Annual OIE/FAO FMD Reference Laboratory Network Report

January – November 2005

FAO World Reference Laboratory and OIE Reference Laboratory for FMD (WRLFMD), Institute for Animal Health, Pirbright, UK: Jean-Francois Valarcher, Nigel Ferris, Nick Knowles, Bob Statham, David Paton

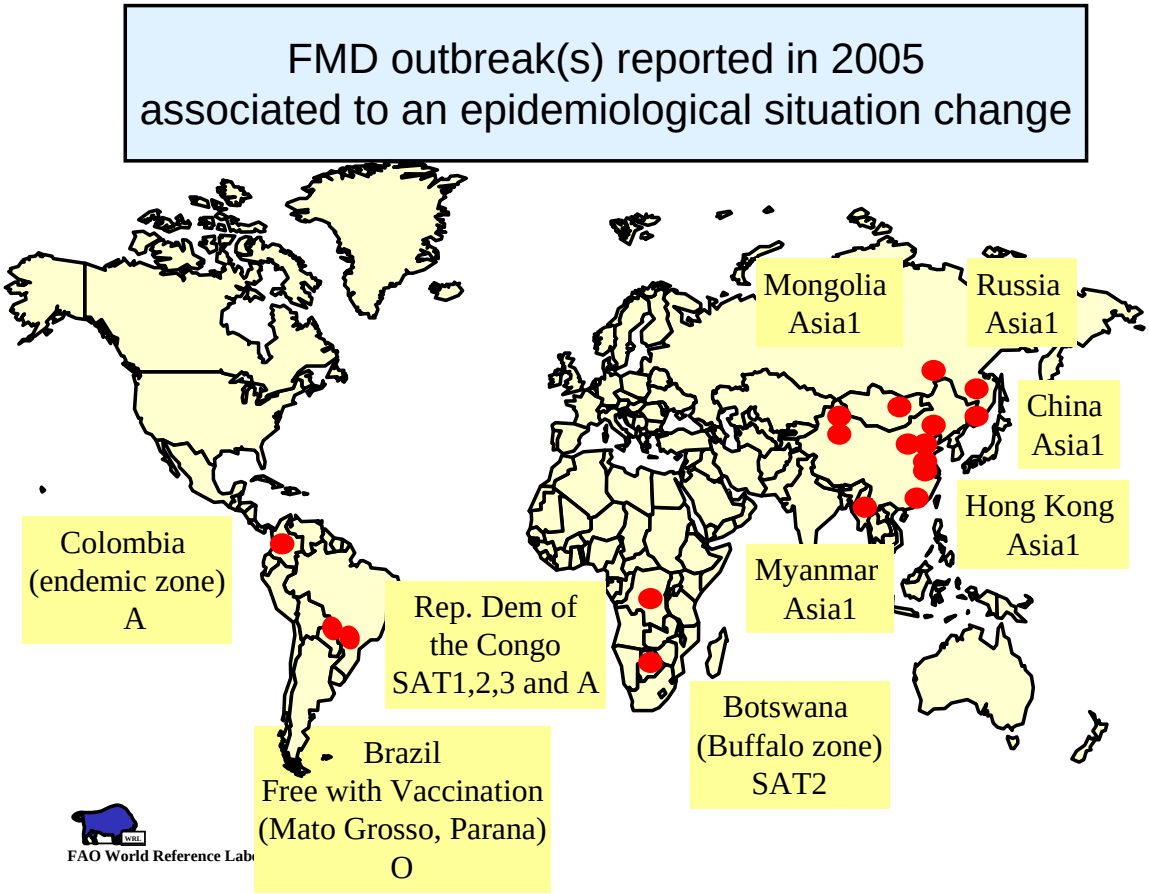
Centro Panamericano de Fiebre Aftosa (PANAFTOSA) and OIE Reference Laboratory for FMD, Rio de Janeiro, Brazil: Ingrid Bergmann, Viviana Malirat, Rossana Allende

Federal Governmental Institute, Centre for Animal Health (FGI ARRIAH) and OIE Reference Laboratory for FMD, Vladimir, Russia: Aleksey Scherbakov, Valery Zakharov

OIE Regional Reference Laboratory for the Sub-Saharan continent, Gabarone, Botswana: Hervé Coupier, Lindani Mozola, George Matlho

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

1.1. Countries that have reported FMD outbreaks in 2005 (January-November) and FMD serotypes related to those outbreaks (where known)



No data are available for 2005 from Handistatus on the global situation by country.

