidemics in a number of countries in the Middle East. This picture somewhat mirrors that seen prior to 2000-2002 when another O PanAsia strain spread into several normally FMD-free countries including Taiwan, Japan, South Africa, UK,

France, Netherlands and South Korea. Although, the O Manisa vaccine is predicted to provide protection against this new PanAsia variant, the vaccine has a slightly poorer serological match compared to that which was found against the O UKG 2001 PanAsia virus. During 2007, this lineage has spread west through **Turkey** to cause outbreaks in Thrace (in February and April, and more recently in September) and through **Jordan, Lebanon, Israel, Palestinian Territory** and into **Egypt**. In addition to Serotype O, there have also been reported outbreaks due to serotype A (Iran 05 lineage) in **Turkey and Jordan**.

In Central Asia, there continue to be sporadic reports of FMD due to Asia 1. In addition to reports from **China** (Qinghai, Gansu and Xinjiang Provinces), in January 2007 this serotype has also caused the first outbreak in **North Korea** since 1960. Although initial analysis indicated that serotype O, had caused this outbreak, subsequent investigation of clinical material collected from affected animals recovered FMDV serotype Asia 1. This outbreak was located in P`yongyan-Si close to the capital. All susceptible livestock (466 cattle and 2630 pigs) in the outbreak were destroyed. Outbreaks of FMD due to serotype O have been reported in **Kazakhstan,** and due to serotype O and serotype A in **Kyrgyzstan**. Elsewhere in Asia, there continue to be reports of FMD in endemic areas including **Vietnam**, **Malaysia**, **Myanmar**, **Bhutan**, **India** and **Laos**. The SEAFMD website (http://www.seafmd-rcu.oie.int/fmd_se_asia.php) provides maps showing countries in southeast Asia that have experienced outbreaks in each month of 2007.

In Africa, new FMD outbreaks have been reported in **Botswana** and **Namibia**. In October 2007, cases of FMD were recognised in cattle in Maun district, Botswana. These outbreaks were located near to the Okavango Delta in the north west of the country and are thought to have arisen via contact of domesticated cattle with wildlife due to damage to control fencing. Initial reports to the OIE indicated serotype SAT1 as the cause: however subsequent analyses of material by both BVI and WRL (IAH) typed the virus as SAT2. Control measures include control of wildlife reservoirs, livestock movement restrictions and vaccination of susceptible animals. In Namibia, FMD cases also due to serotype SAT2 have been reported in the Caprivi Strip in November 2007. At the same time there was an outbreak due to serotye SAT 2 in Kazungula, Zambia. Indications are that the outbreak probably started in Zambia and spread to Namibia due to cattle rustling. Control measures in both these outbreaks include movement restriction and vaccination. In **South Africa**, the area affected by an outbreak of SAT3 in 2006 has now been declared free of FMD.

In South America, outbreaks of FMD (serotype O) have been reported to the OIE from **Bolivia (5)** and **Ecuador (10)** during 2007. In addition, FMDV serotypes O **(9)** and A **(27)** continue to cause outbreaks in **Venezuela**. In many countries of the continent, mass vaccination programmes are being employed to control FMD. A 15 km high surveillance zone (HSZ), not considered FMD-free, was created in the common borders of Argentina, Bolivia, Brazil and Paraguay, which is being closely monitored. Except for this HSZ zone, all the Argentine territory is now FMD-free either with or without vaccination The region considered FMD-free without vaccination has been extended to include Northern Patagonia and the area of FMD-free status with vaccination (suspended due to the 2006 emergency) restored by OIE. In Brazil, despite a large zone with status suspended, the state of Santa Catarina has been established FMD-free without vaccination. Part of the state of Para has been recognized FMD-free with vaccination. Further north, in Colombia, the border with Ecuador, part of the Valley [Valle] and Caqueta, and Western Cundinamarca were declared FMD-free by the OIE. Perú added the central-eastern zone to the already

recognized FMD-free without vaccination zone, reaching 85% of its territory with a free status.

A selection of the viruses received from around the world were further characterised by partial genomic sequencing and serological matching to vaccine strains. Phylogenetic analyses were performed by using complete VP1 gene sequences (see Annex 2).

2. Overall Conclusions

Most of the conclusions of last year are still appropriate to the current situation with:

- FMDV still active in many parts of the world and continuing to threaten FMD-free regions.
- Variable control efforts in different affected areas worldwide
- Mass vaccination ongoing in much of South America, India, China and parts of the Middle East
- A continuing need to review risk and prioritise which vaccine strains should be available
- There have been no reports of outbreaks due to serotype C for the past 3 years. Therefore, it may be appropriate to consider whether continued vaccination against this serotype is necessary. Within geographical regions, the potential risk of improperly inactivated vaccines reintroducing this serotype needs to be balanced against the possibility of undisclosed infection remaining (due to this serotype) in domesticated livestock or wildlife.
- The UK outbreak demonstrated the need to strengthen and implement biosafety policies, to prevent virus release from vaccine manufacturing and research laboratories
- The 2007 outbreak in Cyprus poses questions regarding the diagnostic uncertainty and subsequent trade disruption that arose due to the occurrence of undetected infection in small ruminants.

The recommendation on vaccine strains provided by the FMD FAO World Reference Laboratory to the Executive Committee of the European Commission for the Control of FMD remains unchanged in 2007. O Manisa and A22 Iraq remain the most important vaccine strains for protection against viruses circulating in the Middle East. Since not all of the virus isolates that have been studied show a strong match to these vaccines, emergency vaccine would require the use of high potency vaccines to guarantee protection and there may be a case for developing new vaccine strains with greater antigenic homology. Viruses of the A Iran 96 strain have not been recovered since June 2005, and therefore the importance of this vaccine appears less; it is likely to be relegated from priority in 2008. Asia 1 Shamir remains the vaccine strain of choice for this serotype. In Africa, there is a great diversity of viruses circulating and in some cases, vaccines that provide good matches do not seem to be readily available. In South America, circulating viruses are all of the type that has been indigenous to the continent and are reasonably well matched by O Campos and A24 Cruzeiro, although supplementary strains of serotype A are also used in some countries to improve vaccine match.

Annex 1. Clinical samples and FMDV isolates submitted to reference laboratories of the FMD network during the year in question.

2.1. Tabulation of data on clinical samples received and serotyping results.

2.2. Overview of samples received and serotyping results

During 2007, 858 samples were submitted to the laboratories of the OIE/FAO FMD Reference Laboratories Network for primary or referral diagnosis from 33 countries. Excluding diagnostic material sent to IAH-Pirbright as part of the FMD outbreak in the UK, the WRLFMD received 807 samples from 28 countries, 632 collected in 2007 and 175 collected 2001-6. The RRLSSA received 20 clinical samples from FMD outbreaks from 3 countries (Botswana, Namibia, Zambia). During the same year PANAFTOSA received 13 clinical samples from FMDV episodes, from 3 countries, 6 collected in 2006 and 7 collected in 2007 for referral purposes, as the diagnosis and typing of the agent is performed at the National Laboratory Services of the South American laboratory network, coordinated by PANAFTOSA. 18 samples were submitted to ARRIAH from 2 countries (R. Kazakhstan and R. Kyrgyzstan) and Nagorno-Karabach Republic (NKR).

