

Annual OIE/FAO FMD Reference Laboratory Network Report

January – December 2006

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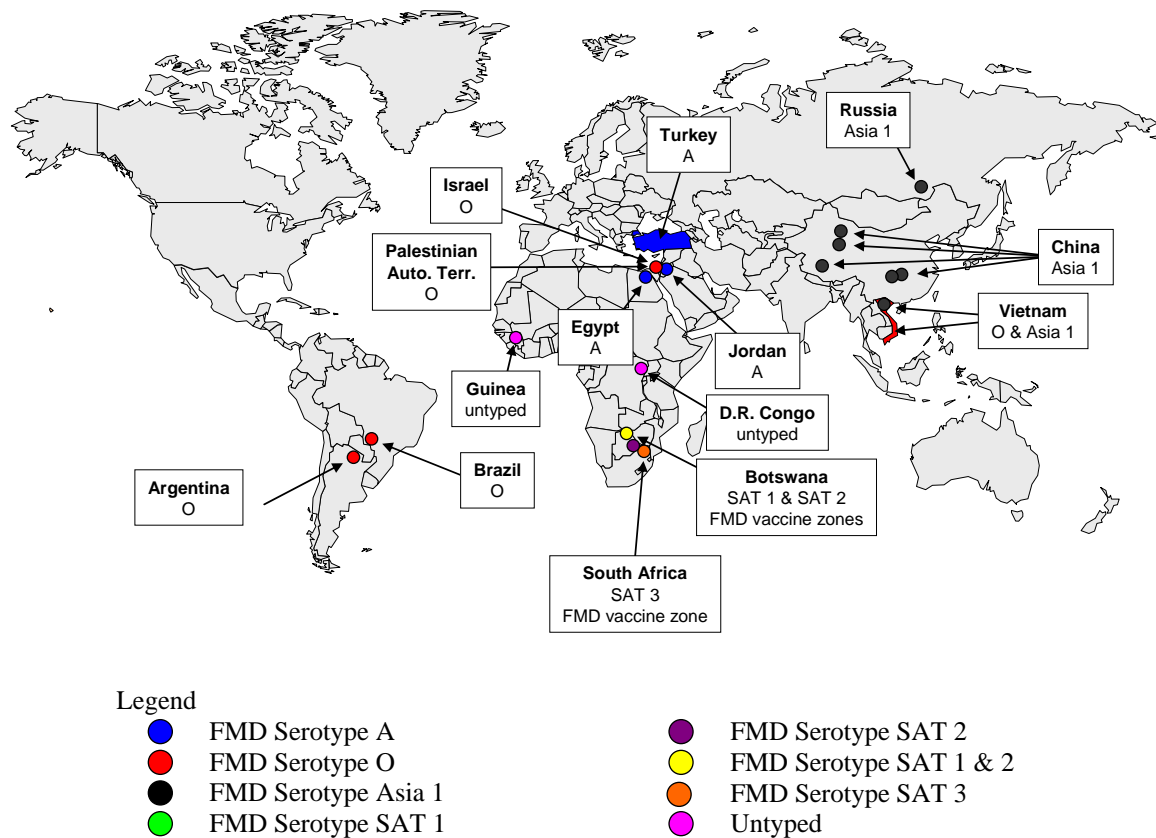
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1. Summary report on FMD outbreaks during period in question from surveillance region covered by reference laboratory

1.1. Countries that have reported FMD outbreaks in 2006 (January-December) that resulted in an epidemiological change. FMD serotypes related to those outbreaks (where known) are indicted.

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. Summary of FMD outbreaks indicative of a change in epidemiological status



1.2. Overview and discussion of outbreak information

No outbreaks were officially reported in FMD-free countries that did not practice vaccination. FMD remained largely confined to traditionally infected areas between January and December 2006. However, **within endemically and sporadically infected parts of the world there have been upsurges of cases, sometimes leading to the submission of samples to reference laboratories and indicating an enhanced risk of collateral spread.** Matching tests to check the availability of suitable vaccines to protect against these strains continue to reveal gaps in cover, especially against serotype A, for example the recent outbreaks due to African serotype A viruses in Egypt and Mauritania. Submission of samples from endemic regions has continued to be mainly in response to perceptions of increased outbreak severity, although in some cases there are proactive projects promoting sample submission. **The majority of viruses have been isolated from samples submitted from Africa and Asia.**

In Africa, FMDV serotype SAT 2 was reported in a formerly FMD-free zone in Botswana in April 2006 leading to cessation of trade with Europe and instigation of vaccination. In June, FMDV SAT 1 was also reported from Northern Botswana from a part of the country where FMDV outbreaks are more common. Cases of FMD caused by SAT3 serotype were reported in Limpopo province, South Africa in August 2006. This outbreak occurred well within the OIE recognized buffer zone (vaccination area) of the FMD control zone of South Africa adjacent to the Kruger National Park and therefore the status of South Africa's FMD free zone without vaccination has not been affected. There were reports to OIE of outbreaks in Guinea, but the serotype was not established. Subsequently, WRL received samples from Mauritania that were found to be serotype A of the indigenous west-Africa toptotype. Since then there have been FMDV outbreaks in Guinea Siguiri Province in the north-east, close to the border with Mali. African toptotypes of serotype O were involved in outbreaks from the Democratic Republic of Congo and from Ethiopia.

In Central Asia, the incidence of FMD due to Asia 1 has apparently declined compared to 2005, although reports of new cases have continued to be received from China throughout 2006. Vietnam has experienced widespread outbreaks of FMD due mainly to serotype O. Asia-1 virus has also been reported in Vietnam, but the strain has affected cattle rather than pigs and is of a lineage indigenous to Southeast Asia and different from that reported in China. The Cathay pig-adapted toptotype of serotype O has been reported in Malaysia and Thailand, the first time that it has been identified in Southeast Asia outside the Philippines, Vietnam and China. The SEAFMD website (<http://www.seafmd-rcu.oie.int/index.php>) provides maps showing countries in southeast Asia that have experienced outbreaks in each month of 2006.

In the Middle-East, three major incursions of FMDV have been observed. One has involved a sublineage of the O PanAsia strain that was first identified in India in 2001, with subsequent spread eastwards into Malaysia (2003-5) and westwards into Pakistan and Iran (2005-6) and then Turkey and Jordan (2006). The second incursion has involved a strain of serotype A, termed A Iran 05, which was first identified in Iran in 2003, with subsequent spread to Saudi Arabia (2005) and to Pakistan, Turkey, and Jordan (2006). The third incursion has involved another strain of serotype A introduced from the horn of Africa into Egypt.

In South America, one outbreak of serotype O was recorded in a formerly FMD-free with vaccination zone in Argentina (Province of Corrientes), in Feb 2006 which has been rapidly brought under control using a “stamping out” and vaccination (polyvalent O, A, and C vaccine) campaign. In Southern Brasil,(State of Parana), an outbreak was declared in January 2006, based on serological results (no viral isolation was attained), of animals with epidemiological links to livestock involved in the FMDV type O outbreaks recorded at the end of the year 2005 in Mato Grosso do Sul State (Brasil). Further investigations (performed during October 2006) carried out in the municipality of Loanda (Paraná) have indicated that FMDV is not circulating In endemic regions of the Continent; FMD outbreaks of type O were recorded in Ecuador and types O and A in Venezuela during the year.

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. **The WRLFMD vaccine recommendations have been changed** to take account of the new serotype A viruses that have entered the Middle East; see Annex 4.

2. 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 2006, 637 samples were submitted to the laboratories of the OIE/FAO FMD Reference Laboratories Network for primary or referral diagnosis from 33 countries. The WRLFMD received 578 samples from 25 countries, 421 collected in 2006 and 157 collected 2004-5. The RRLSSA received 24 clinical samples for FMD diagnosis collected in April and June for virus isolation and characterisation. During the same year PANAFTOSA received 28 clinical samples of FMDV collected between 2003 and 2006, that were isolated in Argentina, Ecuador, and Venezuela 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. Nine samples were submitted to ARRIAH.

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 2006 is in Table 1. A similar summary of samples collected earlier but received in 2006 is provided in Table 2.

Details of the results obtained by WRLFMD can be found at: <http://www.iah.bbsrc.ac.uk/virus/Picornaviridae/Aphthovirus/> 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. Serotyping and confirmatory molecular detection results of samples received in 2006, corresponding to outbreaks that occurred in 2006

Country	No. of samples	Virus isolation in cell culture/ELISA									RT-PCR for FMD (or SVD) virus		Laboratory	
		FMD virus serotypes								Other virus	NVD	Positive		Negative
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1						
ARGENTINA	2	2	-	-	-	-	-	-	-	-	-	2	-	PANAFTOSA
BOTSWANA	37	-	-	-	9	4	-	-	-	-	24	22	15	WRL
BOTSWANA	24	-	-	-	12	4	-	-	-	-	8	-	-	RRLSSA
D.R.OF CONGO	116	42	-	-	-	-	-	-	-	-	74	78	38	WRL
EGYPT	5	-	5	-	-	-	-	-	-	-	-	5	-	WRL
ETHIOPIA	44	8	-	-	-	-	-	-	-	-	36	14	30	WRL
CHINA (HONGKONG)	5	5	-	-	-	-	-	-	-	-	-	5	-	WRL
IRAN	64	50	4	-	-	-	-	-	-	-	10	55	9	WRL
IRELAND	6	-	-	-	-	-	-	-	-	-	6	-	6	WRL
ISRAEL	2	2	-	-	-	-	-	-	-	-	-	2	-	WRL
JORDAN	7	3	3	-	-	-	-	-	-	-	1	6	1	WRL
KENYA	10	-	1	-	3	-	-	-	-	-	6	8	2	WRL
KUWAIT	3	2	-	-	-	-	-	-	-	-	1	2	1	WRL
LAOS	5	4	1	-	-	-	-	-	-	-	-	5	-	WRL
MALAYSIA	5	4	-	-	-	-	-	-	-	-	1	5	-	WRL
MAURITANIA	8	-	7	-	-	-	-	-	-	-	1	7	1	WRL
MONGOLIA	1	-	-	-	-	-	-	-	-	-	1	-	-	ARRIAH
PAKISTAN	53	21	9	-	-	-	-	-	-	-	23	50	3	WRL
RUSSIA	2	-	-	-	-	-	-	2	-	-	-	2	-	ARRIAH
RWANDA	1	-	-	-	-	-	-	-	-	-	1	-	1	WRL
SENEGAL	9	1	-	-	-	-	-	-	-	-	8	-	9	WRL
TANZANIA	1	-	-	-	1	-	-	-	-	-	-	-	-	RRLSSA
TURKEY	21	14	3	-	-	-	-	-	-	-	4	19	2	WRL
TURKEY	4	-	4	-	-	-	-	-	-	-	-	4	-	ARRIAH
UNITED KINGDOM	9	-	-	-	-	-	-	-	-	-	9	-	9	WRL
VIETNAM	11	7	-	-	-	-	-	4	-	-	-	11	-	WRL
ZAMBIA	1	-	-	-	1	-	-	-	-	-	-	-	-	RRLSSA
TOTAL	456	165	37	-	26	8	-	6	-	-	214	302	127	

Table 2. Serotyping and confirmatory molecular detection results of samples collected earlier but received in 2006

Country	Sample year	No. of samples	ELISA/Virus isolation in cell culture								Other virus	NVD	RT-PCR for FMD (or SVD) virus		Laoratory
			FMD virus serotypes							Asia 1			Negative	Positive	
			O	A	C	SAT 1	SAT 2	SAT 3							
BENIN	2005	16	-	-	-	-	-	-	-	-	-	16	16	-	WRL
CHINA (HONGKONG)	2005	10	8	-	-	-	-	-	-	-	-	2	1	9	WRL
ECUADOR	2005	17	17	-	-	-	-	-	-	-	-	-	-	17	PANAFTOSA
ETHIOPIA	2005	4	1	-	-	-	-	-	-	-	-	3	2	2	WRL
ISRAEL	2004	5	5	-	-	-	-	-	-	-	-	-	-	5	WRL
ISRAEL	2005	2	2	-	-	-	-	-	-	-	-	-	-	2	WRL
KENYA	2004	25	4	-	-	1	4	-	-	-	-	16	4	21	WRL
KENYA	2005	31	6	2	-	9	2	-	-	-	-	12	-	31	WRL
MALAYSIA	2005	1	1	-	-	-	-	-	-	-	-	-	-	1	WRL
MYANMAR	2004	1	-	-	-	-	-	-	1	-	-	-	-	1	WRL
NIGER	2005	16	3	-	-	-	1	-	-	-	-	12	10	6	WRL
RWANDA	2005	1	-	-	-	-	-	-	-	-	-	1	1	-	WRL
SAUDI ARABIA	2005	2	-	2	-	-	-	-	-	-	-	-	-	2	WRL
THAILAND	2005	11	6	5	-	-	-	-	-	-	-	-	-	11	WRL
TURKEY	2005	12	5	7	-	-	-	-	-	-	-	-	-	12	WRL
VENEZUELA	2003-2005	9	-	9	-	-	-	-	-	-	-	-	-	9	PANAFTOSA
VIETNAM	2004	7	2	5	-	-	-	-	-	-	-	-	-	7	WRL
VIETNAM	2005	13	6	5	-	-	-	-	2	-	-	-	-	13	WRL
TOTAL		183	66	35	-	10	7	-	3	-	62	34	149		

VI/ELISA FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection ELISA
FMD foot-and-mouth disease
SVD swine vesicular disease
NVD no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected
RT-PCR reverse transcription polymerase chain reaction for FMD (or SVD) viral genome