The SEAFMD website (http://www.seafmd-rcu.oie.int/index.php) provides maps showing countries in the region that have experienced outbreaks in each month of 2005 (Cambodia: not typed, Lao PDR: type O, Peninsular Malaysia: type O and A, Myanmar: type O and Asia 1, Philippines: type O, Thailand: type O and A, Vietnam: type O and A).

PANAFTOSA collects information on outbreaks in South America:
Number of reported FMD-infected farms in South America until week 44.

Country	Total	Type O	Type A	Type C	Clinical – epidemiological diagnosis
Bolivia	0				
Brazil	15	15			
Colombia	1		1		
Ecuador	41	27			14
Perú	0				
Venezuela	2	1	1		
Total	**59**	**43**	**2**	**0**	**14**

1.2. Overview and discussion of outbreak information

Highlighting changes in epidemiological situation, relative risk for disease spread and information gaps.

No FMD outbreaks were officially reported in FMD-free countries not using vaccination. FMD remained largely confined to traditionally infected areas between January and November 2005.

The OIE Scientific Commission for Animal Diseases has, at its meeting held from 13 to 19 January 2005, decided to restore the status “FMD free zone with vaccination” to the zone of Argentina situated north of the 42° parallel and the status “FMD free country with vaccination” to Paraguay. Columbia also gained the status “FMD free with vaccination in two new zones that were officially recognized as such in May 2005.

Since the reporting procedure of the ex-OIE List A diseases has changed, less information about FMD outbreaks in endemic countries is available. Only changes in the epidemiological situation of FMD are now reported in real-time.

For this period, epidemiological changes in FMD situation have occurred in Botswana (Buffalo zone / serotype SAT2), Brazil (Mato Grosso, / serotype O), China (serotype Asia1), Colombia (endemic zone / serotype A), Congo (Rep. Dem of the Congo / SAT1,2,3 and A), Hong Kong (serotype Asia1), Mongolia (serotype Asia1) and Russia (serotype Asia1).

The recent appearance of the Asia 1 serotype in China (east and west), Hong Kong, Mongolia, Myanmar, Russia, Tajikistan, along with the traditional occurrence of this serotype in India, Iran and Pakistan suggested that a single strain of Asia1 could be spreading throughout Asia. By collaborating with FGI ARRIAH (Russia), LVRI (China), PDFMD (India), Pakchong (Thailand), we were able to demonstrate that viruses belonging to five different genetic sub-lineages were responsible for those outbreaks.

At the end of this reporting period, type O FMDV has been recorded in the southern state of Mato Grosso do Sul in Brazil in an area previously free with vaccination.

A selection of the viruses received from various outbreaks 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.

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

Samples collected in 2005 in question:

Country	No. of samples	Virus isolation in cell culture/ELISA FMD virus serotypes							SVD virus	NVD	RT-PCR for FMD (or SVD) virus (where appropriate)			Laboratory
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1			Positive	Negative	Not determined	
Botswana	8					8					8			WRL
Brasil	15	15									13		2	PANAFTOSA
Burkina Faso	10									10		10		WRL
Cameroon	119					in progress								WRL
Colombia	1										1			PANAFTOSA
Cote d'Ivoire	6									6		6		WRL
Ghana	4									4		4		WRL
Hong Kong (China)	16	7						8		1	15	1		WRL
Iran	32	6	20							6	25	7		WRL
Ireland	11									11		11		WRL
Kenya	1				1						1			WRL
Mali	4	3								1	4			WRL
Pakistan	26**	19						2		7	25	1		WRL
Philippines	10	3								7	3	7		WRL
Saudi Arabia	14	11								3	11	3		WRL
Senegal	3									3		3		WRL
Sudan	3	3									3			WRL
Togo	16	4	1							11	3	13		WRL
Venezuela	7	2	5								7			PANAFTOSA
Vietnam	5	5									5			WRL
Zambia	2				2						2			WRL
Total	313	78	27		3	8		10		70	126	66	2	