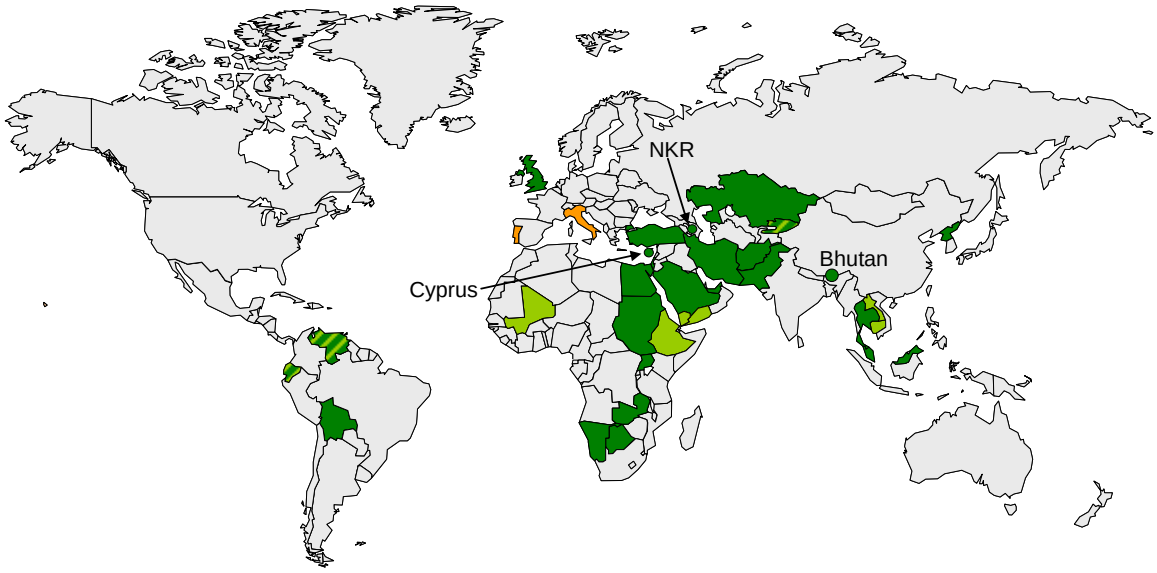


Figure 2. Summary of samples received to OIE network laboratories during 2007.

Legend:
- Samples collected in 2007
- Samples collected in previous years
- Samples collected in 2007 for SVD diagnosis

A summary of serotyping and confirmatory molecular detection results for clinical samples and FMD isolates collected by the OIE/FAO FMD Reference Laboratories Network in 2007 is in Annex 1, Table 1. A similar summary of samples collected earlier but received in 2007 is provided in Annex 1, Table 2.

Details of the results obtained by WRLFMD can be found at: http://www.wrlfmd.org/ Serotyping data from this laboratory can be searched on-line via the FMD BioPortal: http://fmd.ucdavis.edu/bioportal/. Details of the results obtained by PANAFTOSA can be found at: http://www.panaftosa.org.br.

Table 1. Virological testing and serotyping of samples received in 2007, corresponding to outbreaks that occurred in 2007

Country	No. of samples	Virus isolation in cell culture/ELISA										RT-PCR: FMD virus or SVD virus[4]		
		FMD virus serotypes							SVD virus	NVD	NT			
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1				Positive	NVD	NT
AFGHANISTAN	45	8	3	-	-	-	-	-	-	34	-	18	27	-
BHUTAN	33	7	-	-	-	-	-	-	-	26	-	28	5	-
BOLIVIA	3[1]	2	-	-	-	-	-	-	-	-	1	3	-	-
BOTSWANA	6	-	-	-	-	4	-	-	-	2	-	5	1	-
CYPRUS	270	-	-	-	-	-	-	-	-	270	-	-	270	-
ECUADOR	2[2]	-	-	-	-	-	-	-	-	-	2	2	-	-
EGYPT	37	-	-	-	-	-	-	-	-	37	-	7[3]	30	-
IRAN	40	29	6	-	-	-	-	-	-	5	-	36	4	-
ISRAEL	10	10	-	-	-	-	-	-	-	-	-	10	-	-
ITALY[4]	15	-	-	-	-	-	-	-	15	-	-	15	-	-
MALAYSIA	9	6	2	-	-	-	-	-	-	1	-	9	-	-
MALTA	9	-	-	-	-	-	-	-	-	9	-	-	9	-
NAMIBIA	5	-	-	-	-	3	-	-	-	2	-	5	-	-
NORTH KOREA	2	1	-	-	-	-	-	1	-	-	-	2	-	-
PAKISTAN	52	42	-	-	-	-	-	-	-	10	-	45	7	-
PORTUGAL[4]	5	-	-	-	-	-	-	-	1	4	-	1	4	-
SAUDI ARABIA	5	5	-	-	-	-	-	-	-	-	-	4	1	-
SUDAN	22	-	-	-	-	1	-	-	-	21	-	1	21	-
THAILAND	1	-	-	-	-	-	-	-	-	1	-	-	1	-
TURKEY	30	17	8	-	-	-	-	-	-	5	-	29	1	-
UGANDA	31	1	-	-	-	-	-	-	-	30	-	5	26	-
UAE	2	2	-	-	-	-	-	-	-	-	-	2	-	-
UNITED KINGDOM	3774	95	-	-	-	-	-	-	-	674	3005	98	3113	563
VENEZUELA	2[2]	-	-	-	-	-	-	-	-	-	2	2	-	-
ZAMBIA	3	-	-	-	-	3	-	-	-	-	-	3	-	-
TOTAL	**4413**	**225**	**19**	**-**	**-**	**11**	**-**	**1**	**16**	**1131**	**3010**	**330**	**3520**	**563**

Data for IAH and PANAFTOSA: FMD (foot-and-mouth disease); SVD (swine vesicular disease); VI/ELISA (FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection ELISA); NVD (no FMD, SVD or vesicular stomatitis virus detected); NT (not tested); RT-PCR (reverse transcription polymerase chain reaction for FMD (or SVD) viral genome).

Samples from PANAFTOSA: [1] one samples was submitted as inactivated material in Trizol; [2] All samples were submitted after inactivation with Trizol; [3] FMDV type O diagnosed from sequencing studies; [4] samples from Italy and Portugal submitted for SVDV characterisation

Table 2. Virological testing and serotyping of samples collected earlier but received in 2007

The following samples were additionally received by the OIE/FAO World Reference Laboratory for Foot and Mouth Disease in 2007 :

Country	Sample year	No. of samples	Virus isolation in cell culture/ELISA									RT-PCR for FMD (or SVD) virus	
			FMD virus serotypes							SVD virus	NVD		
			O	A	C	SAT 1	SAT 2	SAT 3	Asia 1			Positive	Negative
CAMBODIA	2006	4	1	2	-	-	-	-	-	-	1	4	-
EGYPT	2006	4	1	3	-	-	-	-	-	-	-	4	-
ECUADOR	2006	4[1]	-	-	-	-	-	-	-	-	-	3	-
ETHIOPIA	1998	1	-	-	-	-	-	-	-	-	1	1	-
	2000	16	-	1	-	-	-	-	-	-	15	10	6
	2001	9	-	-	-	-	-	-	-	-	9	4	5
	2003	10	-	-	-	-	-	-	-	-	10	2	8
	2004	8	1	-	-	-	-	-	-	-	7	5	3
	2005	3	-	-	-	-	-	-	-	-	3	2	1
	2006	20	4	-	-	-	-	-	-	-	16	11	9
ITALY	2005	2	-	-	-	-	-	-	-	2	-	2	-
	2006	24	-	-	-	-	-	-	-	24	-	22	2
KYRGYZSTAN	2004	1	-	-	-	-	-	-	1	-	-	1	-
	2006	2	2	-	-	-	-	-	-	-	-	2	-
LAOS	2006	3	-	3	-	-	-	-	-	-	-	3	-
MALI	2006	17	3	2	-	-	-	-	-	-	12	7	10
PAKISTAN	2006	6	1	-	-	-	-	-	-	-	5	5	1
SUDAN	2006	3	-	2	-	-	-	-	-	-	1	2	1
THAILAND	2006	11	-	10	-	-	-	-	-	-	1	11	-
VENEZUELA	2006	3[2]	-	-	-	-	-	-	-	-	1	2	1
VIETNAM	2006	2	-	-	-	-	-	-	-	-	2	2	-
YEMEN	2006	29	3	-	-	-	-	-	-	-	26	17	12
TOTAL		**182**	**16**	**23**	**-**	**-**	**-**	**-**	**1**	**26**	**110**	**117**	**58**

Data for IAH and PANAFTOSA: FMD (foot-and-mouth disease); SVD (swine vesicular disease); VI/ELISA (FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection ELISA); NVD (no FMD, SVD or vesicular stomatitis virus detected); NT (not tested); RT-PCR (reverse transcription polymerase chain reaction for FMD (or SVD) viral genome).