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

3.1. Tabulated data on isolates typed genetically and antigenically

3.1.1. Summary of genetic typing

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
Serotype O						
O/Corrientes/Arg/06 (MC2146)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Corrientes/Arg/06 (MC2147)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/COD/3/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/6/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/7/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/10/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/11/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/13/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/15/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/19/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/21/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/36/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/47/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/51/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/53/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/55/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/57/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/58/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/59/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/60/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/63/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/64/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/65/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/66/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/68/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/71/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/77/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/80/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/81/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/82/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/83/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/90/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/91/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/92/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/93/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/95/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/99/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/100/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/101/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/102/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/104/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/105/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/COD/106/2006	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
O/Pichincha/Ecu/05 (1/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Esmeraldas/Ecu/05 (8/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Esmeraldas/Ecu/05 (10/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Esmeraldas/Ecu/05 (37/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Imbabura/Ecu/05 (23/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/El oro/Ecu/05 (16/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/El oro/Ecu/05 (12/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/El oro/Ecu/05 (28/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (40/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (44/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (33/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (20/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (31/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (24/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (32/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Manabí/Ecu/05 (54/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/Guayas/Ecu/05 (13/05)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 16	PANAFTOSA
O/ETH/2/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/4/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/19/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/20/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/21/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/27/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/ETH/43/2006	VP1	639	EA-3	n.d.	Annex 2, Fig. 4	WRLFMD
O/HKN/17/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/18/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/19/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/20/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/22/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/23/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/24/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/25/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/1/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/2/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/3/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/4/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/HKN/5/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	WRLFMD
O/IRN/8/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/9/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/10/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/11/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/12/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/13/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/14/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/15/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/16/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/17/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/18/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/19/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/20/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/21/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
O/IRN/22/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/23/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/24/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/25/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/26/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/27/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/28/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/IRN/29/2006	VP1		in progress			WRLFMD
O/IRN/30/2006	VP1		in progress			WRLFMD
O/IRN/31/2006	VP1		in progress			WRLFMD
O/IRN/32/2006	VP1		in progress			WRLFMD
O/IRN/33/2006	VP1		in progress			WRLFMD
O/IRN/34/2006	VP1		in progress			WRLFMD
O/IRN/35/2006	VP1		in progress			WRLFMD
O/IRN/37/2006	VP1		in progress			WRLFMD
O/IRN/38/2006	VP1		in progress			WRLFMD
O/IRN/39/2006	VP1		in progress			WRLFMD
O/IRN/42/2006	VP1		in progress			WRLFMD
O/IRN/43/2006	VP1		in progress			WRLFMD
O/IRN/44/2006	VP1		in progress			WRLFMD
O/IRN/45/2006	VP1		in progress			WRLFMD
O/IRN/46/2006	VP1		in progress			WRLFMD
O/IRN/47/2006	VP1		in progress			WRLFMD
O/IRN/48/2006	VP1		in progress			WRLFMD
O/IRN/49/2006	VP1		in progress			WRLFMD
O/IRN/50/2006	VP1		in progress			WRLFMD
O/IRN/51/2006	VP1		in progress			WRLFMD
O/IRN/52/2006	VP1		in progress			WRLFMD
O/IRN/53/2006	VP1		in progress			WRLFMD
O/IRN/55/2006	VP1		in progress			WRLFMD
O/IRN/56/2006	VP1		in progress			WRLFMD
O/IRN/58/2006	VP1		in progress			WRLFMD
O/IRN/59/2006	VP1		in progress			WRLFMD
O/IRN/60/2006	VP1		in progress			WRLFMD
O/IRN/61/2006	VP1		in progress			WRLFMD
O/IRN/64/2006	VP1		in progress			WRLFMD
O/ISR/7/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/8/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/9/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/10/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/11/2004	VP1	632	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/1/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/2/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/Snir/ISR/05*	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	Kimron Veterinary Institute, Israel
O/ISR/1/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/ISR/2/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/JOR/5/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/JOR/6/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/JOR/7/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/KEN/23/2004	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/24/2004	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
O/KEN/29/2004	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/30/2004	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/4/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/6/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/10/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/14/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/26/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KEN/27/2005	VP1	639	EA-2	n.d.	Annex 2, Fig. 3	WRLFMD
O/KUW/2/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/KUW/3/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/LAO/2/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/LAO/3/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/LAO/4/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/LAO/5/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/MAY/9/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/MAY/1/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/MAY/2/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/MAY/3/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/MAY/5/2006	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/NGR/3/2005	VP1	639	WA	n.d.	Annex 2, Fig. 5	WRLFMD
O/NGR/10/2005	VP1	639	WA	n.d.	Annex 2, Fig. 5	WRLFMD
O/NGR/14/2005	VP1	639	WA	n.d.	Annex 2, Fig. 5	WRLFMD
O/PAK/4/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/6/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/8/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/9/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/10/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/11/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/12/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/14/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/15/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/PAK/16/2006	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/SEN/8/2006	VP1	639	WA	n.d.	Annex 2, Fig. 5	WRLFMD
O/TAI/1/2005	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/TAI/5/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/TAI/6/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/TAI/8/2005	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/TAI/9/2005	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/TAI/10/2005	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/TAI/14/05*	VP1	639	SEA	Mya98	Annex 2, Fig. 6	Thailand RRL
O/TAI/15/05*	VP1	639	SEA	Mya98	Annex 2, Fig. 6	Thailand RRL
O/TAI/21/05*	VP1	639	SEA	Mya98	Annex 2, Fig. 6	Thailand RRL
O/TAI/35/05B2*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TAI/53-2/05*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TAI/54-1/05B1*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TAI/54-2/05B1*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TAI/64-1/05*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TAI/64-2/05*	VP1	639	Cathay	n.d.	Annex 2, Fig. 6	Thailand RRL
O/TUR/1/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/TUR/2/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/TUR/3/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
O/TUR/4/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/TUR/5/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 8	WRLFMD
O/1423/TUR/2006*	VP1	601	ME-SA	PanAsia	Annex 2, Fig. 8	FMDI-Ankara, Turkey
O/VIT/7/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/VIT/8/2004	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/VIT/6/2005	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/VIT/7/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/VIT/9/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/11/2005	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/12/2005	VP1	550	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/17/2005	VP1	639	ME-SA	PanAsia	Annex 2, Fig. 7	WRLFMD
O/VIT/1/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/2/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/3/2006	VP1	639	Cathay	n.d.	Annex 2, Fig. 7	WRLFMD
O/VIT/4/2006	VP1	637	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/VIT/5/2006	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/VIT/6/2006	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD
O/VIT/7/2006	VP1	639	SEA	Mya98	Annex 2, Fig. 7	WRLFMD

Serotype A

A/EGY/1/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/EGY/2/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/EGY/3/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/EGY/4/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/EGY/5/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/EGY/2006	VP1	639	Africa	n.d.	data not shown	EGYPT
A/IRN/4/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/IRN/5/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/IRN/5/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/IRN/7/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/IRN/54/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/IRN/57/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/JOR/2/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/JOR/3/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/JOR/4/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/KEN/12/2005	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/KEN/29/2005	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/KEN/3/2006	VP1	639	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/LAO/1/2006	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/MAU/1/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/3/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/4/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/5/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/6/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/7/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/MAU/8/2006	VP1	636	Africa	n.d.	Annex 2, Fig. 9	WRLFMD
A/PAK/1/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/PAK/3/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/PAK/5/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/SAU/15/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/SAU/16/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TAI/2/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
A/TAI/3/2005	VP1	633	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/TAI/4/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/TAI/7/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/TAI/11/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/TAI/1/05R2B2*	VP1	636	Asia	n.d.	Annex 2, Fig. 11	Thailand RRL
A/TAI/3-3/05*	VP1	636	Asia	n.d.	Annex 2, Fig. 11	Thailand RRL
A/TAI/4/05R1*	VP1	636	Asia	n.d.	Annex 2, Fig. 11	Thailand RRL
A/TAI/6/05*	VP1	636	Asia	n.d.	Annex 2, Fig. 11	Thailand RRL
A/TUR/6/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/7/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/8/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/9/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/10/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/11/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/12/2005	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/551/05*	VP1	152	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/560/05*	VP1	153	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/562/05*	VP1	152	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/563/05*	VP1	152	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/1/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/1/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/TUR/2/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/2/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/TUR/3/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/3/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/TUR/4/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/4/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 18	FGI ARRIAH
A/TUR/6/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/7/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/8/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/9/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/10/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/11/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/12/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/14/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/16/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/17/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/18/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/19/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/20/2006	VP1	639	Asia	Iran-05	Annex 2, Fig. 10	WRLFMD
A/TUR/161/06*	VP1	144	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/175/06*	VP1	145	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/194/06*	VP1	150	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/195/06*	VP1	148	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/TUR/210/06*	VP1	148	Asia	Iran-05	Annex 2, Fig. 10	Sinan Aktas, Turkey
A/1266/TUR/2006*	VP1	474	Asia	Iran-05	data not shown	FMDI-Ankara,

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
						Turkey
A/1416/TUR/2006*	VP1	538	Asia	Iran-05	data not shown	FMDI-Ankara, Turkey
A/Merida/Ven/05 (21366)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Apure/Ven/05 (21303)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Merida/Ven/05 (21244)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Tachira/Ven/05 (21290)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Barinas/Ven/05 (21040)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Falcon/Ven/05 (21281)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Bolivar/Ven/05 (21029)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Merida/Ven/05 (21185)*	VP1	639	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/Zulia/Ven/05 (21105)*	VP1	636	Euro-SA	n.d.	Annex 2, Fig. 17	PANAFTOSA
A/VIT/6/2004	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/9/2004	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/10/2004	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/11/2004	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/12/2004	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/8/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/10/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/13/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/14/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
A/VIT/18/2005	VP1	636	Asia	n.d.	Annex 2, Fig. 11	WRLFMD
Serotype Asia 1						
Asia1/MYA/1/2005	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/Khabarovsk/RUS/Dec2005*	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	FGI ARRIAH
Asia1/Amursky/RUS/Dec2005*	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	FGI ARRIAH
Asia1/Chita/RUS/2006*	VP1	633	n.d.	n.d.	Annex 2, Fig. 12 Annex 2, Fig. 19	FGI ARRIAH
Asia1/Amursky/RUS/Feb2006*	VP1	633	n.d.	n.d.	Annex 2, Fig. 19	FGI ARRIAH
Asia1/VIT/15/2005	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/16/2005	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/8/2006	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/9/2006	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/10/2006	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/11/2006	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	WRLFMD
Asia1/VIT/3/06R2B1*	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	Thailand RRL
Asia1/VIT/4/06R2B1*	VP1	633	n.d.	n.d.	Annex 2, Fig. 12	Thailand RRL
Serotype SAT1						
SAT1/BOT/12/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/13/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/14/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/15/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/16/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/17/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/18/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/20/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/BOT/22/2006	VP1	663	WZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/21/2004	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/11/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/13/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD

FMDV isolate	Region sequenced	No. of bases	Topotype	Strain	Reference for dendrogram	Laboratory
SAT1/KEN/16/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/17/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/18/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/19/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/24/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/31/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/32/2005	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/5/2006	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/9/2006	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
SAT1/KEN/10/2006	VP1	663	NWZ	n.d.	Annex 2, Fig. 13	WRLFMD
Serotype SAT2						
SAT2/BOT/1/2006	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/BOT/5/2006	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/BOT/8/2006	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/BOT/24/2006	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/13/2004	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/17/2004	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/22/2004	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/32/2004	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/7/2005	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/KEN/8/2005	VP1	648	n.d.	n.d.	Annex 2, Fig. 14	WRLFMD
SAT2/NGR/15/2005	VP1	648	n.d.	n.d.	Annex 2, Fig. 15	WRLFMD

n.d., none defined

*, not WRLFMD Ref. No.