Samples received at WRL in year in question, but collected earlier

Country	Year	No. of samples	on in cell culture/ELISA FMD virus serotypes							VSV		SVD virus	NVD	RT-PCR for I virus (where
			O	A	C	SAT 1	SAT 2	SAT 3	Asia 1	New Jersay	Indiana			Positive
Ecuador	2004	22	10							11	1			22
Hong Kong (China)	2004	1	1											1
Iran	2004	12		2					3				7	4
Kenya	2003-2004	14		2	1		7						4	14
Lao PDR	2003	1		1										1
Mali	2004	16		1									15	
Myanmar	2004	4	4											4
Pakistan	2004	2											2	2
Thailand	2004	9	1	2									6	9
Togo	2004	1	1											
Venezuela	2004	8	1	7										8
Zambia	2004	16					6						10	7
Total		106	18	15	1	6	7		3	11	1		44	50

FMDV	foot-and-mouth disease virus
VI/ELISA	FMDV serotype identified following virus isolation in cell culture and antigen detection ELISA
RT-PCR	reverse transcription polymerase chain reaction for FMD viral genome
NVD	no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected
*	two samples were positive for O and Asia1
VSV	Vesicular stomatitis virus

2.2. Overview and discussion of samples received and serotyping results

Overview highlighting changes in patterns of sample receipts and information gaps.

In 2005, FAO WRLFMD received 366 clinical samples or FMDV isolates, collected between 2003 and 2005, for virus isolation and characterisation (TABLE 2). Samples were collected in 21 countries located in Europe, Asia and Africa. European samples were collected in the Republic of Ireland and were negative for FMDV by several techniques. African FMDV isolates were collected in ten countries (Botswana, Burkina Faso, Cote d`Ivoire, Ghana, Kenya, Mali, Senegal, Sudan, Togo and Zambia) between 2003 and 2005. FMD viruses obtained from the Middle East and from southern Asia were collected in three countries (Saudi Arabia, Iran and Pakistan) between 2004 and 2005. Strains collected in southeast Asia between 2004 and 2005 were obtained from Hong Kong, Myanmar, Philippines, Thailand and Vietnam.

FMD virus types O, A, C, SAT 1, SAT 2 and Asia 1 were isolated at the WRLFMD from the above listed submissions. As usual, type O was the most prevalent identified serotype. All of these viruses were further characterised by partial genomic sequencing (complete VP1 gene). In addition, complete VP1 sequences were received from FGI ARRIAH, LVRI-China and Pakchong-Thailand Regional Laboratories for comparison to sequences compiled in WRLFMD database.
A selection of specimens was also further studied regarding their antigenic relationship to vaccine strains.

During the same year PANAFTOSA received a total of 53 clinical samples, collected between 2004 and 2005, material that was sent for additional virus characterisation (molecular and/or antigenic, including vaccine matching) (TABLE 2), as the primary isolation and characterization is carried out in the country of origin.
FMD virus types O and A and Vesicular Stomatitis Virus New Jersey and Indiana 1 were characterized at PANAFTOSA from the above listed submissions by partial genomic sequencing (complete VP1 gene of FMDV and partial NS gene of VSV), and antigenic characterization was carried out by Indirect Sandwich ELISA and/or Complement Fixation Test Subtyping was carried out by Complement Fixation Test and selected specimens were studied regarding their antigenic relationship to vaccine strain by r relationship and Expectancy of Protection (EPP) assay.