[1] All samples were submitted after inactivation with Trizol; [2]two samples was submitted as inactivated material in Trizol.

Annex 2. Genetic and antigenic typing of FMD virus isolates submitted to the Reference Laboratories

2.1. Tabulated data on isolates typed genetically and antigenically

Table 3: Summary of genetic typing

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Laboratory
FMDV A					
A/AFG/6/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/AFG/7/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/AFG/44/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/CAM/1/2006	VP1	636	ASIA	n.d.	WRLFMD
A/CAM/2/2006	VP1	636	ASIA	n.d.	WRLFMD
A/EGY/6/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/EGY/7/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/EGY/9/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/ETH/6/2000	VP1	639	AFRICA	n.d.	WRLFMD
A/IRN/3/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/IRN/15/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/IRN/36/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/IRN/37/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/IRN/38/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/IRN/39/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/LAO/6/2006	VP1	636	ASIA	n.d.	WRLFMD
A/LAO/7/2006	VP1	636	ASIA	n.d.	WRLFMD
A/LAO/8/2006	VP1	636	ASIA	n.d.	WRLFMD
A/MAY/1/2007	VP1	636	ASIA	n.d.	WRLFMD
A/MAY/3/2007	VP1	636	ASIA	n.d.	WRLFMD
A/MAI/12/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/MAI/16/2006	VP1	636	AFRICA	n.d.	WRLFMD
A/SUD/1/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/SUD/3/2006	VP1	639	AFRICA	n.d.	WRLFMD
A/TAI/1/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/2/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/3/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/4/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/6/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/7/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/8/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/9/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/10/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TAI/11/2006	VP1	636	ASIA	n.d.	WRLFMD
A/TUR/2/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/5/2007	VP1	639	ASIA	Irn-05	WRLFMD

A/TUR/7/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/8/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/10/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/12/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/24/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/TUR/25/2007	VP1	639	ASIA	Irn-05	WRLFMD
A/Apure/Ven/06	VP1	639	Euro-SA	n.d.	PANAFTOSA
A/Portuguesa/Ven/07	VP1	639	Euro-SA	n.d.	PANAFTOSA

FMDV Asia 1

Asia1/KRG/1/2004	VP1	633	n.d.	n.d.	WRLFMD
Asia1/NKR/2/2007	VP1	633	n.d.	n.d.	WRLFMD

FMDV O

O/AFG/29/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/34/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/36/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/37/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/39/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/42/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/43/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/AFG/45/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/BHU/11/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/BHU/12/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/BHU/18/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/CAM/4/2006	VP1	639	ME-SA	PanAsia	WRLFMD
O/EGY/8/2006	VP1	639	ME-SA	O1 Sharquia-like	WRLFMD
O/ETH/46/2006	VP1	639	EA-3	n.d.	WRLFMD
O/ETH/48/2006	VP1	639	EA-3	n.d.	WRLFMD
O/ETH/3/2004	VP1	639	EA-3	n.d.	WRLFMD
O/ETH/54/2006	VP1	639	EA-3	n.d.	WRLFMD
O/ETH/62/2006	VP1	639	EA-3	n.d.	WRLFMD
O/IRN/1/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/4/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/5/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/6/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/7/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/8/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/9/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/10/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/11/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/13/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/14/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/16/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/17/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/18/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/19/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD

O/IRN/20/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/21/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/22/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/23/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/24/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/26/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/27/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/28/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/29/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/30/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/31/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/32/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/33/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/IRN/34/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/ISR/1/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/ISR/3/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/ISR/5/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/ISR/7/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/ISR/9/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/KAZ/1/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/KAZ/2/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/KAZ/3/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/KRG/1/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/KRG/2/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/NKR/1/2007	VP1	639	ME-SA	PanAsia 2	ARRIAH
O/KRG/1/2006	VP1	639	ME-SA	O-194-like	WRLFMD
O/KRG/2/2006	VP1	639	ME-SA	O-194-like	WRLFMD
O/MAY/4/2007	VP1	639	SEA	Mya-98	WRLFMD
O/MAY/5/2007	VP1	639	SEA	Mya-98	WRLFMD
O/MAY/6/2007	VP1	639	SEA	Mya-98	WRLFMD
O/MAY/7/2007	VP1	639	SEA	Mya-98	WRLFMD
O/MAY/9/2007	VP1	639	SEA	Mya-98	WRLFMD
O/MAI/11/2006	VP1	639	WA	n.d.	WRLFMD
O/MAI/15/2006	VP1	639	WA	n.d.	WRLFMD
O/MAI/17/2006	VP1	639	WA	n.d.	WRLFMD
O/NKR/1/2007	VP1	639	ME-SA	vaccine-like*	WRLFMD
O/SAU/1/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/SAU/2/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/SAU/3/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/SAU/4/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/SAU/5/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/1/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/3/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/4/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/6/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/9/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/11/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD

O/TUR/13/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/14/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/15/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/16/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/18/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/20/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/23/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/27/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/28/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/29/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/TUR/30/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/UGA/18/2007	VP1	639	EA-2	n.d.	WRLFMD
O/UAE/1/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/UAE/2/2007	VP1	639	ME-SA	PanAsia 2	WRLFMD
O/YEM/3/2006	VP1	639	EA-3	n.d.	WRLFMD
O/YEM/4/2006	VP1	639	EA-3	n.d.	WRLFMD
O/YEM/29/2006	VP1	639	EA-3	n.d.	WRLFMD
O/EGY/25/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/26/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/27/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/28/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/29/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/30/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/EGY/31/2007	partial VP1	142	ME-SA	PanAsia 2	WRLFMD
O/UKG/7B/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/7/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/93/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UIKG/150/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/643/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/1153/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/800/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/1421/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/1484/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/1679/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/UKG/2366/2007	CG	~8179	EURO-SA	O1 BFS 1860	WRLFMD
O/Santa Cruz/Bol/07	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Pichincha/Ecu/06 (03-06)	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Pichincha/Ecu/06 (04-06)	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Pichincha/Ecu/06 (17-06)	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Imbabura/Ecu/07 (013-07)	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Pichincha/Ecu/07 (s.n.)	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Trujillo/Ven/06	VP1	639	Euro-SA	n.d.	PANAFTOSA
O/Trujillo/Ven/06	VP1	639	Euro-SA	n.d.	PANAFTOSA

FMDV SAT2

SAT2/BOT/2/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/BOT/3/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/BOT/5/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/BOT/6/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/NMB/1/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/NMB/4/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/SUD/1/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/ZAM/1/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/ZAM/2/2007	VP1	648	n.d.	n.d.	WRLFMD
SAT2/ZAM/3/2007	VP1	648	n.d.	n.d.	WRLFMD

* initial virus isolated in North Korea associated with the investigation into the outbreak in 2007

n.d., not designated

Figure 3 Molecular characterisation (based on VP1 sequence) of serotype O FMDV causing outbreaks in the United Kingdom.