3.1.2. Summary of antigenic typing

Table 3. Summary of Antigenic characterisation of FMD field isolates by matching with vaccine strains.
r₁ values were obtained by VNT or ELISA

FMDV Serotype A

Strain	A22		A Irn 96		A May97		A 5925		A Sau95		A Irn 01		A Eri98/ Irn99*	A Erit 98	A22 Iraq		A 4164	A Irn99	A Irn87	A Ken 35/80	A15	A22/ 550 ARRI AH
	vnt	elisa	vnt	vnt	elisa	vnt	elisa	vnt	elisa	vnt	elisa	vnt	vnt	vnt	elisa	elisa	elisa	elisa	elisa	vnt	vnt	
A Car 036/05	0.29		0.21	0.16																		
A Car 115/05	0.22		0.30	0.08																		
A Car 116/05	0.22		0.30	0.08																		
A Car 36/05														0.25								
A Egy 01/06	0.23	0.17	0.25	0.21	0.06			0.32	0.42	0.3	0.83	0.60					<0.17	0.21	0.23	0.38		
A Egy 01/06													0.45									
A Egy 02/06	0.24	0.14	0.16	0.20	<0.03			0.30	0.50	0.2	1.00	0.95					0.25	0.23	0.14	0.38		
A Egy 02/06													0.41									
A Eth 16/05	0.13		0.21	0.22																		
A Eth 16/05														0.22								
A Irn 04/05	>1.00		0.11					0.43														0.17
A Irn 05/05	0.71		0.11					0.51														0.15
A Irn 05/06	0.48		0.09																			0.15
A Irn 05/06								0.09								0.5			0.06			
A Irn 07/06	0.38		0.09																			0.14
A Irn 07/06								0.2								0.5			0.03			
A Ken 12/05	0.13		0.30	0.33																		
A Ken 12/05														0.24								
A Mau 01/06		0.03			0.14						0.13								0.09	0.53		
A Mau 03/06		0.03			0.15						0.13								0.06	0.61		
A May 5/05	0.12		0.19	0.58																		
A Pak 01/06					0.43			0.3		>1.0						>1.0	0.22		0.03			
A Pak 05/06					0.13			0.08		>1.0						0.09	0.14		0.22			

Strain	A22		A Irn 96	A May97		A 5925		A Sau95		A Irn 01		A Eri98/ Irn99*	A Eri 98	A22 Iraq		A 4164	A Irn99	A Irn87	A Ken 35/80	A15	A22/ 550 ARRI AH	
	vnt	elisa	vnt	vnt	elisa	vnt	elisa	vnt	elisa	vnt	elisa	vnt	vnt	vnt	elisa	elisa	elisa	elisa	elisa	vnt	vnt	
A Sau 15/05	0.29	>0.88	0.12	0.16	0.17		0.50	0.35	>1.0													>0.89
A Sau 15/05												0.14										
A Sau 16/05	0.25	>0.88	0.12	0.17	0.15		0.58	0.39	>1.0													>1.0
A Sau 16/05												0.14										
A Tur 01/06	0.42	0.21	0.08	0.11		0.41	0.32	0.21	0.26													0.29
A Tur 01/06												0.15										
A Tur 02/06												0.15										
A Tur 04/06							0.11		0.35						0.15	0.43			0.16			
A Tur 08/06							0.25		0.43						0.53	0.13			0.06			
A Tur 09/06							1.0								0.86				0.19			
A Tur 12/06							0.43		0.35						0.71	0.16			0.07			
A Tur 14/06							<0.07		>1.0						0.22				0.14			
A Tur 16/06							0.09		0.31						1.0				0.14			
A Tur 18/06							0.43		0.21						0.61	0.06			0.10			
A Tur 2/06	0.36	0.29	0.07	0.18		0.48	0.56	0.20	0.50							0.30						
A Tur 20/06							0.09		>1.0						0.3				0.43			
A Tur 3/06	0.39		0.09	0.13		0.48																
A Vit 06/04			0.11	0.31								0.09		0.11								0.10
A Vit 08/05			0.15	0.51								0.11		0.15								0.16
A Vit 10/04			0.15	0.31								0.11		0.15								0.12
A Vit 18/05			0.20	0.36								0.10		0.20								0.18

* antiserum raised against vaccine containing two virus strains

FMDV Serotype O

Strain	O1	O	O	O	O	O Tai
	Campos vnt	Manisa vnt	Lausanne vnt	3039 elisa	4174 elisa	189/87 elisa
O Corrientes/Arg/06 60 days post vaccine*	70.00					0
O Corrientes/Arg/06 22 days post revacc*	97.00					0
O Irm 13/2006		>1.0		0.75	0.34	>1.0
O Irm 14/2006		>1.0		0.61	0.25	>1.0
O Irm 16/2006		>0.86		0.61	0.38	>1.0
O Irm 20/2006		>0.86		0.53	0.25	>1.0
O Irm 26/2006		1.0		nd	0.27	>1.0
O Isr 01/05		0.07				
O Isr 11/04		>1.0				
O Kuw 02/06		>0.80	0.69			
O Kuw 03/06		0.74	0.57			
O May 04/06		>1.0				
O May 06/06		>1.0				
O May 4/05		>1.0				
O May 6/05		>1.0				
O Vit 01/06		0.33				
O Vit 07/04		>1.0				
O Vit 12/05		0.19				

* Antigenic match of O/Corrientes/Arg/06 to vaccine strain O₁ Campos studied by Expectancy of Protection (EPP) assay as provided by National Reference Laboratory (SENASA, Argentina). The r₁ value for this sample obtained by CF against O₁ Campos was 0.53.

FMDV Serotype C

Strain	C Ober		C Ken	C	C Phi
	vnt	elisa	267/67 elisa	Noville elisa	7/84 elisa
C Eth 6/05	0.44	0.19	0.75	0.56	0.14
C Eth 7/05	0.39	0.13	0.59	0.30	0.10

FMDV Serotype Asia 1

Strain	As Ind	As Shamir 3/89	
	8/79 vnt	vnt	elisa
Asia1 Vit 15/2005	0.25	0.36	
Asia1 Vit 16/2005	0.24	0.39	
Asia1 Amursky/2005 ^a		0.18-0.25	0.25
Asia1 Mongolia/2005 ^a		0.25	

^a Results from ARRIAH

FMDV Serotype SAT 1

Strain	Sat 105	Sat 109
	vnt	vnt
SAT 1 BOT/06/06*	0.82	0.71

* RRLSSA isolates

FMDV Serotype SAT 2

Strain	Sat 2 Eritrea	Sat 251	Sat 287
	vnt		
Sat2 Bot 01/05	0.51		
Sat2 Bot 02/05	0.48		
Sat2 Ken 13/04	0.93		
Sat2 Ken 17/04	0.65		
Sat2 Ken 22/04	0.63		
Sat2 Ken 07/05	0.45		
Sat2 Ken 08/05	0.74		
Sat 2 Bot 04/06		0.74	0.79

Acknowledgement

For the work carried out at Pirbright, the majority of the vaccine strains and vaccine antisera used for these tests have been supplied to WRL by Merial. Some strains and/or antisera were supplied to WRL by ARRIAH and the Thai Regional Reference Laboratory at Pakchong

Interpretation of r_1 values

In the case of VNT:

$r_1 \geq 0.3$ 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

3.2. Overview and discussion of typing results

3.2.1. FMDV serotype O

3.2.1.2. Africa

From West Africa, indigenous viruses of the West-Africa topotype were recognized from **Senegal** and **Niger**, fairly similar to viruses isolated in previous years from **Mali** (2005) and **Togo** (2004-5) (see Annex 2, Figure 5).

From Central and East Africa, indigenous viruses of different East Africa (EA) topotypes (EA-2, EA-3 and EA-4) were recognised. **Ethiopian** viruses from 2005 and 2006 were very diverse comprising several sublineages within the EA-3 topotype (2005 and 2006) as well as a new EA-4 topotype (2005) (see Annex 2, Figure 4); viruses isolated from **Uganda** in 1998 were also found to belong to this new topotype (data not shown). **Kenyan** and **Sudanese** viruses from 2005 represented sublineages of EA-2 and EA-3 topotypes, respectively (see Annex 2, Figure 3). Forty-two viruses from the **Democratic Republic of Congo** were similar to one another and belonged to the EA-2 topotype (Annex 2, Figure 3); they were related to viruses received earlier from **Uganda** (2004) and **Kenya** (2002). Nineteen viruses isolated from samples taken in the **Cameroon** in 2005 were all closely related (<2.5% different) and were most closely related to recent isolates from **Togo** and **Mali** (~11% nt differences) (data not shown).

3.2.1.3. Asia

From the Middle East and South Asia, four sublineages of the PanAsia strain (ME-SA topotype) have been recorded since the beginning of 2005, of which two have been represented by isolations from samples collected in 2006 (Annex 2, Figure 8).

- One sublineage included viruses from **Israel** and **Turkey** (2005) with slightly less closely related viruses recorded from **Iran** and **Israel** the previous year.
- A second sublineage comprised isolates from **Kuwait** (2006) and **Saudi Arabia** (2005).
- A third sublineage was exclusively from **Pakistan** (2005).
- A fourth sublineage has been actively spreading since 2001 when it was first recorded in **India**, with subsequent recognition in **Nepal** (2003), **Bhutan** (2003-4) and **Malaysia** (2003-5). In 2005 and 2006, the virus has been recognized in **Pakistan** and **Iran** and in 2006, for the first time in **Turkey** and **Jordan** (Annex 2, Figure 8).

From Southeast Asia, as for previous years, porcine virus isolates from **Hong Kong** belonged to the CATHAY topotypes and were all closely related to each other (Annex 2, Figure 6).

Nine VP1 sequences were received from the OIE FMD Regional Reference Laboratory (RRL) in **Thailand**. Three were from viruses isolated from cattle and belonged to the Southeast Asia (SEA) topotype (Annex 2, Figure 6). The remaining six sequences were from

isolates from pigs and belonged to the CATHAY toptype (Annex 2, Figure 6). This is the first known occurrence of this toptype in **Thailand**. In December 2005, the CATHAY toptype was also found in **Malaysia** for the first time (Annex 2, Figure 7).

Fourteen isolates of serotype O collected from **Vietnam** (2004-2006) were characterized. These represented three separate serotype O toptypes (SEA, ME-SA and CATHAY) (Annex 2, Figure 7). Interestingly, two separate lineages of the CATHAY toptype were represented indicating at least two separate introductions of these viruses into **Vietnam**. Incomplete zoo-sanitary measures and shortage of vaccine have led to widespread outbreaks of FMD affecting cattle and pigs. Four samples from **Laos** fell within two distinct lineages of the PanAsia strain (ME-SA toptype), as was previously found for samples collected in 2003 (Annex 2, Figure 6). FMDV O was identified in six samples received from **Malaysia** (one of which was collected in 2005); four fell with the PanAsia strain and one belonged to the SEA toptype (Mya98 strain) (no virus was isolated from the sixth sample) (Annex 2, Figure 7).

3.2.1.3. South America

From **Argentina**, the virus responsible for the outbreaks recorded in the FMD-free with vaccination area in Corrientes, belonged to the EURO-SA toptype, being indigenous to the continent, and with homology values between 90-93% to the strains that have sporadically re-appeared in the Southern Cone of the continent in the years 2000, 2002 and 2003 (Annex 2, Figure 16).

From **Ecuador**, where FMD is still endemic, further EURO-SA toptype viruses were from a different lineage than that causing the emergence in the Southern Cone (Annex 2, Figure 16).

3.2.2. FMDV serotype A

3.2.2.1. Africa

From North East Africa, viruses from **Egypt** were all closely related to each other and most closely related to viruses from East Africa, especially a recent isolate from **Kenya** (2005) (Annex 2, Figure 9). These viruses are not closely related to the new type A Iran 05 strain circulating in the Middle East.

From West Africa, an indigenous virus type was recognized from **Mauritania** (Annex 2, Figure 9). It is of a lineage not detected since 1998 in **Gambia** and somewhat distinct from more recently isolated type A viruses from the region (**Mali** 2004, **Togo** 2005). No samples were received from outbreaks reported to OIE in 2006 by the neighbouring state of **Guinea**. Three virus isolates collected in the **Cameroon** in 2005 were closely related to each other (<1.5% different) and most closely related to viruses isolated in **Eritrea** in 1997-98 and the **Cameroon** in 2000 (8.3-10.3% nt differences) (data not shown).

3.2.2.2. Asia

From the Middle East, no viruses of the A Iran 96 or A Iran 99 toptypes were recognised in 2006. Rather the new "A Iran 05" strain was widespread (Annex 2, Figure 10). Having been first recognised in **Iran** in 2003, it became a serious problem there in 2005, and was

recognised at the end of the same year in **Saudi Arabia**. Partial VP1 sequences sent from the SAP Institute, Turkey (later confirmed by complete VP1 sequencing performed in the WRLFMD), indicate that this strain was found in various parts of **Turkey** during 2005 (Annex 2; Figure 10) and extensive outbreaks ensued with spread into **Turkish Thrace** close to the borders of Greece and Bulgaria in early 2006. Samples sequenced at ARRIAH showed similar genetic characteristics from complete VP1 sequences (Annex 2, Figure 18). In 2006, the strain was also recognised in **Pakistan** and **Jordan** (Annex 2; Figure 10).

From **Southeast Asia**, viruses from **Vietnam** were related to sequences of viruses from **Thailand**, **Malaysia** and **Laos** from 2003 and 2004 (Annex 2, Figure 11). Sequencing of samples collected in **Thailand** and **Malaysia** during 2005 indicates that serotype A viruses in these two countries have high similarity (Annex 2, Figure 11)

3.2.2.2. South America

From **Venezuela**, where FMD is still endemic, isolates were placed within the indigenous EURO-SA toptype (Annex 2, Figure 17).

3.2.3. FMDV serotype Asia 1

3.2.3.1. Asia

Complete VP1 sequences of isolates from Amursky and Chita in Eastern **Russia** were obtained by ARRIAH (Annex 2, Figure 19). VP1 sequences received by WRL from ARRIAH (from Amursky, Khabarovsk and Chita) were found to be closely related to previous outbreak viruses in the region (Annex 2, Figure 12). The sequences of **Vietnamese** isolates received from the Thailand RRL were closely related to each other and next most closely related to viruses from **Thailand** (1998) and **Myanmar** (2005) (Annex 2, Figure 12). This lineage only occurs in Southeast Asia and is distinct from Asia 1 viruses circulating in other Asian countries.

3.2.4. FMDV serotype SAT 1

3.2.4.1. Africa

SAT 1 isolates from **Kenya** (2004-6) divide into three sublineages (according to location) within the North West Zimbabwe toptype (Annex 2, Figure 13).

SAT 1 was isolated from samples from **Zambia**, **Tanzania** and from an outbreak from the buffalo zone in **Botswana** by RRLSSA, Botswana. SAT 1 FMDV isolated at WRL from samples derived from cattle and buffalo that were received from RRLSSA, Botswana in 2006 were closely related to each other within the West Zimbabwe toptype (Annex 2, Figure 13).

3.2.5. FMDV serotype SAT 2

3.2.5.1. Africa

Fifty-two **Cameroon** isolates from 2005 were found to be closely related to each other (<2% different) and most closely related to SAT2/LIB/1/2003 (7.42% nt difference), SAT2/NGR/15/2005 (8.02% nt difference) and SAT2/SAU/6/2000 (8.50% nt difference) (data not shown).