3. Genetic and antigenic typing of FMD virus isolates submitted to the Reference Laboratory during the year in question

3.1 Tabulated data on isolates typed genetically and antigenically

3.1.1. Summary of genetic typing (one table for each serotype)

FMDV isolate	**Region sequenced (bases)**	**Subtyping result**	**Reference for dendrogram**	
Serotype O				
O/HKN/13/2004	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/9/2005	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/10/2005	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/11/2005	VP1 (142)	O Cathay	Fig..5.5	WRLFMD
O/HKN/12/2005	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/13/2005	VP1 (142)	O Cathay	Fig..5.5	WRLFMD
O/HKN/14/2005	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/15/2005	VP1 (639)	O Cathay	Fig..5.5	WRLFMD
O/HKN/16/2005	VP1 (142)	O Cathay	Fig..5.5	WRLFMD
O/IRN/8/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.2	WRLFMD
O/IRN/9/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.2	WRLFMD
O/IRN/12/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.2	WRLFMD
O/MAI/1/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/MAI/2/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/MAI/3/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/MYA/4/2004	VP1 (639)	O SEA (Mya98)	Fig. 5.7	WRLFMD
O/MYA/1/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL

O/MYA/2/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/MYA/3/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/MYA/4/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/MYA/5/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/PAK/1/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/2/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/3/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/7/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/9/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/10/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/11/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/12/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PAK/13/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.3	WRLFMD
O/PHI/1/2005	VP1 (639)	O Cathay	Fig. 5.6	WRLFMD
O/PHI/2/2005	VP1 (639)	O Cathay	Fig. 5.6	WRLFMD
O/PHI/3/2005	VP1 (639)	O Cathay	Fig. 5.6	WRLFMD
O/SAU/4/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/5/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/6/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/7/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/8/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/9/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/10/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/11/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/12/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/13/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SAU/14/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.4	WRLFMD
O/SUD/1/2005	VP1 (639)	O EA-3	Fig. 5.1	WRLFMD
O/SUD/2/2005	VP1 (639)	O EA-3	Fig. 5.1	WRLFMD
O/SUD/3/2005	VP1 (639)	O EA-3	Fig. 5.1	WRLFMD
O/TAI/8/2004	VP1 (639)	O SEA (Mya98)	Fig. 5.7	WRLFMD
O/TAI/20/04R2*	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.7	TRRL
O/TAI/36/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/TAI/37/04*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/TOG/1/2004	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/TOG/1/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/TOG/3/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/TOG/4/2005	VP1 (639)	O WA	Fig. 5.1	WRLFMD
O/VIT/1/2005	VP1 (639)	O Cathay	Fig. 5.7	WRLFMD
O/VIT/3/2005	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.7	WRLFMD
O/VIT/4/2005	VP1 (639)	O SEA	Fig. 5.7	WRLFMD
O/VIT/1/05*	VP1 (639)	O Cathay	Fig. 5.7	TRRL
O/VIT/2/05*	VP1 (639)	O Cathay	Fig. 5.7	TRRL
O/VIT/3/05*	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.7	TRRL
O/VIT/4/05*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/VIT/5/05*	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.7	TRRL
O/VIT/6/05*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/VIT/7/05*	VP1 (639)	O Cathay	Fig. 5.7	TRRL
O/VIT/8/05*	VP1 (639)	O ME-SA (PanAsia)	Fig. 5.7	TRRL
O/VIT/9/05*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/VIT/10/05*	VP1 (639)	O SEA (Mya98)	Fig. 5.7	TRRL
O/Eldorado/MS/Bra/05 (4523-2)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4523-3)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4523-4)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4583-7)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA