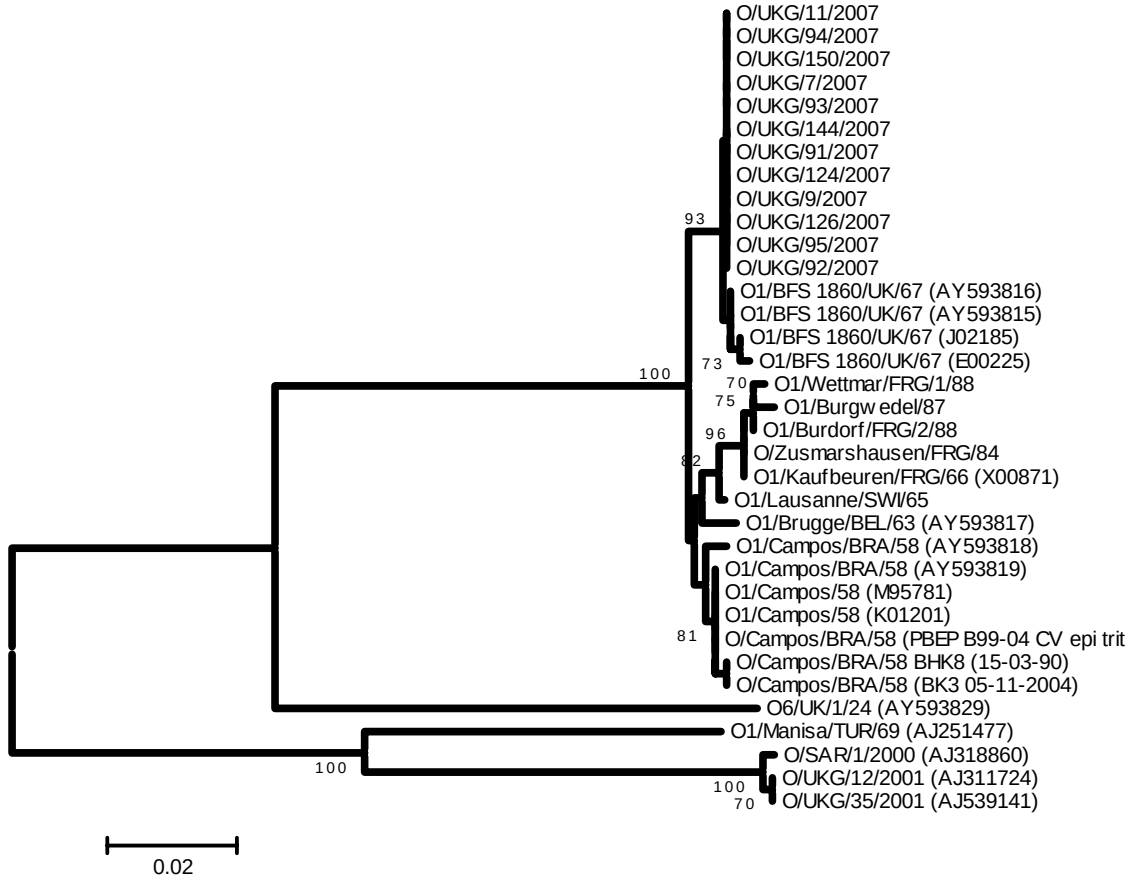


Figure 4: Recently characterised FMDV isolates from the Asia-1 serotype

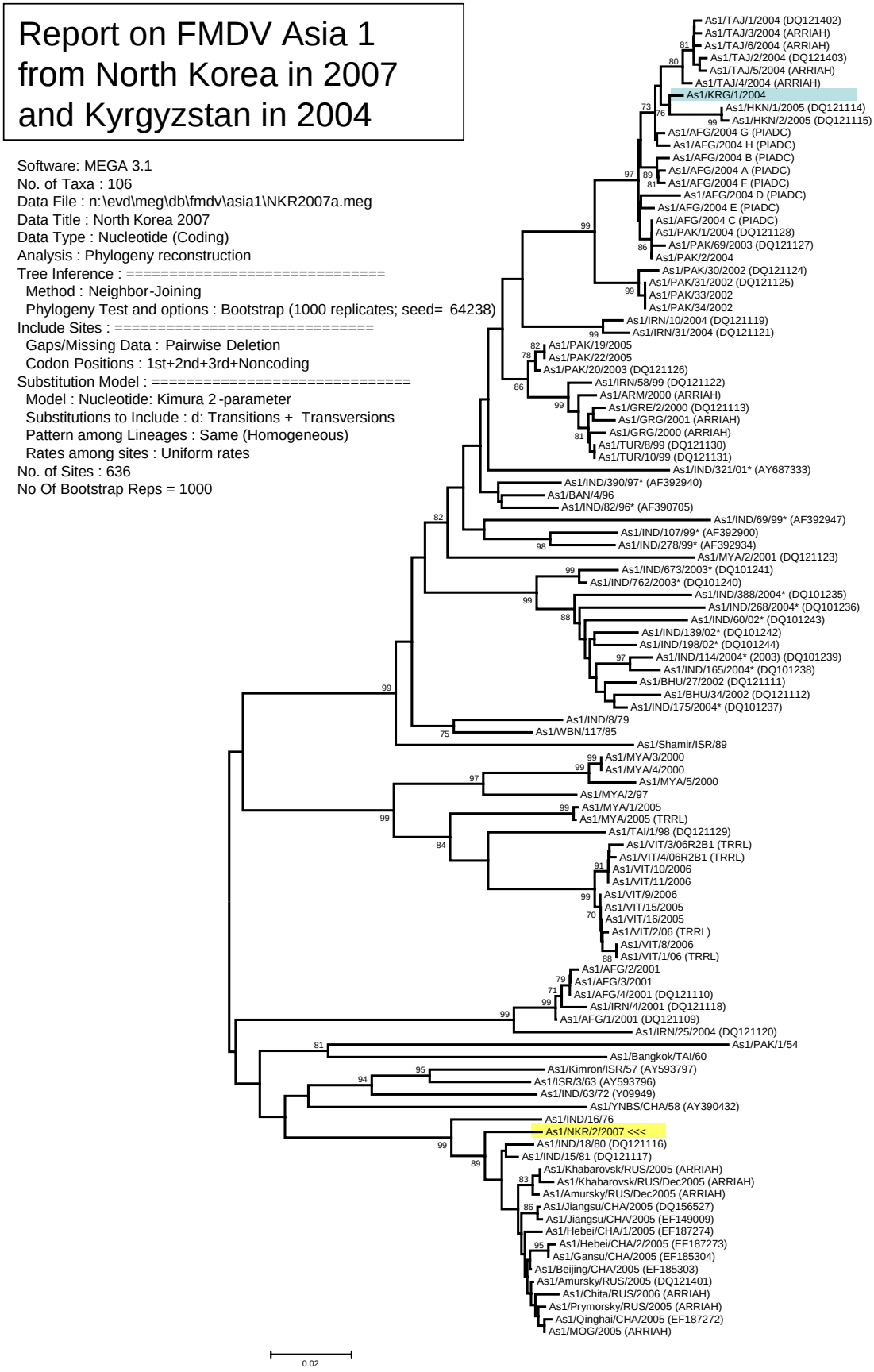


Figure 5: SAT 2 viruses characterised from southern Africa

Report on FMDV SAT2 from Botswana, Namibia and Zambia in 2007

Software: MEGA 3.1
No. of Taxa : 154
Data File : n:\evd\meg\db\fmdv\sat2\ZAM2007a.meg
Data Title : Zambia & Namibia 2007
Data Type : Nucleotide (Coding)
Analysis : Phylogeny reconstruction
Tree Inference : ==========
  Method : Neighbor-Joining
  Phylogeny Test and options : Bootstrap (1000 replicates; seed: 64238)
Include Sites : ==========
  Gaps/Missing Data : Pairwise Deletion
  Codon Positions : 1st+2nd+3rd+Noncoding
Substitution Model : ==========
  Model : Nucleotide: Kimura 2parameter
  Substitutions to Include : d: Transitions +Transversions
  Pattern among Lineages : Same (Homogeneous)
  Rates among sites : Uniform rates
No. of Sites : 648
No Of Bootstrap Reps = 1000
Only bootstrap values of 70% or greater are shown