SAT 2 was isolated from an outbreak in the FMD free without vaccination zone (Zone 7, see Annex 1, Figure 2) by RRLSSA, Botswana. Three samples received by WRL from Botswana were sequenced and shown to be closely related to viruses from previous outbreaks in **Zimbabwe** (2001-02) and **Botswana** (2002) (Annex 2, Figure 14). They were distinct from viruses causing an outbreak in **Botswana** in 2005 (see Annex 2, Figure 14). An isolate from African buffalo collected was not closely related to the cattle outbreak viruses (see Annex 2, Figure 14). **Kenyan** SAT 2 viruses from 2004 were similar to others derived from contemporary cases in **Tanzania** and **Malawi** (Annex 2, Figure 14).

A SAT 2 virus from **Niger** (2005) was closely related to the virus responsible for the 2003 outbreak in **Libya** (where SAT 2 does not normally occur) providing evidence of the risk posed to the southern Mediterranean from outbreaks in sub-Saharan states (see Annex 2, Figure 15).

3.2.6. FMDV serotype C

3.2.6.1. Africa

The complete VP1 sequences of two type C isolates from **Ethiopia** were determined. Both were said to originate from 1983. Both were essentially identical to each other and to a virus (vaccine strain?) received from Ethiopia in 1971 (C/ETH/1/71) (data not shown). These viruses were distinct from other FMDV C viruses which have occurred in East Africa (Kenya and Uganda).

4. Antigenic Typing

4.1 Overview of Typing Results

The results of all antigenic characterizations of FMD field isolates by matching with vaccine strains are given in Table 3.

4.1.2. Serotype O

FMDV serotype O isolates collected in **Iran, Israel, Kuwait, Malaysia, and Vietnam** or Africa (**Cameroon, Egypt, Ethiopia, Kenya**) between 2005 and 2006 were further characterized by VNT and/or ELISA. This confirmed the utility of **O₁ Manisa** to all serotype O isolates tested except for an isolate from **Israel** (O ISR/1/2005) that was closely related to viruses circulating in the area (Turkey/Lebanon/Israel) and an isolate from **Vietnam** (O VIT 12/2005) which is classified by VP1 sequencing as a member of the Cathay topotype.

The type O isolate responsible for the outbreaks recorded in the FMD-free with vaccination area in Corrientes, **Argentina** was subtyped as O₁ (National Reference Laboratory,

SENASA, Argentina). Vaccine matching gave satisfactory results by Expectancy of Protection (EPP, by VNT), and by 'r' values obtained by Complement Fixation test, with vaccines containing strain O₁ Campos (National Reference Laboratory, SENASA, Argentina).

4.1.3. Serotype A

The best match, by VNT, for the type A virus from the 2006 outbreak in **Egypt** was afforded by vaccine containing A Eritrea 98. Additional African serotype A viruses (from **Cameroon, Ethiopia, Kenya** and **Togo**) were also tested for cross-reaction with the A Eritrea vaccine strain. All showed a rather poor match with this vaccine strain. A potency test conducted for The European Commission for Control of FMD at the Friedrich Loeffler Institute in Germany in August, found that a high potency A22 Iraq vaccine could protect against A Egypt 2006 despite a poor predicted serological match. The only vaccine that provided a match to the **Mauritanian** viruses was A Ken 35/80.

A22 Iraq vaccine was recommended by WRL to provide protection against the "**A Iran 05**" strain of FMDV. This is based on serological tests which have and continue to indicate a moderate match despite the lack of a close genetic relationship (isolates tested from **Iran, Saudi Arabia, Jordan** and **Turkey**). This recommendation has been supported by subsequent reports that the A22 vaccine has proved to be effective against the "A Iran 05" strain in Turkey, in the field.

A May 97 vaccine showed an acceptable match to serotype A viruses isolated from **Malaysia** (2005) and **Vietnam** (2004-5).

4.1.3. Serotype Asia 1

Two isolates of Asia 1 from **Vietnam** had an acceptable match with vaccine strain Asia 1 Shamir.

Isolates collected in 2005 from **Russia** and **Mongolia** were also acceptable matches with vaccine strain Asia 1 Shamir.

4.1.4. Serotype SAT 1 and 2

The SAT1 isolates tested from **Botswana** all matched SAT 1 105 and 109 reference vaccine strains and BVI vaccine was effective in controlling the outbreak.

A selection of African SAT 2 isolates matched with the SAT 2 Eritrea vaccine strain.

A new recommendation on vaccine strains has been provided by the FMD FAO World Reference Laboratory to the Executive Committee of the European Commission for the Control of FMD (Annex 4). A22 Iraq has been moved from medium to high priority and A Eritrea 98 from low to medium priority.

5. Overall Conclusions

FMDV is still active in many parts of the world and continues to threaten FMD-free regions.

Efforts to control FMD in affected regions are extremely variable. Substantial initiatives appear to be taking place to increase vaccination in India and China, two of the largest animal producing regions affected by FMD. In South America, the outbreaks of disease in southern Brazil and northern Argentina have led to concern that virus still circulates in areas that are supposedly “FMD-free with vaccination”. Despite the efforts of the Commission for the Control of FMD in South East Asia, the situation in the region has not improved in the last year, with major outbreaks in Vietnam, incursions into Malaysia and westward spread of the pig-adapted Cathay topotype. In some parts of the world, particularly parts of Africa, there is little in the way of effective control.

Knowledge concerning the types of FMD virus circulating is related to disease control efforts in the country or region involved. In countries where the disease does not occur or occurs only sporadically, there is a good likelihood that outbreaks will lead to samples being collected and submitted to laboratories for detailed analysis. In contrast, viruses in primary endemic countries which are the main reservoir of infection are much less likely to be studied in a systematic way leading to gaps in our knowledge. Cumulative results over many years have led to a fairly good understanding of the different virus topotypes to be found in different regions, but new strains, for example of serotype A, continue to emerge from incompletely understood sources. Surveillance can be improved by continuing efforts to solicit sample submissions; however, proper epidemiological studies are also needed to complement laboratory-based virus characterisation.

The vaccines held in reserves by different FMD-free regions do not appear to give optimal protection against the full range of FMD viruses from endemic regions and therefore there is a continuing need to review risk and prioritise which vaccine strains should be available. Continuation of vaccination against serotype C remains questionable since there is little evidence for continued circulation of this serotype and use of improperly inactivated vaccine carries a risk of its reintroduction.

Annex 1

1.3. Overview and discussion of outbreaks of FMD in Botswana

In April 2006 Botswana had an outbreak of FMD in Bobonong Extension Area, Selibe Phikwe veterinary district (Zone 7) which was an FMD free without vaccination zone. The outbreak was caused by a SAT 2 strain similar to the Matsiloje outbreak which was closely related to the strain circulating in the adjoining Zimbabwean side of the border (see Figure 2). This strain was different to the one involved in the Pandamatenga outbreak of August 2005. Correlation values with BVI vaccine strain were between 0.6 and 1.0 and the disease was effectively and quickly controlled using the BVI vaccine.

In June 2006 an outbreak of FMD was confirmed in cattle at Muchenje extension area in Kasane Veterinary district (Buffalo Zone). The outbreak was caused by a SAT 1 strain differing by 9%, 11% and 13%, respectively, from SWA/2/89, BOT /1/68 and the 1998 isolate from Botswana. The recent appearance of FMD outbreaks in vaccinated herds prompted BVI and Department of Animal Health to do a detailed study of the virus in buffaloes. The testing of samples is still in progress.

The Department of Animal Health will present at a meeting of The OIE Scientific Commission for Animal Diseases, to be held at end of November, a proposed zonation for approval.

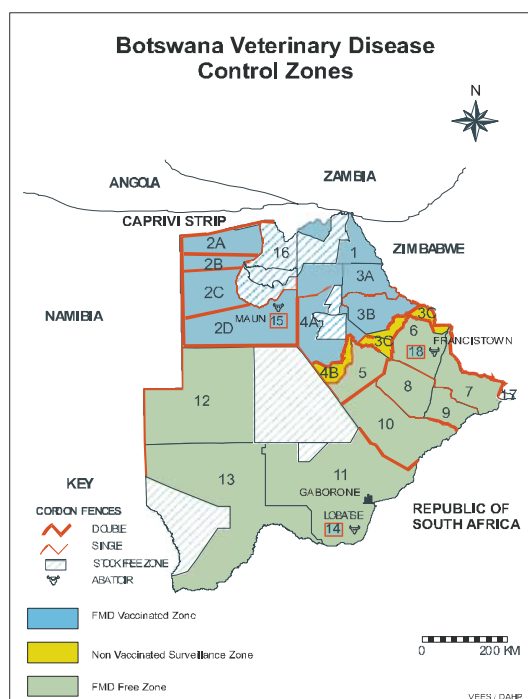
Zambia had an outbreak in June 2006 caused by a SAT 1 serotype differing only by 3% from the 2004 strain. The outbreak was in Namwala village, Namwala veterinary district of the Southren Province.

SAT 1 serotype virus was isolated from samples received from Tanzania (unknown location) in June 2006.

A selection of the viruses received from the above outbreaks were further characterised by partial genomic sequencing and serological matching to vaccine strains except the Tanzania outbreak at BVI, WRL and OVI. Phylogenetic analyses were performed by using complete VP1 gene sequences.

In conclusion, the reoccurrence of FMD outbreaks of SAT types in the SADC region emphasised the need for continuous surveillance for the disease. For most of the outbreaks in 2006 isolates were shown to have a very good matching with BVI vaccine strains by VNT indicating the appropriateness of use of these vaccines.

Figure 2. FMD Control Zones in Botswana



Annex 2

Figure 3. FMDV serotype O collected in Kenya (2004-2006) and the Democratic of the Congo (2006).

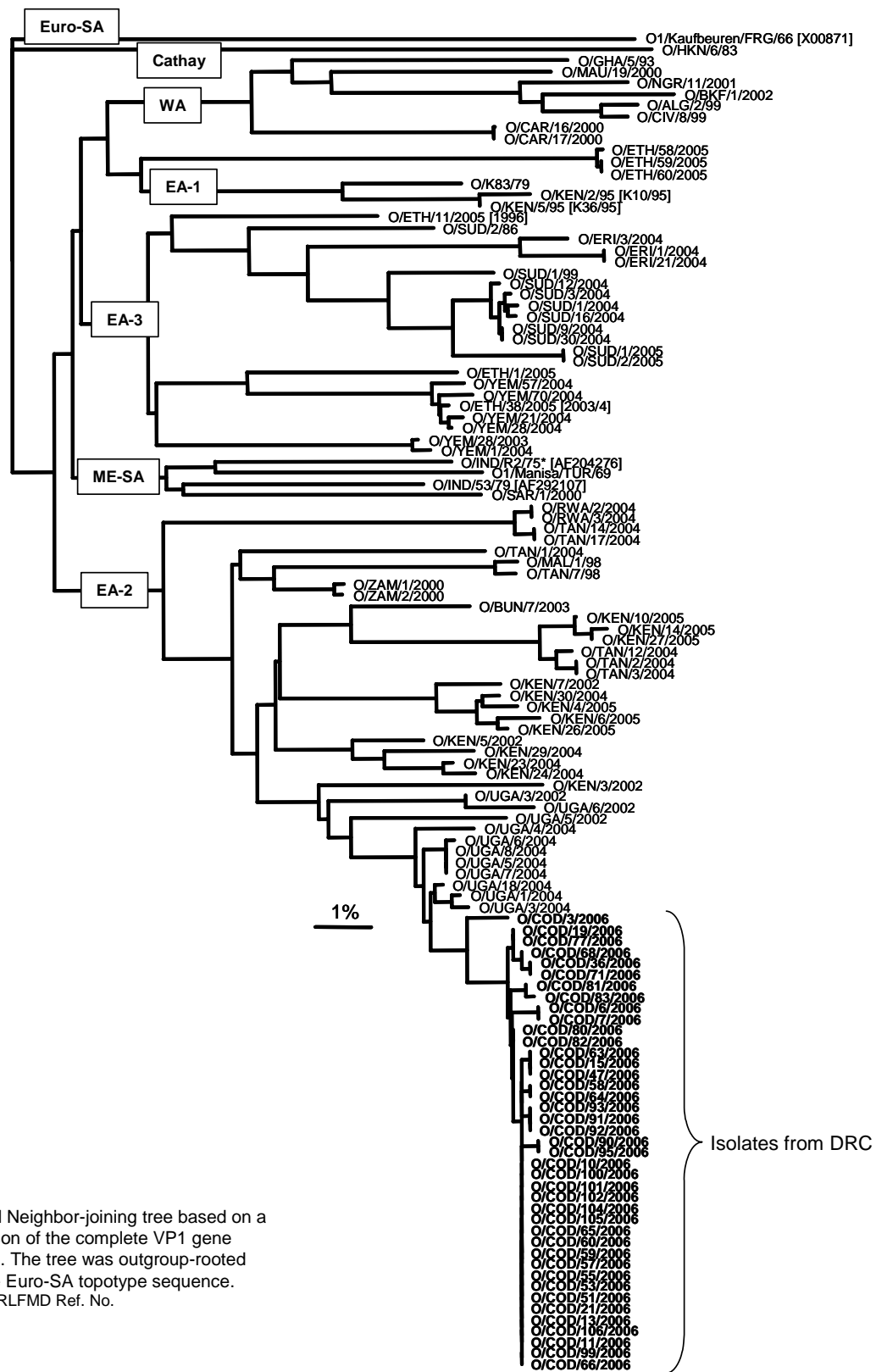


Figure 4. FMDV serotype O collected in Ethiopia in 2006.