O/Eldorado/MS/Bra/05 (4583-8)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4583-9)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4583-10)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4583-11)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4593-50058-2)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (4593-50058-3)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (814-4)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (815-3)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Eldorado/MS/Bra/05 (837-4)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Pichincha/Ecu/04 (050/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Pichincha/Ecu/04 (064/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Cotopaxi/Ecu/04 (067/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Los Ríos/Ecu/04 (071/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Carchi/Ecu/04 (072/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Los Ríos/Ecu/04 (074/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Esmeraldas/Ecu/04 (097/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Cotopaxi/Ecu/04 (099/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Imbabura/Ecu/04 (101/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Pichincha/Ecu/04 (106/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Trujillo/Ven/05 (21378)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Zulia/Ven/05 (21386 IBHK)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
O/Mérida/Ven/04 (21237/04)	VP1 (639)	O Euro-SA	Fig. 5. 17	PANAFTOSA
Serotype A				
A/IRN/32/2004	VP1 (636)	A Asia (Irn96)	Fig. 5.10	WRLFMD
A/IRN/33/2004	VP1 (639)	A Asia (Irn96)	Fig. 5.10	WRLFMD
A/IRN/1/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/2/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/4/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/5/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/7/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/10/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/13/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/14/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/16/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/IRN/17/2005	VP1 (636)	A Asia (Irn96)	Fig. 5.10	WRLFMD
A/IRN/18/2005	VP1 (639)	A Asia	Fig. 5.10	WRLFMD
A/KEN/1/2003	VP1 (639)	A Africa	Fig. 5.8	WRLFMD
A/KEN/2/2003	VP1 (639)	A Africa	Fig. 5.8	WRLFMD
A/LAO/36/2003	VP1 (636)	A Asia	Fig. 5.11	WRLFMD
A/MAI/4/2004	VP1 (639)	A Africa	Fig. 5.9	WRLFMD
A/TAI/6/2004	VP1 (636)	A Asia	Fig. 5.11	WRLFMD
A/TAI/9/2004	VP1 (636)	A Asia	Fig. 5.11	WRLFMD
A/TOG/9/2005	VP1 (639)	A Africa	Fig. 5.9	WRLFMD
A24/Bogotá/Cundinamarca/Col/05	VP1 (639)	A Euro- SA (A24)	Fig. 5. 18	PANAFTOSA
A/Apure/Ven/05 (21335)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Táchira/Ven/05 (21351)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Mérida/Ven/05 (21366-A)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Mérida/Ven/05 (21369)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Mérida/Ven/05 (21374)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Táchira/Ven/04 (20904)	VP1 (636)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Táchira/Ven/04 (21203)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Táchira/Ven/04 (21211)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Barinas/Ven/04 (21218)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA

A/Táchira/Ven/04 (21229)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Yaracuy/Ven/04 (21270)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
A/Barinas/Ven/04 (21283)	VP1 (639)	A Euro- SA	Fig. 5. 18	PANAFTOSA
Serotype C				
C/KEN/1/2004	VP1 (633)		Fig. 5.12	WRLFMD
Serotype Asia1				
Asia1/Armenia/2000	VP1 (611)		Fig. 5.16	ARRIAH
Asia1/JiangSu/CHA/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/WuXi/JS/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/YanQuing/BJ/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/SanHe/HeB/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/Zhangjiakou/HeB/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/JingNing/GS/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/TongRen/QH/China/2005	VP1 (633)		Fig. 5.16	LVRI
Asia1/Georgia/2000	VP1 (622)		Fig. 5.16	ARRIAH
Asia1/Georgia/2001	VP1 (625)		Fig. 5.16	ARRIAH
Asia1/HKN/1/2005	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/HKN/2/2005	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/HKN/3/2005	VP1 (633)		not shown	WRLFMD
Asia1/HKN/4/2005	VP1 (633)		not shown	WRLFMD
Asia1/HKN/5/2005	VP1 (633)		not shown	WRLFMD
Asia1/HKN/6/2005	VP1 (633)		not shown	WRLFMD
Asia1/HKN/7/2005	VP1 (633)		not shown	WRLFMD
Asia1/HKN/8/2005	VP1 (633)		not shown	WRLFMD
Asia1/IRN/25/2004	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/IRN/30/2004	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/IRN/31/2004	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/Mongolia/2005	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/PAK/2/2004	VP1 (633)		Fig. 5.16	WRLFMD
Asia1/Amursky/RUS/2005	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/Khabarovsk/RUS/2005	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/Prymorsky/RUS/2005	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/TAJ/1/2004*	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/TAJ/2/2004*	VP1 (633)		Fig. 5.16	ARRIAH
Asia1/TAJ/3/2004*	VP1 (633)		not shown	ARRIAH
Asia1/TAJ/4/2004*	VP1 (633)		not shown	ARRIAH
Asia1/TAJ/5/2004*	VP1 (633)		not shown	ARRIAH
Asia1/TAJ/6/2004*	VP1 (633)		not shown	ARRIAH
Serotype SAT1				
SAT1/KEN/1/2005	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/27/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/28/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/29/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/30/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/31/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/32/2004	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/1/2005	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD
SAT1/ZAM/2/2005	VP1 (663)	SAT1 NWZ	Fig. 5.13	WRLFMD