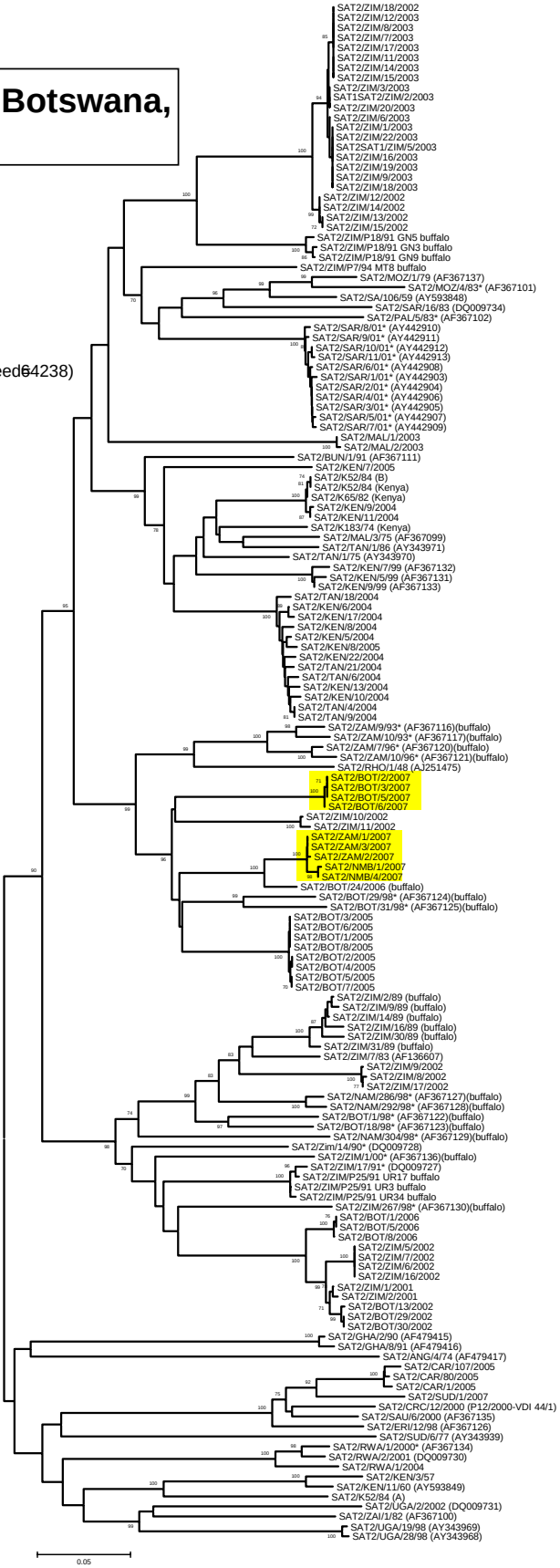


Figure 6: The new A-Iran-05 lineage. Figure shows relationship between the isolates recovered from this lineage and highlights recently characterised viruses from Iran that appear to be more divergent from the main A-Iran-05 lineage.

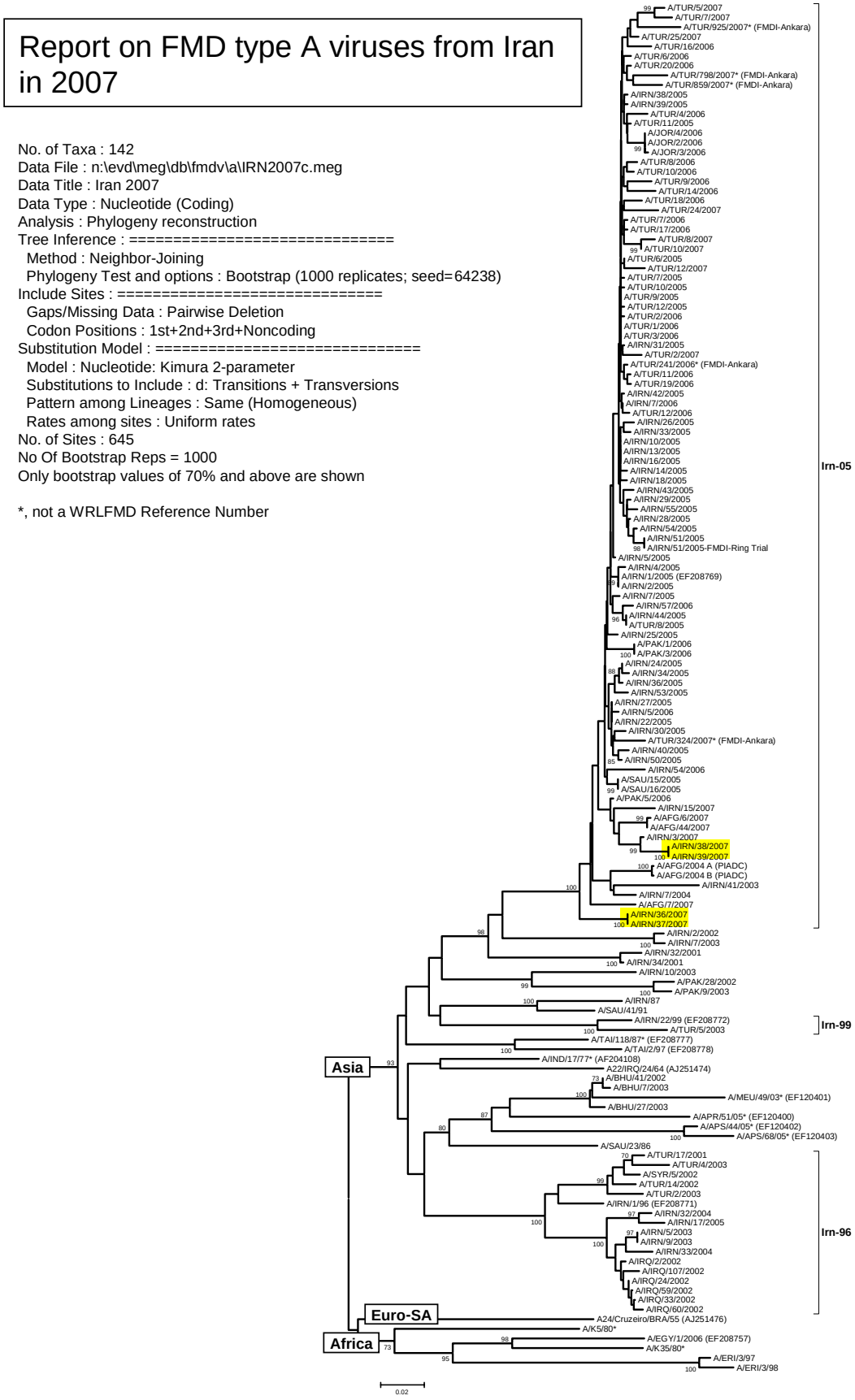


Figure 7: Type O viruses characterized from South America (Complete VP1 sequences: 639 n; MEGA software, version 4; Method: Neighbor-joining; Model: p-distance)