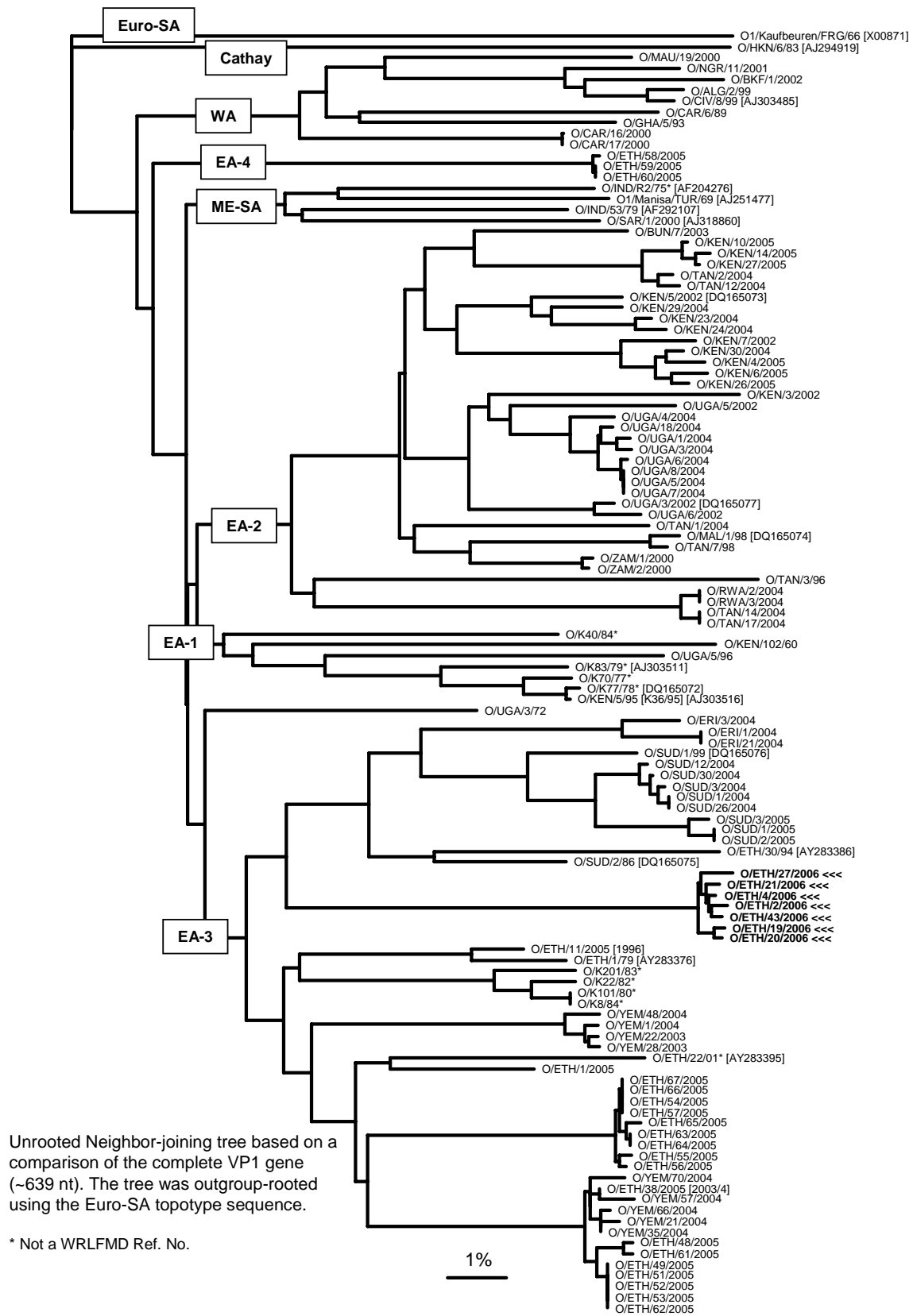


Figure 5. FMDV serotype O collected in Niger (2005) and Senegal (2006).

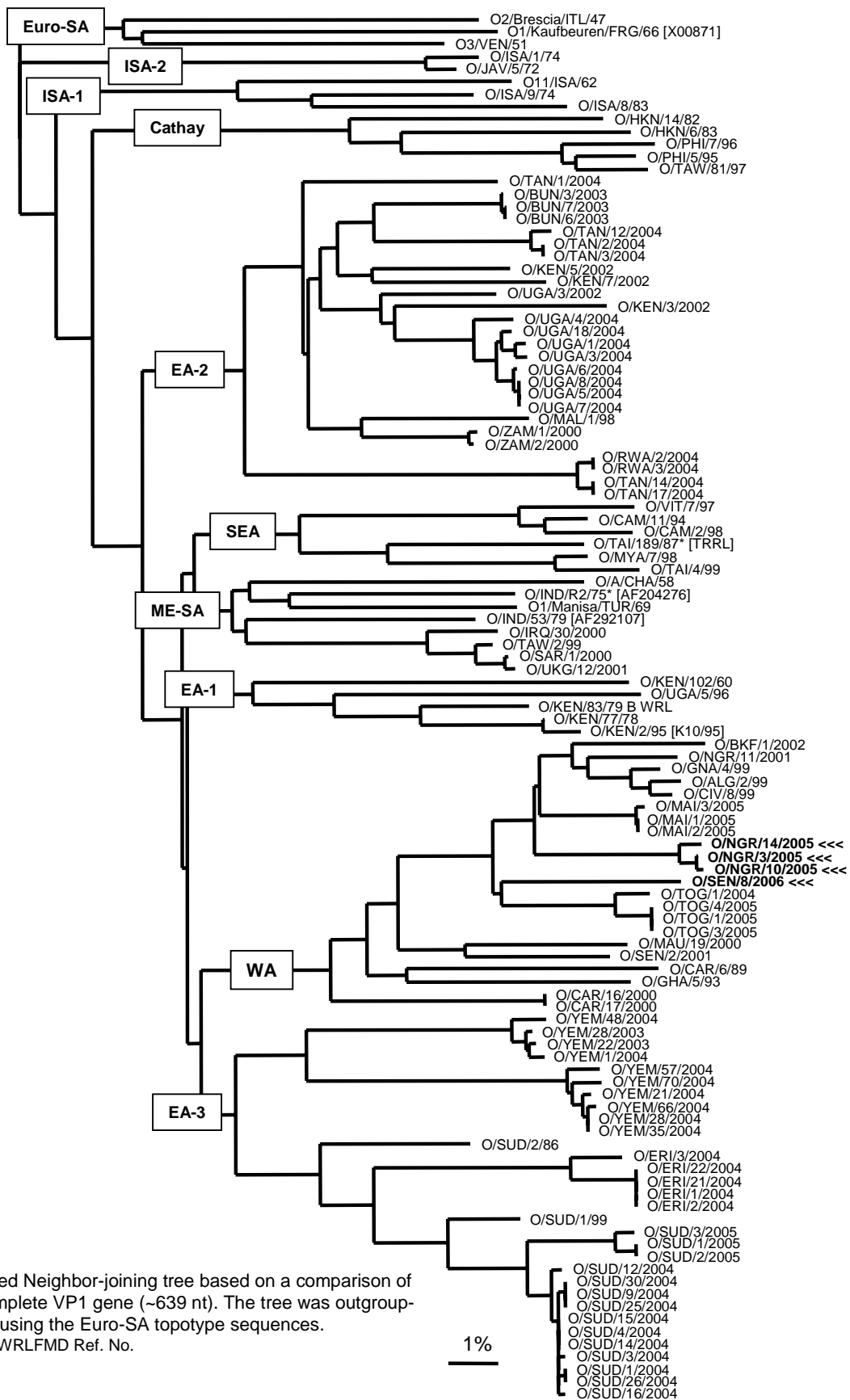
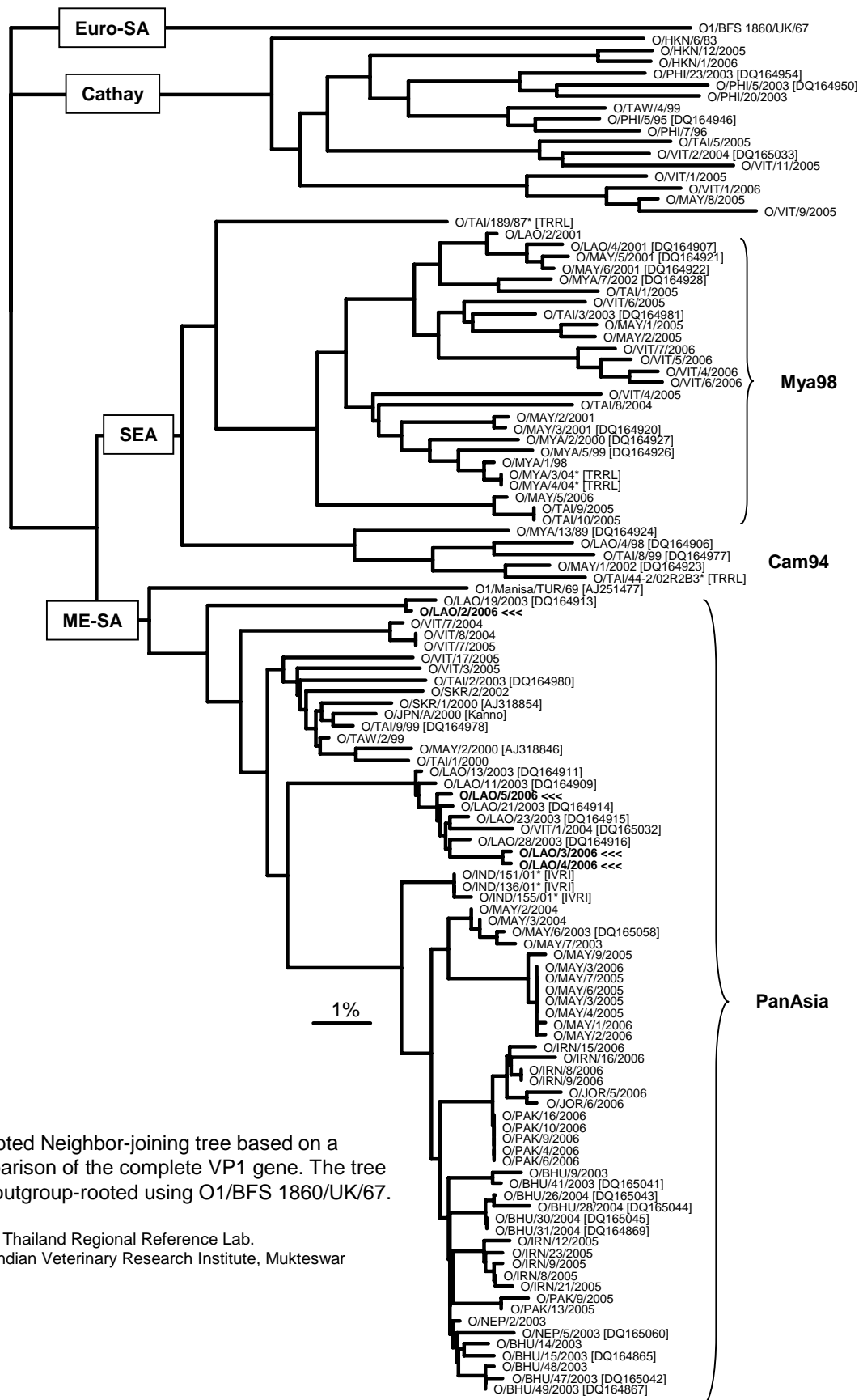


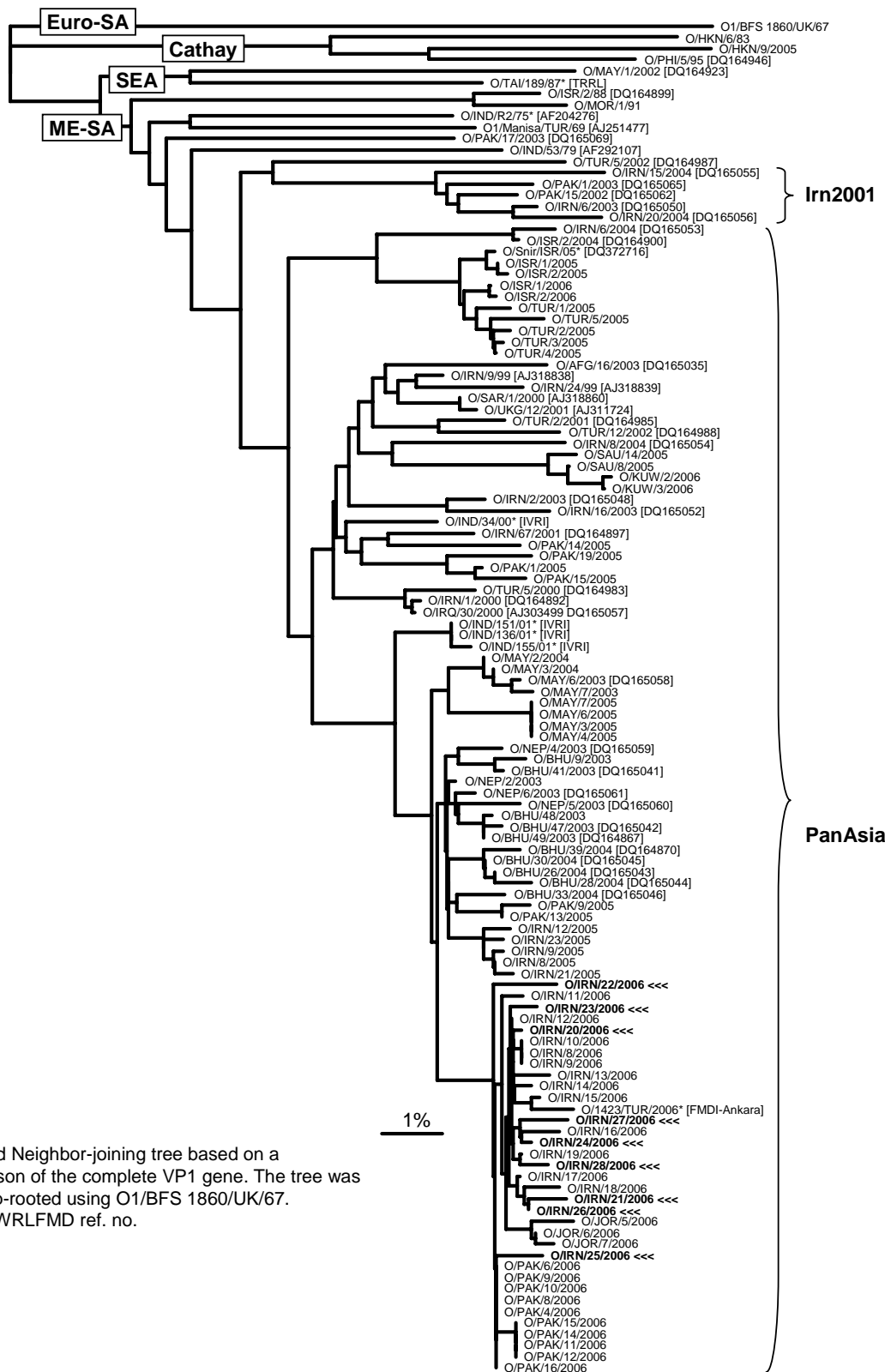
Figure 7. FMDV serotype O collected in Malaysia (2005-2006) and Laos (2006).



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using O1/BFS 1860/UK/67.

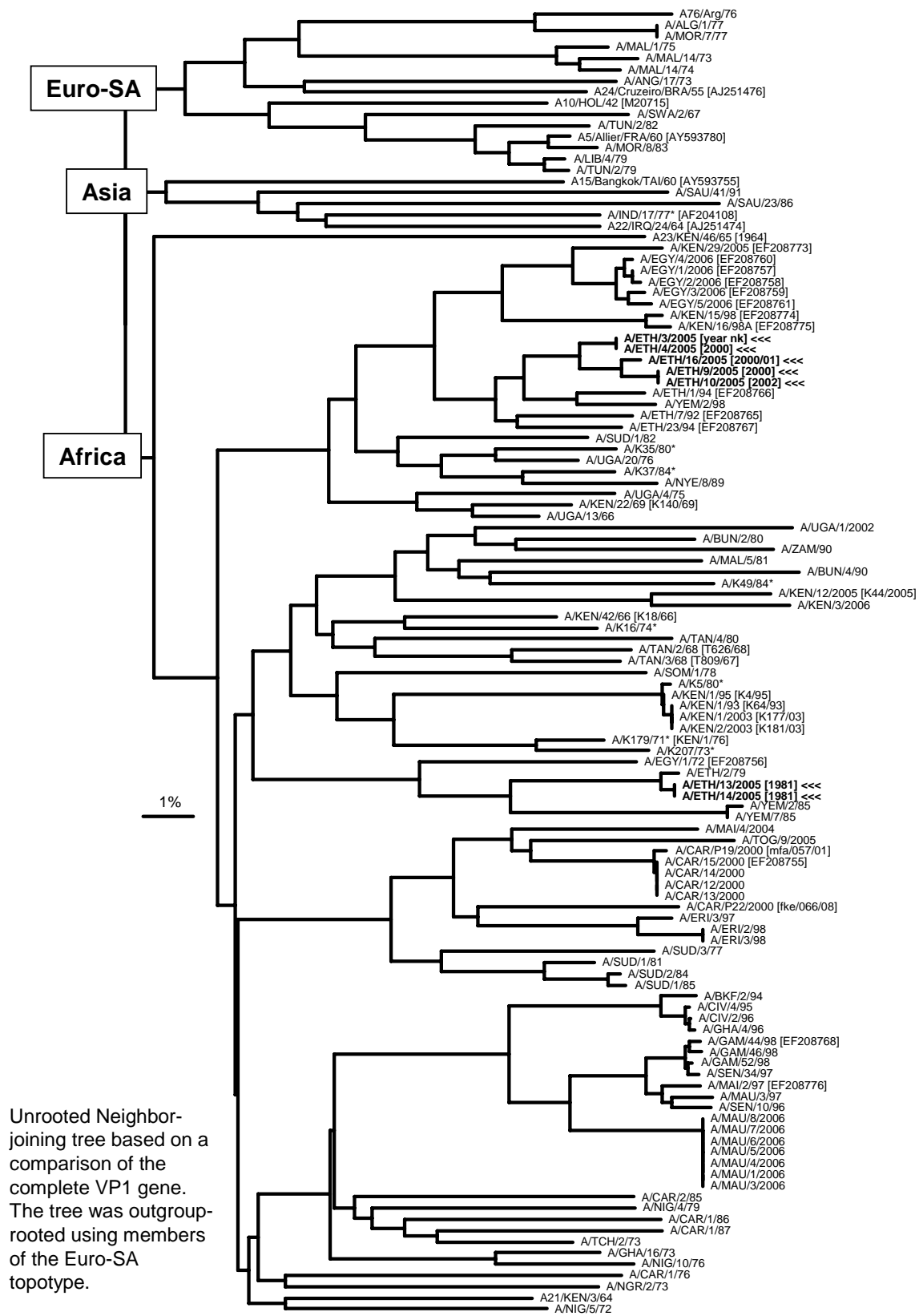
TRRL, Thailand Regional Reference Lab.
IVRI, Indian Veterinary Research Institute, Mukteswar

Figure 8. FMDV serotype O from the Middle East (Turkey, Iran, Jordan, Israel, Pakistan)



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using O1/BFS 1860/UK/67. *, not a WRLFMD ref. no.

Figure 9. FMDV serotype A collected in Ethiopia in 1981 and 2000-2002.



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using members of the Euro-SA topospecies.

Figure 10. FMDV serotype A collected in Iran, Turkey, Jordan, Pakistan, Saudi Arabia.

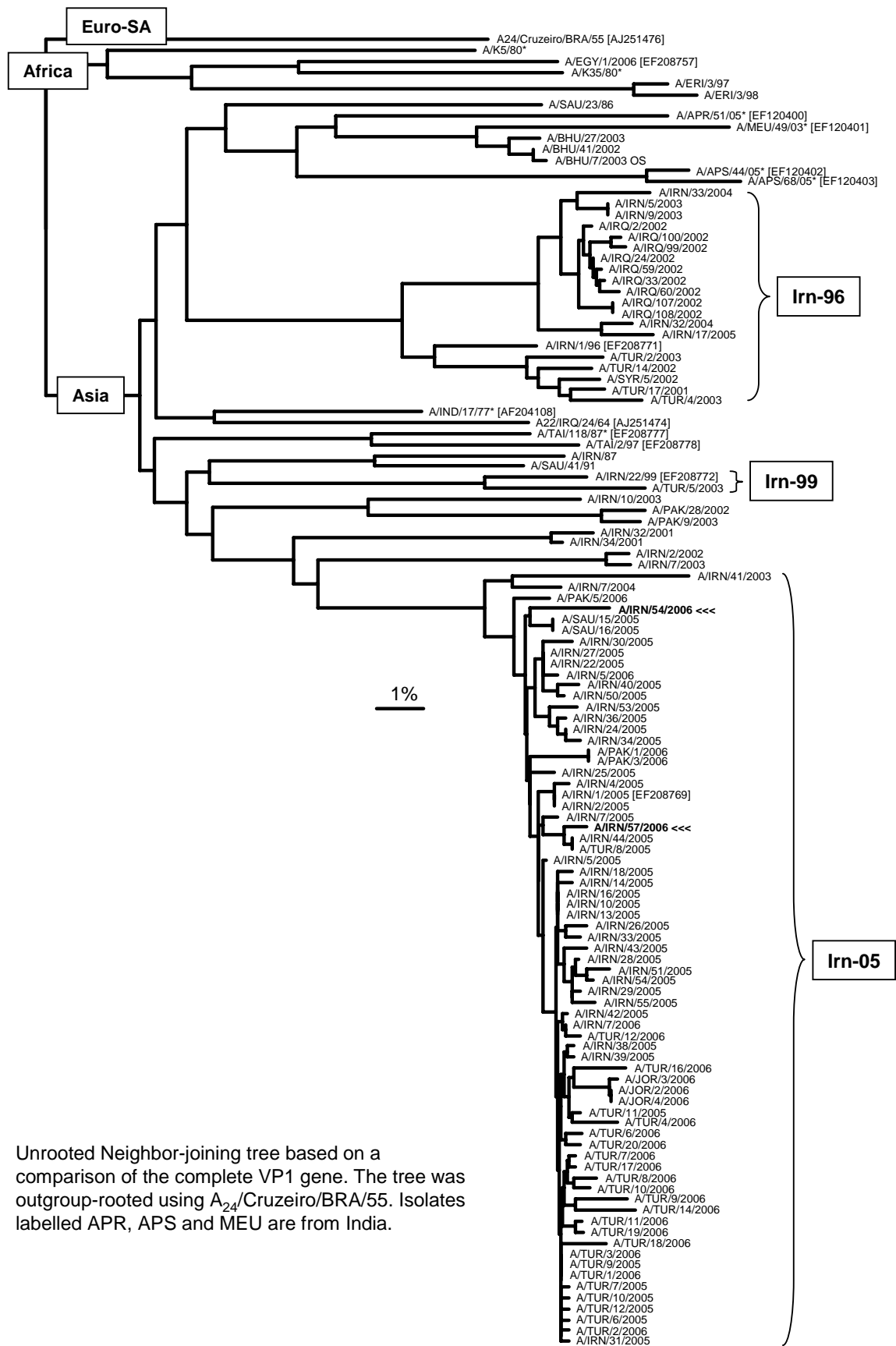


Figure 11. FMDV serotype A collected in Southeast Asia in 2004-2006.