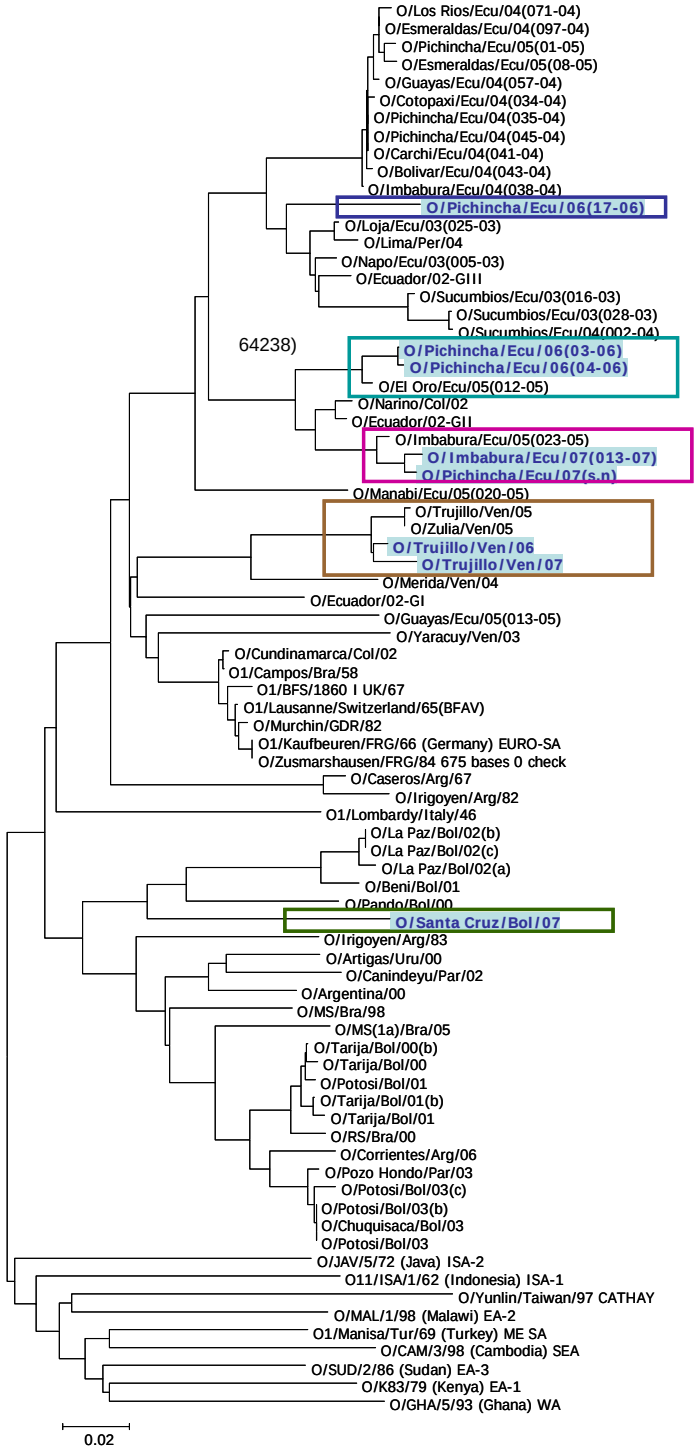
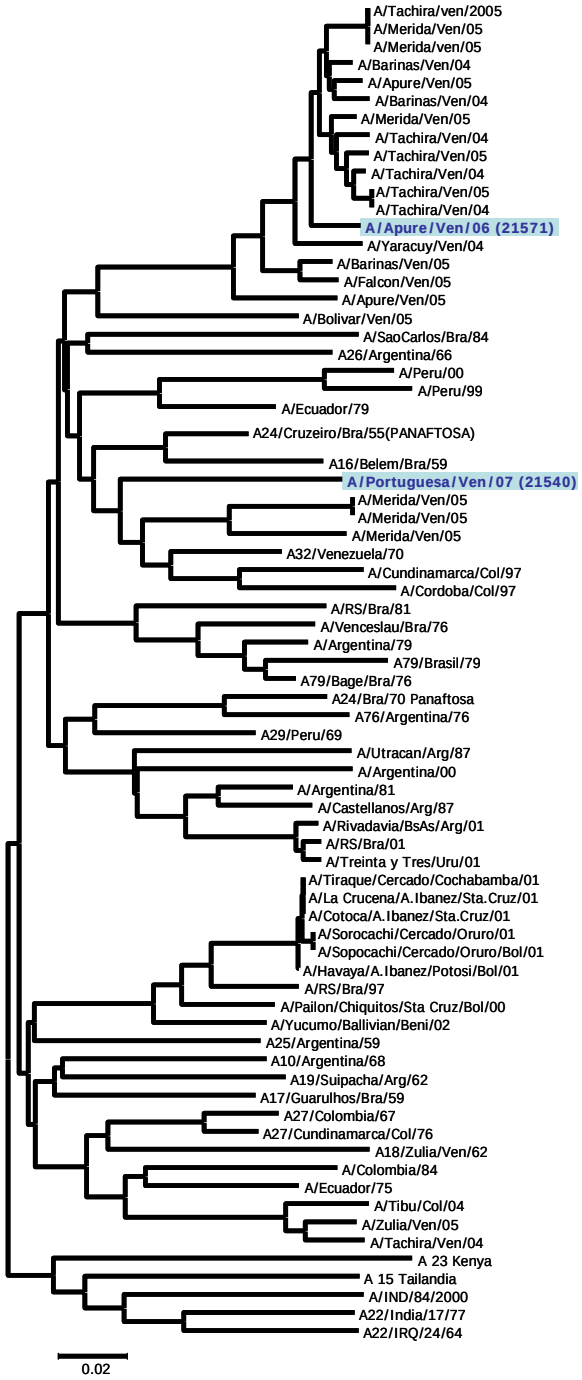


Figure 8: Type A viruses characterized from South America (Complete VP1 sequences: 639 n; MEGA software, version 4; Method: Neighbor-joining; Model: p-distance)



Summary of antigenic typing

Summary of Antigenic characterisation of FMD field isolates by matching with vaccine strains.
r_1 values were obtained by VNT or ELISA

Table 4 FMDV Serotype A

Isolates	A22		A Ind 17/82	A Tur06	IRN96	May-97		A Eri98	A SAU95 1634		A IRN87	A KEN 35/80
	VNT	ELISA	VNT	VNT	VNT	VNT	ELISA	VNT	VNT	ELISA	ELISA	ELISA
AFG 7/2007	0.33		0.14									
AFG 44/1007	0.32		0.14									
ETH 6/2000	0.2							0.46				
ETH 6/2000											<0.05	<0.15
IRN 1/2005				>1.0								
IRN 4/2005				>1.0								
IRN 7/2005				>1.0								
IRN 54/2006	0.49			0.98	0.20							
IRN 57/2006	0.21			0.66	0.15							
MAI 12/2006	0.61							0.43				
MAI 16/2006	0.21							0.21			0.03	0.16
JOR 3/2006	0.44	0.52				0.28	0.32	0.19	0.21	0.32	0.12	0.23
JOR 4/2006	0.59	0.44				0.22	0.19	0.17	0.18	0.18	0.09	0.19
SUD 1/2006	0.13							0.53				
SUD 1/2006											<0.02	<0.13
SUD 3/2006	0.11							0.34				
TUR 02/2007	0.66											
TUR 08/2007	>0.82											
TUR 24/2007	0.81											
TUR 25/2007	0.61											
A Vit 08/05			0.15									
A Vit 18/05			0.18									

Table 5. FMDV Serotype O (from WRLFMD)