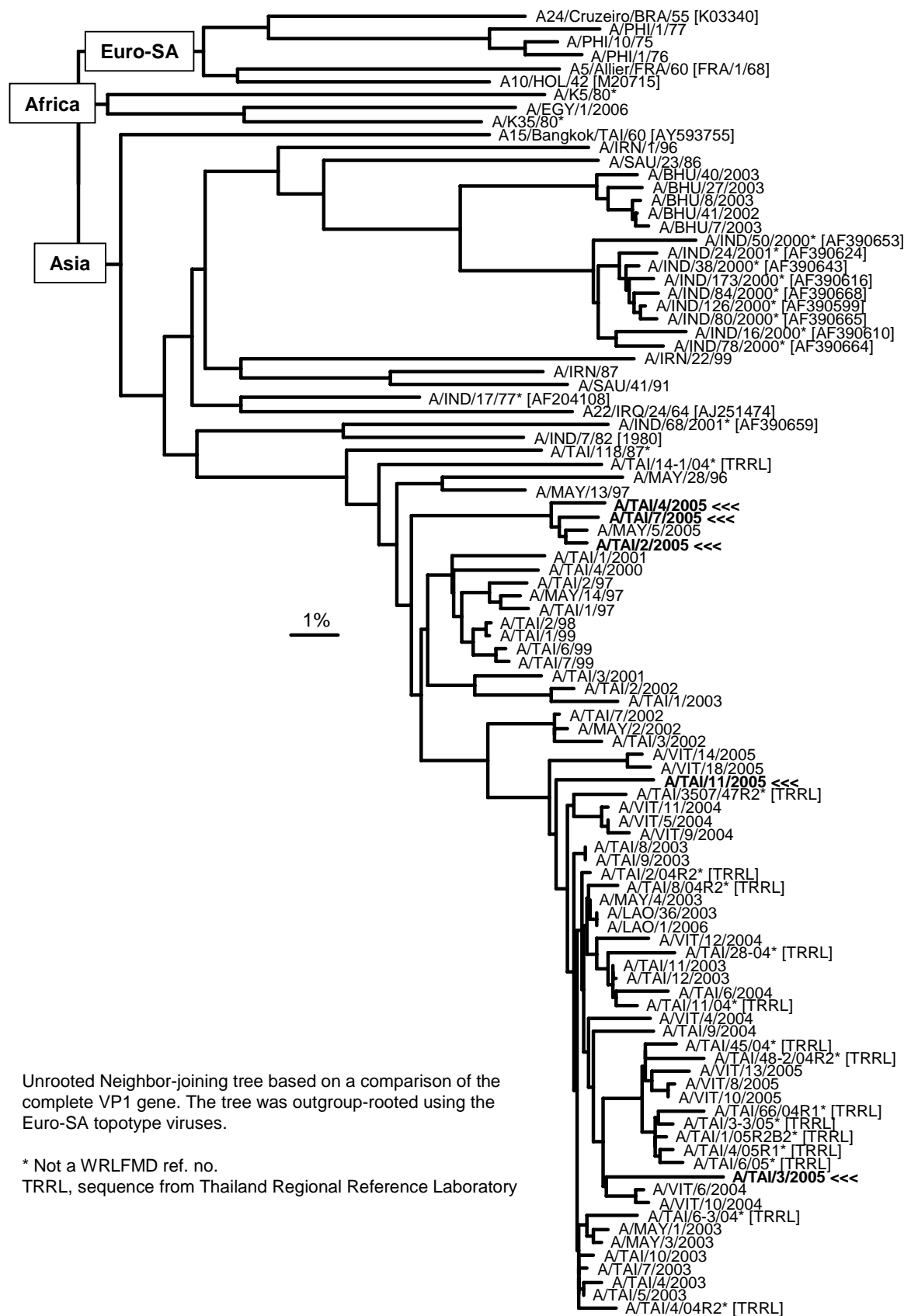
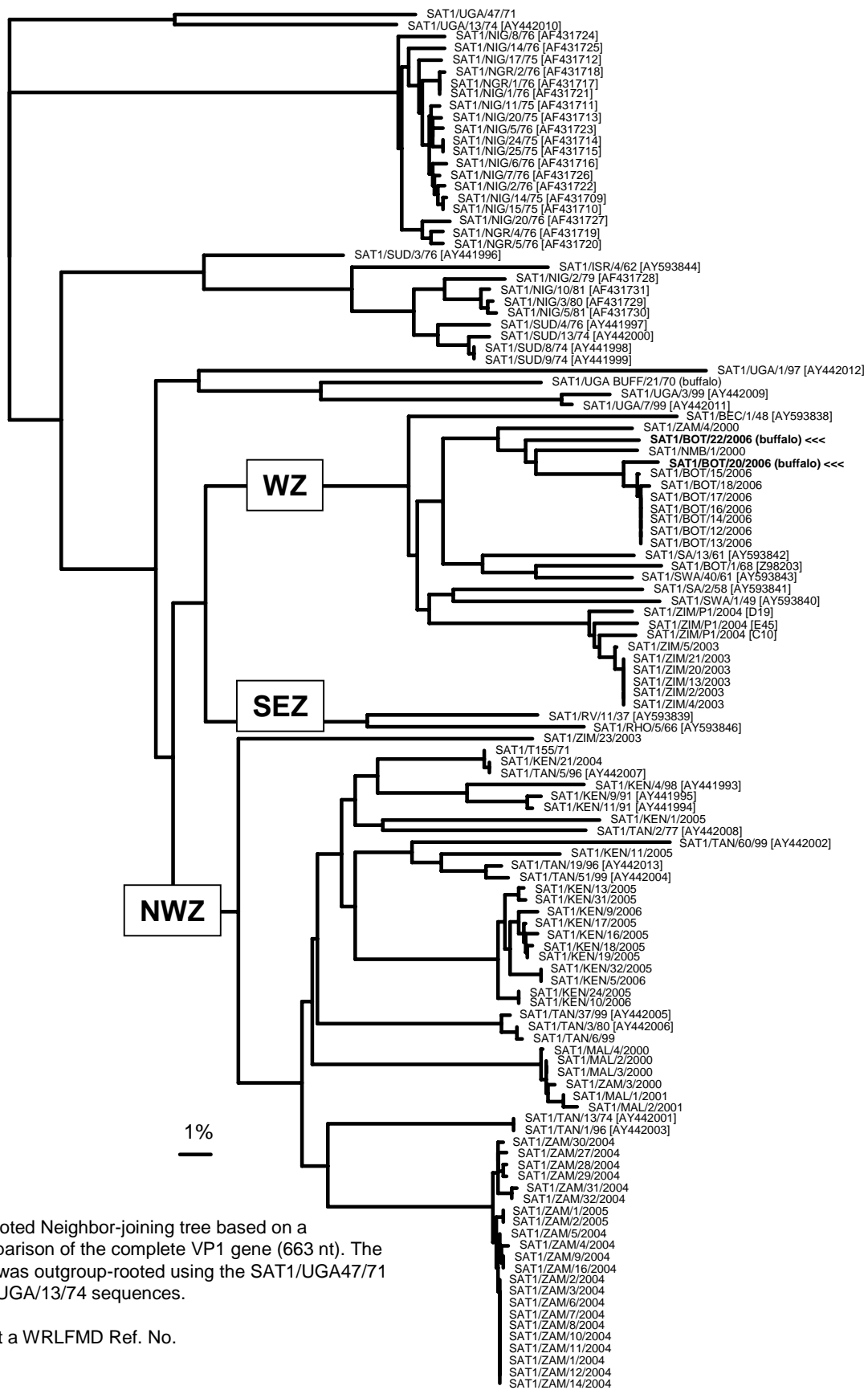


Figure 13. FMDV serotype SAT1 collected in Botswana in 2006



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (663 nt). The tree was outgroup-rooted using the SAT1/UGA47/71 and UGA/13/74 sequences.

*, not a WRLFMD Ref. No.

Figure 14. FMDV serotype SAT 2 collected in Kenya and Botswana.

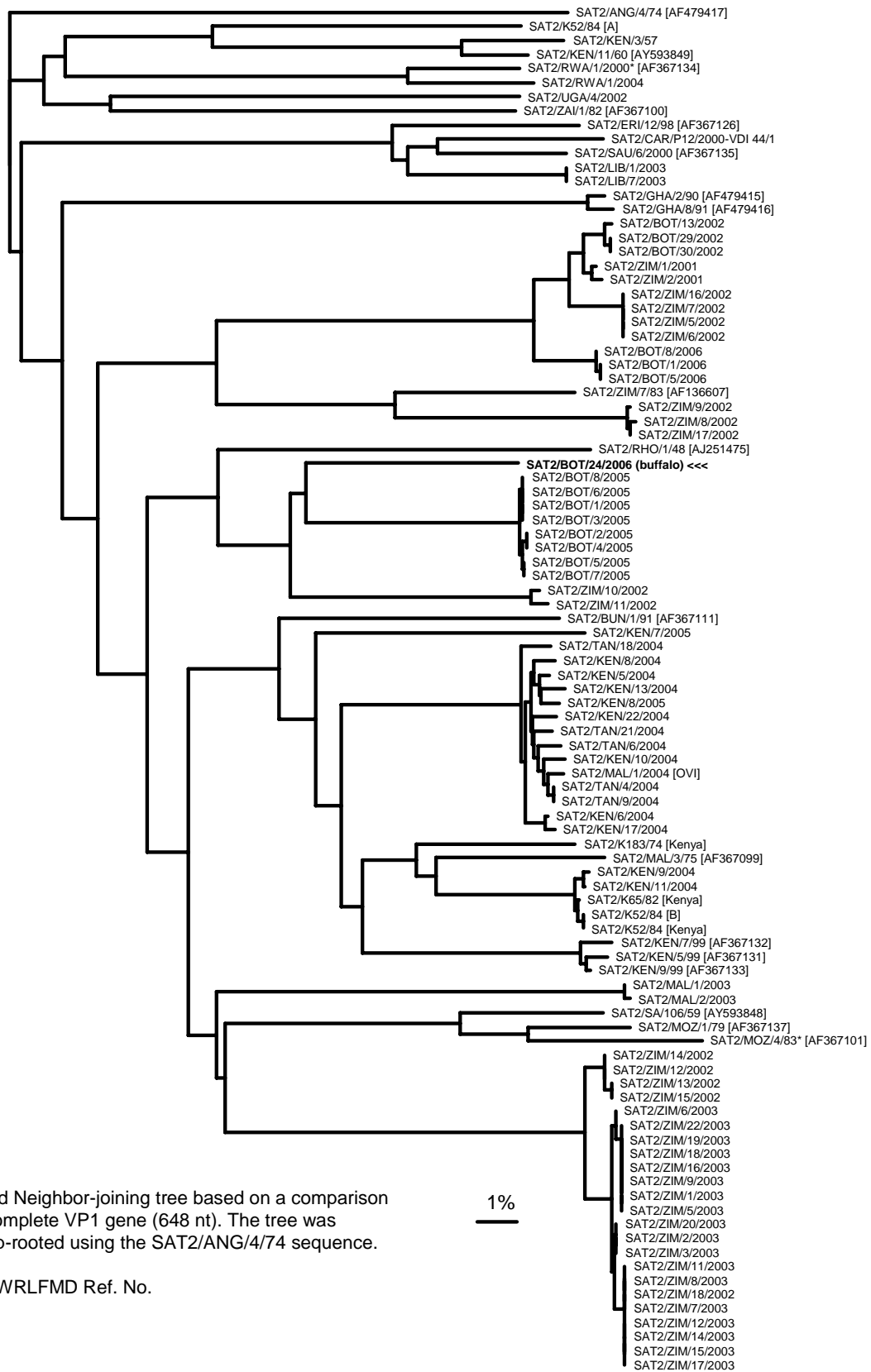


Figure 15. FMDV serotype SAT2 collected in Niger in 2005.

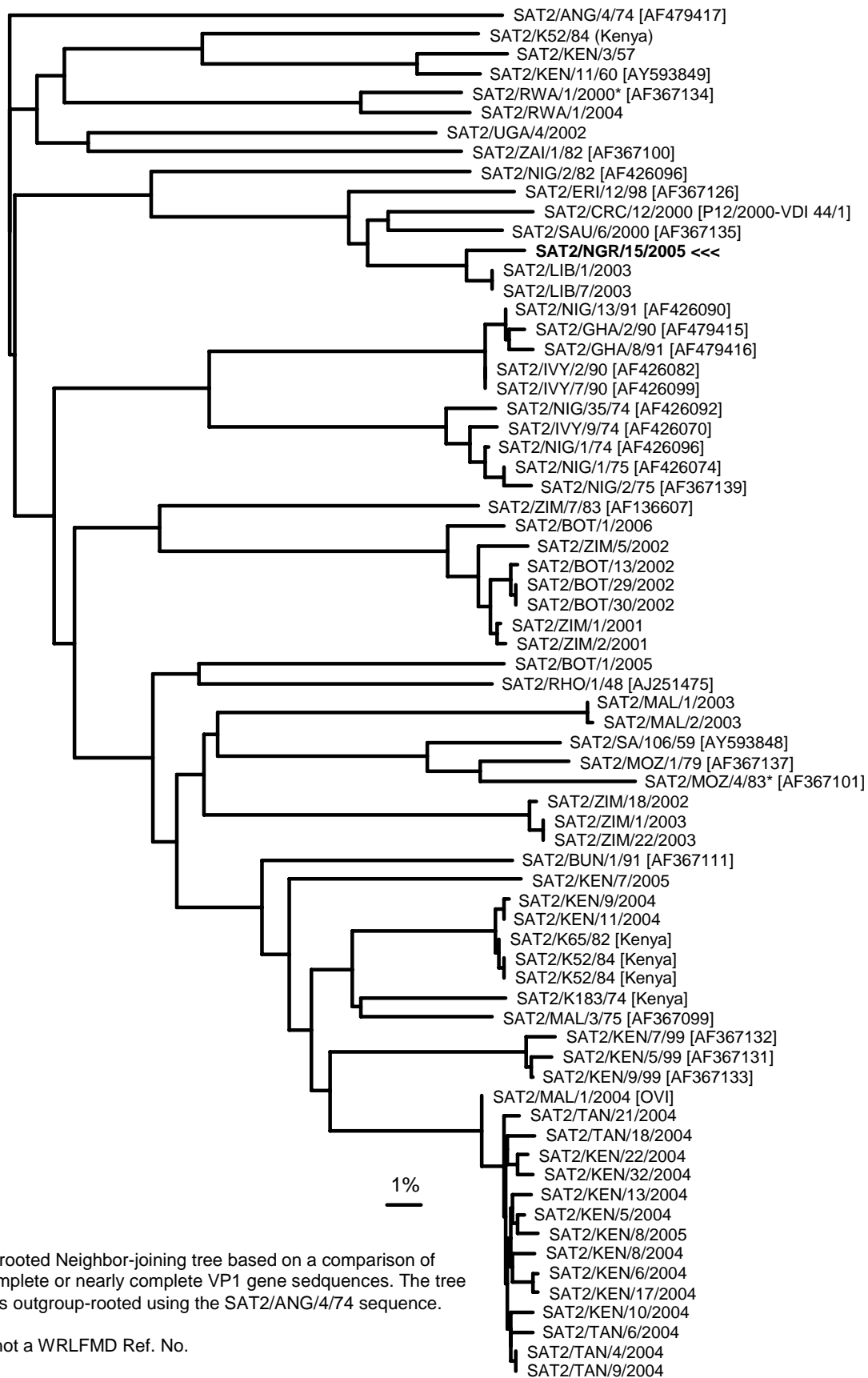


Figure 16. Neighbour-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in South America.

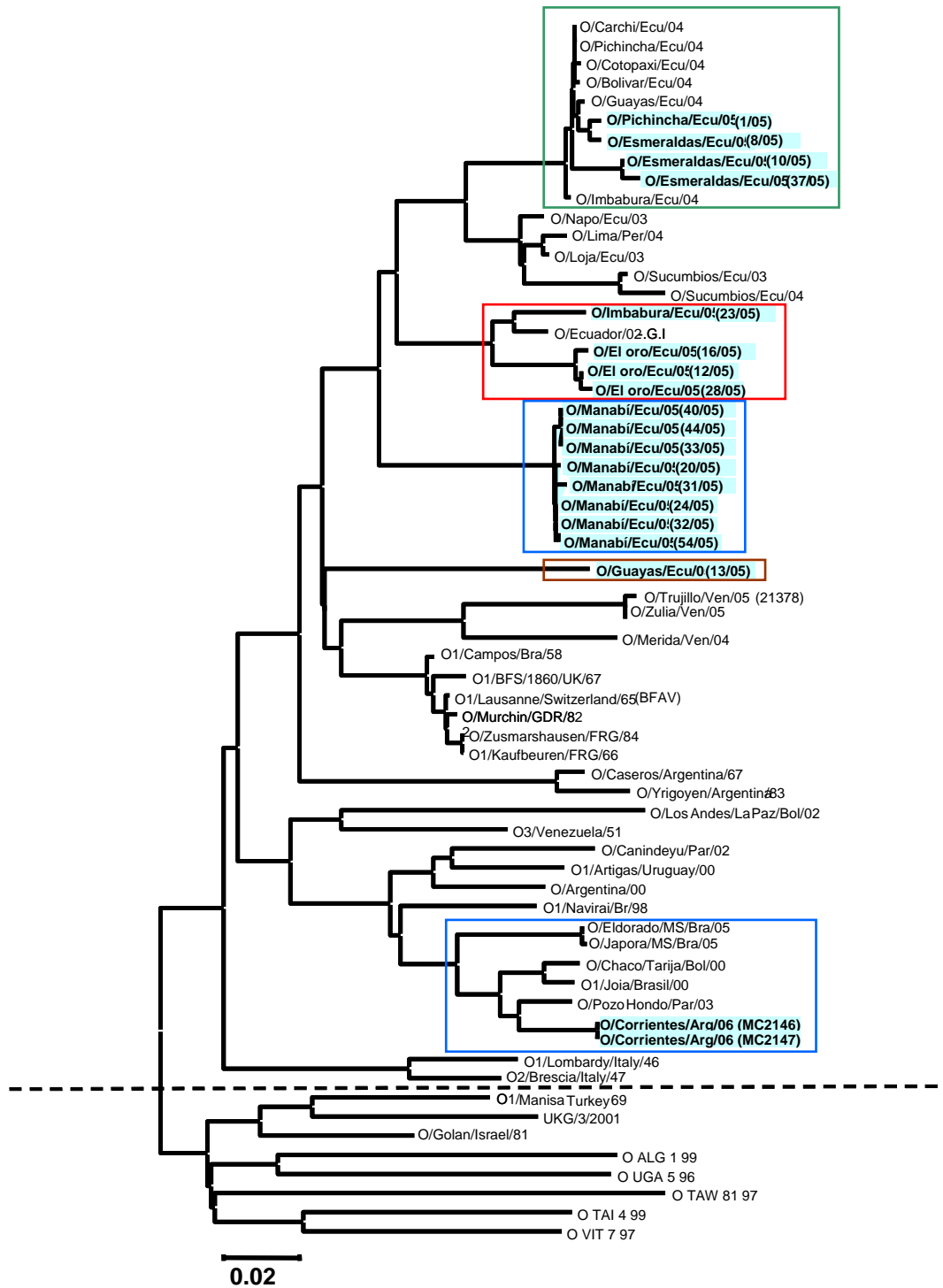


Figure 17. Neighbor-joining tree comparing the complete VP1-coding sequences of type A FMDV collected in South America.

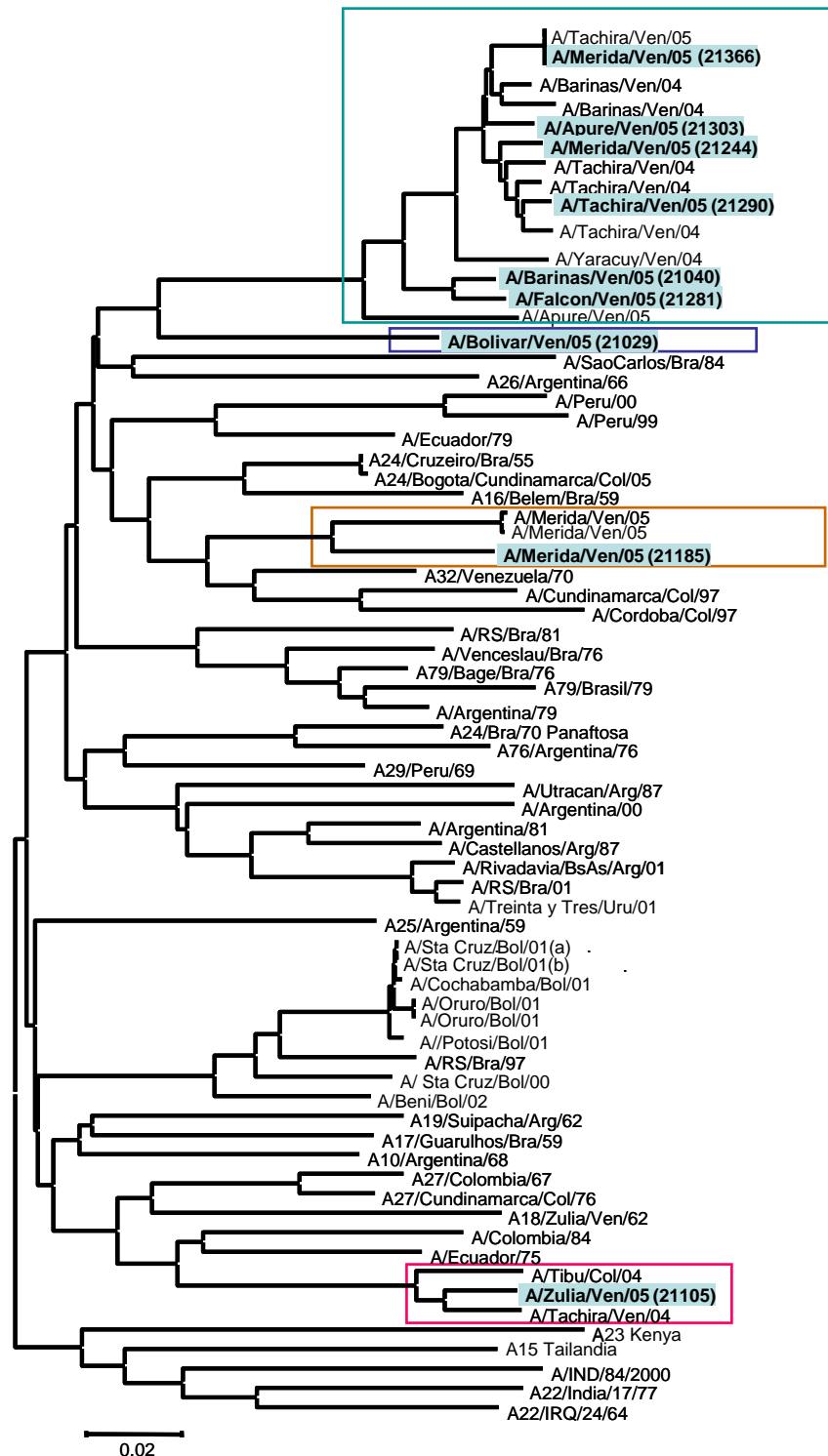


Figure 18. Phylogenetic tree produced by ARRIAH with complete VP1 gene sequences showing the genetic relationships between the FMD type A viruses. VS- Vaccine strain.

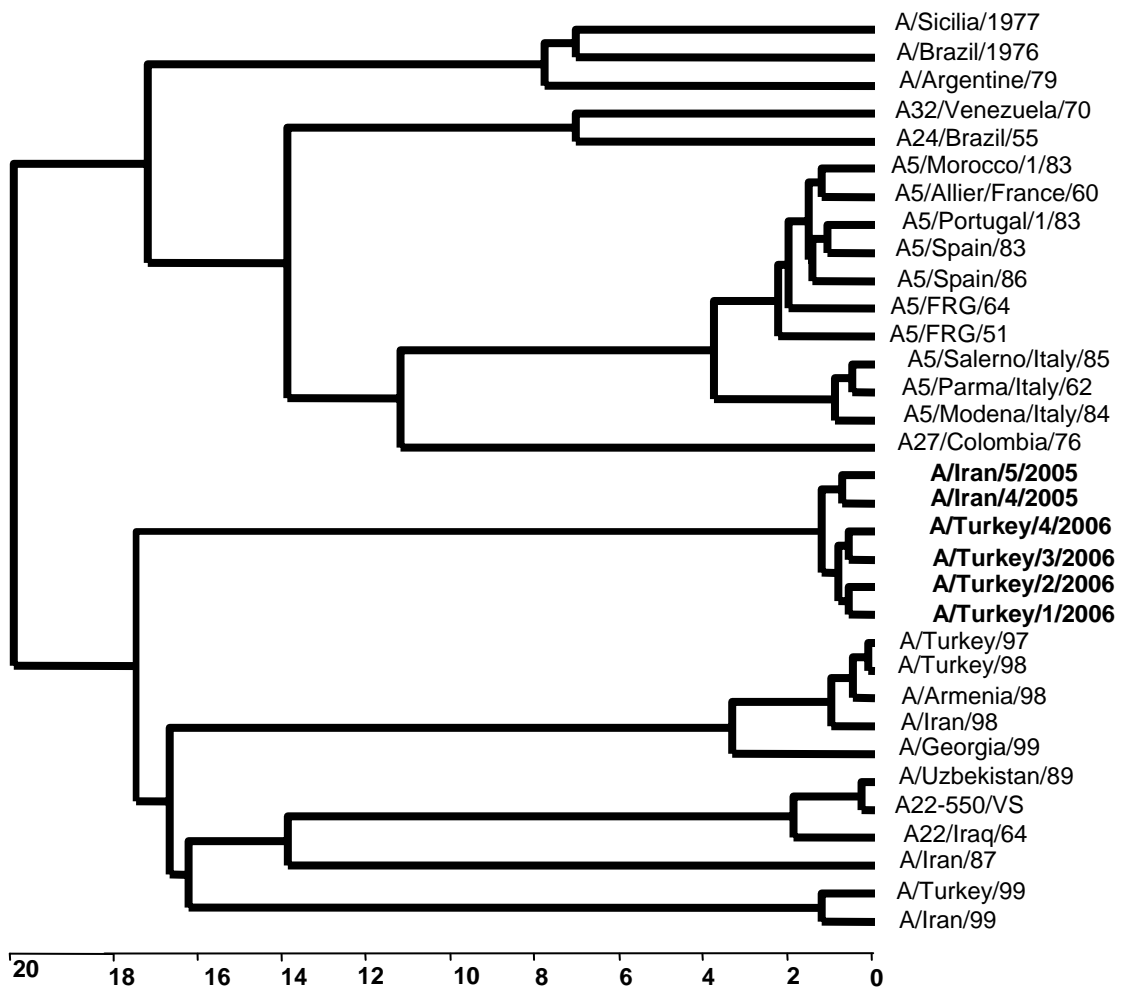
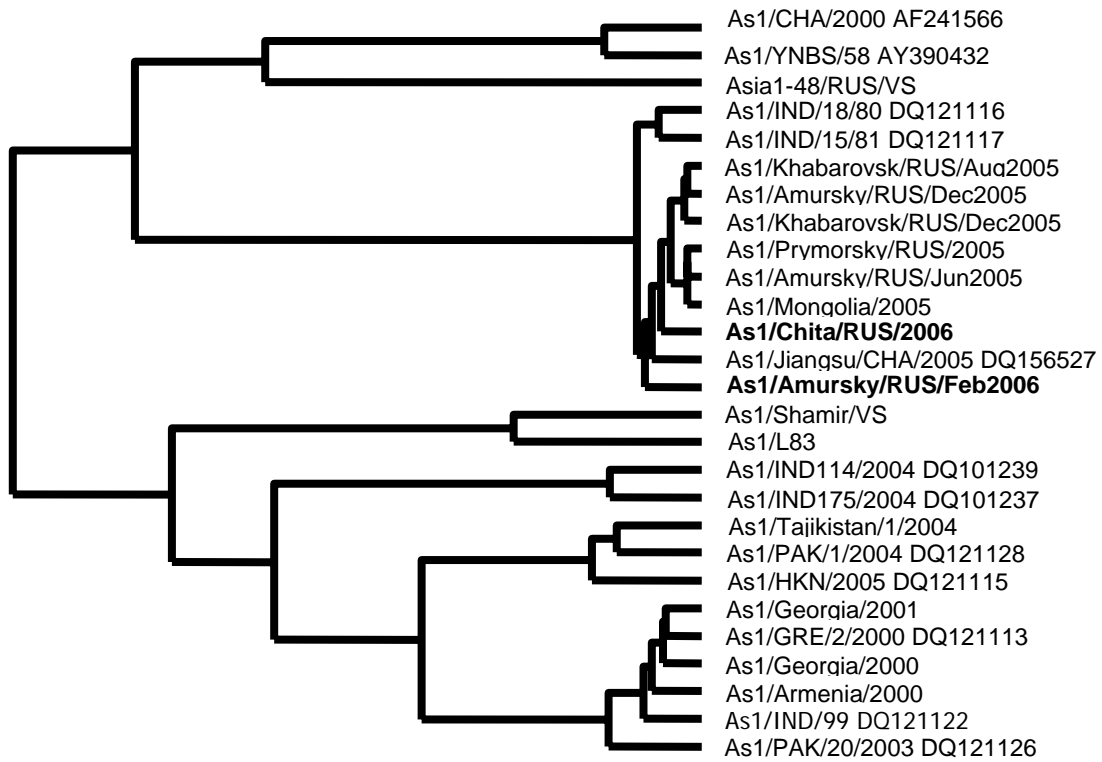


Figure 19. Phylogenetic tree produced by ARRIAH showing the genetic relationships based on complete VP1 gene sequences between the FMD type Asia-1 viruses. VS- Vaccine strain.



Annex 4. Recommendations from the WRL on FMD virus strains to be included in FMDV antigen banks – 2006 (not in order of importance)

High Priority

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

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