Isolates	VNT	VNT	LPBE				VNT	VNT	VNT	VNT
	O Man	O Ind R2/75	O Phi95	O 4174	O Campos	O Manisa	O BFS	O Camp	O Kauf	O Laus
AFG 29/2007	0.59									
AFG 34/2007	0.57									
AFG 36/2007	0.55									
AFG 37/2007	0.50									
AFG 42/2007	0.79									
AFG 43/2007	0.56									
AFG 45/2007	0.61									
ETH 67/05	>0.93									
ETH 2/2006	0.76									
ETH 21/2006	0.39									
ETH 43/2006	0.55									
ETH 48/06	>0.93									
IRN 29/2006	0.63									
IRN 34/2006	0.64	0.66								
IRN 47/2006	>0.71									
IRN 52/2006	0.64									
ISR 1/2006	>0.77		1.0	0.13	0.76	0.33				
ISR 2/2006	>0.87									
ISR 3/2007	0.91									
ISR 5/2007	>0.74									
ISR 9/2007	0.56	0.45								
MAI 11/06	>0.75									
MAI 17/06	0.66									
JOR 5/2006	>90									
JOR 6/2006	>0.82	0.58	1.0	0.17	0.76					
PAK 4/2006	<0.15									
PAK 4/2006	<0.09									
PAK 4/2006			1.0		0.38					
PAK 8/2006	0.78									
PAK14/2006	>1.0									
PAK14/2006			0.66		0.38					
PAK7/2007	0.55									
PAK20/2007	0.45									
PAK48/2007	0.48	0.46								
PAK50/2007	0.53									
TUR 1/05	0.76									
TUR 4/05	>0.93		0.66		0.25					
TUR 5/05	>1.0		0.50	0.17	0.38					
TUR 11/2007	0.45									
TUR 13/2007	0.53	0.62								
TUR 29/2007	0.51									
TUR 30/2007	0.53									
UAE 1/2007	0.78	1.00								
O UKG 7/2007	0.64						>0.93	>1.0	0.85	0.72
O UKG 9/2007	0.51						>1.0	>1.0	1.0	>1.0
O UKG 11/2007	0.57						>1.0	0.60	0.79	0.58
O VIT 03/05		0.55								
O VIT 11/05		0.48								
O VIT 12/05		0.51								
O VIT 01/06		0.70								

Table 6: Antigenic characterisation of serotype O FMD field isolates by matching with vaccine strains - r_1 values were obtained by VNT (from ARRIAH)

Isolates	VNT			
	O Manisa	**O_1 N 1618**	**O Taiwan 3/97**	**O Russia/2000**
O/KAZ/1/2007	0.85	1.0	0.71	>1.0
O/KRG/1/2007		0.49		0.68
O/KRG/2/2007		0.43		0.34
O/NKR1/2007		0.36		0.5

Interpretation of r_1 values

In the case of VNT:

r_1 = ≥ 0.3 suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.
r_1 = < 0.3 suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect.

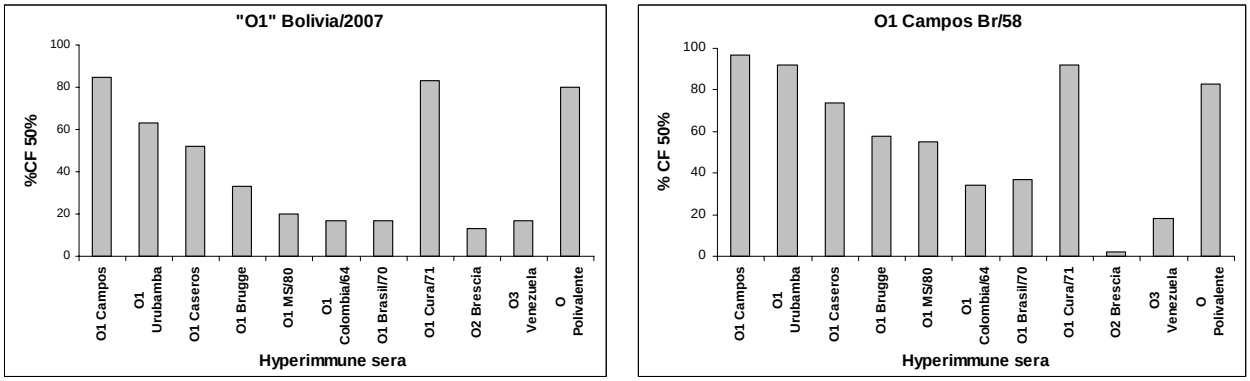
In the case of ELISA:

r_1 = 0.4-1.0 suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.
r_1 = 0.2-0.39 suggests that the field isolate is antigenically related to the vaccine strain. The vaccine strain might be suitable for use if no closer match can be found provided that a potent vaccine is used and animals are preferably immunised more than once.
r_1 = <0.2 suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect

Summary of antigenic typing of South American strains (from PANAFTOSA)

Summary of Antigenic characterisation of FMD field isolates: antigenic profile and matching with vaccine strains.

Figure 9. Antigenic profile determined using complement fixation test (CF 50%);



Vaccine matching:
r values obtained by CF50%. Expectancy of protection (EPP) determined with two reference serum panels (average 30 sera) at 30 days post-vaccination (dpv) and at 30 days post re-vaccination (dpR) by ELISA-CFL.

r Value (CF 50%)

Viral isolate	r1 *
Bolivia/07 - 6100	0.69
Bolivia/07 - 6133	0.73
O1Campos Br/58	1

*** r1 ≥ 0.25 is considered within the same subtype**

Expectancy of Protection (EPP) against vaccine strain O1Campos
ELISA-CFL/EPP*

Viral isolate	30dpv	30 dpR
O1 Bolivia/2007	65	99

*** EPP ≥ 70 (30 cattle) at 30 dpR is considered that the vaccine strain will protect**

Annex 3. Discussion of sequencing and typing results

Molecular characterisation: sequencing
FMDV serotype O:

Europe
VP1 and full-genome sequencing has been performed on viruses recovered from all the infected premises from the FMD outbreak in United Kingdom. These viruses were all closely related to each other and derived from O1/BFS 1860 (Figure 3) used as a vaccine and FMDV reference strain. Full genome sequences have also been recovered from field samples, providing high resolution molecular epidemiological data to allow the reconstruction of transmission trees between the affected farms.

Middle East/Asia
During 2007, further analysis of serotype O viruses from the Middle East (Turkey, Jordan, Israel, Iran, UAE and Bhutan) has been performed. In addition, 5 FMDV isolates obtained from a wild oryx sampled in Saudi Arabia have also been sequenced. All these viruses are derived from the new PanAsia II lineage widely circulating in the region and closely related to each other (and other viruses previously characterised from other countries in the region). It was not possible to recover full-length VP1 sequences from recent material obtained from FMD outbreaks in Egypt: however, partial sequencing indicates that the causative virus is also of the PanAsia II lineage. The samples received from Bhutan represent the most easterly reports of this new FMDV lineage. In contrast, further to the East, a previous lineage of PanAsia appears to be still circulating in Cambodia as shown by material sent to the WRLFMD in 2007.

Two serotype O isolates supplied from Kyrgyzstan were also characterised and shown to be from the ME-SA topotype, but sharing closest relationship with historical viruses from Russia (from 1958 and 1976) rather than to contemporary serotype O viruses from the Middle East and Asia. Elsewhere, 3 FMDV isolates from Yemen have been sequenced belonging to the East-Africa-3 topotype and 5 viruses isolated from material sent from Malaysia have been characterised as belonging to the Mya-98 lineage within the SEA topotype (sharing closest nucleotide identity to a previously characterised isolate from Thailand).

Africa
Sequencing of 3 FMDV serotype O isolates from Mali showed that they were members of the West African topotype most closely related to other viruses recently characterised from the region (Senegal, Mali and Togo). Five viruses from Ethiopia (collected in 2004 and 2006), were closely related to other viruses from the region in the EA-3 topotype. Sequencing of an FMDV serotype O isolate from Uganda showed that it was most closely related to other FMD viruses from Uganda (collected in 2004) within the East Africa-2 topotype.

South America
From Bolivia, the virus responsible for the outbreaks recorded during the emergency, belonged to the EURO-SA topotype, being indigenous to the continent, with homology values of about 90-93% to strains that have circulated in the country in Beni and Pando states in the years 2000-2002, but not closely related to the strains responsible for the sporadic re-appearance in the Southern Cone of the continent in the years 2000, 2002, 2003, 2005 and 2006, nor to those circulating in Ecuador and Venezuela. In the latter countries, where FMD is still endemic, further EURO-SA topotype viruses were recorded from different lineages (Figure 7).

FMDV serotype A:

Middle East/Asia

During 2007, FMDV isolates belonging to the A-Iran-05 lineage have been collected from Turkey, Iran, Afghanistan. The spread of the Iran-05 lineage of serotype A through the Middle East (Iran, Turkey and Jordan) was described in last years report. Interestingly, within Iran these viruses appear to fall into two separate lineages: one of these, comprising viruses collected in Sistan (Figure 6) in the east of the country, is rooted some distance from the majority of recent isolates collected from Iran: closer to the ancestral root of this lineage. This might indicate a separate introduction (common to these two viruses) into Iran possibly from the East (Pakistan or Afghanistan). Further isolates from the region are required to investigate this question.

From southeast Asia, isolates collected from Thailand (9), Laos (3) and Cambodia (2) in 2006 have been characterised. Within countries, these isolates group together and are all characterised as members of the ASIA topotype of serotype A. Two serotype A viruses from Malaysia were sequenced: the phylogenetic tree indicates separate introductions of these viruses into the country.

Africa

Two additional serotype A viruses from Mali have also been sequenced. Phylogenetically, these viruses represent two discrete lineages within the Africa topotype of serotype A. The presence of these two lineages has been separately reported in Mali (2004 and 1997). Three additional isolates from the recent FMD Serotype A outbreak in Egypt were characterised. All were identical to each other and closely related to other field material received to the WRL from the 2006 outbreaks. Three further African serotype A viruses (2 from Sudan and 1 from Ethiopia) were analysed and shown to be closely related to other viruses from the regions where they were collected, within the AFRICA topotype of serotype A.

South America

From Venezuela, where FMD is still endemic, isolates were placed within the indigenous EURO-SA topotype (Figure 8).

FMDV serotype A:

Asia

Field material received to the WRLFMD from North Korea showed that FMDV isolated was of the Asia-1 serotype. This finding supported by serological testing of affected animals and demonstrated that the North Korean isolate shared highest nucleotide identity (98.3%) to Russian isolates of the Asia-1 serotype collected in 2005 (Figure 4). An additional Asia-1 isolate from Kyrgyzstan (collected in 2004) was also analysed (see Figure 4).

FMDV serotype SAT2:

Africa

The phylogenetic tree presented in Figure 5, shows the relationships between the recently characterised isolates recovered from material sent from Botswana, Zambia and Namibia. The isolates from Zambia and Namibia are closely related to each other (share ~ 99.2 % nucleotide identity) and to a buffalo virus collected in Botswana (Muchenje, Kasane) in 2006. However, the samples from Botswana (from Maun in 2007) are more distantly related to these isolates. A single SAT2 isolate (SUD 1/2007) from Sudan has also been sequenced and was most closely related to other North African viruses of the SAT2 serotype.

Antigenic typing: Vaccine matching

Serotype O:

Three isolates (O UKG 7, 9, 11/2007) from 2007 FMD outbreak in UK were antigenically analysed for type O vaccine matching to provide advice on the vaccine selection should the emergency vaccination strategy be used. As expected from the sequence data, the results from two dimensional VNT showed that these field strains were closest matched to O BFS, O Campos , O Lausanne and O Kaufbeuren vaccine strains, and also moderately matched to O Manisa vaccine strain.

A number of isolates (from Israel, United Arab Emirates, Jordan, Iran and Turkey) representative of the new PanAsia II lineage were characterised. All field isolates generated r-values indicative of a protective response with O1 Manisa vaccine. However, it has been noted that O Manisa appears to have only a moderate match against some isolates of this currently circulating O PanAsia II strain. This indicates that highly potent O Manisa vaccines should be used to ensure good effect against strains currently circulating in the Middle East and western Asia. A potency test was conducted by the European Community Reference Laboratory at IAH to test the protection afforded by O Manisa vaccine against a representative of the O PanAsia II lineage - O Iran 34/2006, for which the r_1 by neutralisation test value for match to O Manisa was 0.6. The potency test was conducted according to the guidelines of the European Pharmacopoiea using O Manisa vaccine formulated from the EU antigen bank and the level of protection was scored as 3.5 PD_{50} (3 PD_{50} is the minimum recommended, whilst 6 PD_{50} is preferred for emergency vaccination).

Viruses from Pakistan, Ethiopia, Mali were further characterised by two dimensional virus neutralisation test (2dm VNT) and liquid phase blocking ELISA (LPBE). r-values from 2dm VNT showed that all of these isolates were antigenically matched with O1 Manisa vaccine strains, which indicated that the currently predominant type O virus can be covered by a vaccine present in vaccine banks. Furthermore, isolate O PAK 4/2006 was well matched to O PHI 95 and relatively close to O Campos by LPBE. Four field isolates received from Vietnam (1, 3, 11 and 12/2007) along with two of the above isolates (O PAK 20/2007 and O TUR 13/2007) have showed antigenic matching to O Ind R2/75 vaccine strain. In contrast, 2 field isolates received from Yemen (O YEM 4, 29/2006) in the EA-3 topotype showed no antigenic matching with either O Manisa or O Ind R2/75 vaccines.

The type O isolate responsible for the outbreaks recorded in Bolivia was subtyped as O_1. Vaccine matching gave satisfactory results by 'r' values obtained by Complement Fixation test and by Expectancy of Protection (EPP, by ELISA) with sera at 30 days post-revaccination, with vaccines containing strain O_1 Campos.

Serotype A:

Viruses of the A-Iran-96 strain that were previously dominant in the Middle East have not been received at WRL since June 2005 (a single isolate from Iran). The strain has been superseded by A Iran 05 and all of the many subsequent isolates from Iran (n=33; 2005, 2006, 2007), as well as from Turkey (n=32; 2005, 2006, 2007), Pakistan (n=9; 2006, 2007), Saudi Arabia (n=2; 2006), Jordan (n=3; 2006) and Afghanistan (n=3; 2007) have been of the A Iran 05 strain. Therefore, the importance of A-Iran-96 as a vaccine strain is reduced and the strain may be moved to medium priority next year. Within the new A-Iran-05 lineage, vaccine matching has been performed on isolates received from Iran, Afghanistan, Jordan and

Turkey. In common with other isolates from this lineage, it was anticipated that the A22 vaccine would provide adequate protection. However, in-vitro matching data for some isolates (such as IRN 57/2006) indicates a moderate or poor match between A22 and the field strain. This is an area of concern, confirming that high potency A22 vaccines should be used and indicating that a new vaccine strain used to protect against these viruses may be required. Additional serotype A viruses from Ethiopia, Sudan, Mali and Vietnam (outside of the A-IRN-05 lineage) were also characterised by VNT and LPBE during 2007. The results showed that only two isolates from Vietnam provide some match to A22 vaccine strain; the rest failed to match to either A22 or A Ind 17/82 strains. Isolates from Ethiopia, Mali and Sudan showed antigenic matching to A Eritrea vaccine strain. Three further FMDV type A isolates (A EGY 6, 7 and 9/2006) from Egypt have also been antigenically analysed by two dimensional VNT. The results showed that these provide some match to A SAU95 vaccine strain.

Annex 4. Recommendations from the WRL on FMD virus strains to be included in FMDV antigen banks (within categories not in order of importance)

High Priority

O Manisa (*covers PanAsia strain)*
O BFS or Campos
A24 Cruzeiro
Asia 1 Shamir
A22 Iraq
SAT 2 Saudi Arabia *(or equivalent)*
A Iran ’96

Medium Priority

A Eritrea
SAT 2 Zimbabwe
AIran 87 or A Saudi Arabia 23/86 *(or equivalent)*
SAT 1 South Africa
A Malaysia 97 *(or Thai equivalent such as A/NPT/TAI/86)*
A Argentina 2001
O Taiwan 97 *(pig-adapted strain or Philippine equivalent)*
A Iran ’99

Low Priority

A15 Bangkok related strain
A87 Argentina related strain
C Noville
SAT 2 Kenya
SAT 1 Kenya
SAT 3 Zimbabwe
A Kenya