Serotype SAT2				
SAT2/BOT/1/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/2/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/3/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/4/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/5/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/6/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/7/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/BOT/8/2005	VP1 (648)		Fig. 5.15	WRLFMD
SAT2/KEN/5/2004	VP1 (648)		Fig. 5.14	WRLFMD
SAT2/KEN/6/2004	VP1 (648)		Fig. 5.14	WRLFMD
SAT2/KEN/8/2004	VP1 (648)		Fig. 5.14	WRLFMD
SAT2/KEN/9/2004	VP1 (648)		Fig. 5.14	WRLFMD
SAT2/KEN/10/2004	VP1 (648)		Fig. 5.14	WRLFMD
SAT2/KEN/11/2004	VP1 (648)		Fig. 5.14	WRLFMD
*, not a WRLFMD Ref. No.				
O/IRN/20/2005		in progress		
O/IRN/21/2005		in progress		
A/IRN/22/2005		in progress		
O/IRN/23/2005		in progress		
A/IRN/24/2005		in progress		
A/IRN/25/2005		in progress		
A/IRN/26/2005		in progress		
A/IRN/27/2005		in progress		
A/IRN/28/2005		in progress		
A/IRN/29/2005		in progress		
A/IRN/30/2005		in progress		
A/IRN/31/2005		in progress		
O/PAK/14/2005		in progress		
O/PAK/15/2005		in progress		
O/PAK/16/2005		in progress		
O/PAK/17/2005		in progress		
O+Asia1/PAK/19/2005		in progress		
O/PAK/20/2005		in progress		
O/PAK/21/2005		in progress		
O+Asia1/PAK/22/2005		in progress		
O/PAK/24/2005		in progress		
O/PAK/25/2005		in progress		
O/Pakistan vaccine		in progress		

3.1.2. Summary of antigenic typing

FMDV isolate	**Vaccines matched**	**r value by ELISA**	**r value by CF50**	**r value by VNT**
Serotype O				
O Afg 2003/16	O Manisa			>1.0
O Bhu 2004/39	O Manisa			0.5
O Bhu 2004/40	O Manisa			0.44
O Eri 2004/1	O Manisa			0.43

O Eri 2004/2	O Manisa		0.36
O Eri 2004/3	O Manisa		0.04
O Hkn 2005/9	O Manisa		0.4
	O 3039		0.5
O Hkn 2005/15	O Manisa		0.33
	O Taiwan 3/97		0.21
	O 3039		0.51
O Irn 2004/6	O Manisa		0.47
O Irn 2004/15	O Manisa		0.62
O Irn 2004/20	O Manisa		0.47
O Irn 2005/12	O Manisa		>1.0
O Irn 2005/20	O Manisa		>1.0
O Irn 2005/23	O Manisa		>1.0
O May 2004/2	O Manisa	1	0.65
	3039	1	
	4147	0.61	
	O Phi 95	1	
	O Tai 189/87	0.86	
	O TNN 24/84	0.71	
O May 2004/3	O Manisa	>1.0	0.5
	3039	1	
	4147	0.71	
	O Phi 95	>1.0	
	O Tai 189/87	1	
	O TNN 24/84	0.86	
O Mai 2005/1	O Manisa		>1.0
O Mya 2004/1	O Manisa		0.6
O Mya 2004/2	O Manisa		0.69
O Pak 2005/3	O Manisa		0.81
O Pak 2005/7	O Manisa		0.65
O Pak 2005/9	O Manisa		>1.0
O Pak 2005/12	O Manisa		>1.0
	O TNN 24/84	0.75	
O Pak 2005/14	O Manisa		>1.0
O Pak 2005/16	O Manisa		>1.0
O Pak 2005/17	O Manisa		>1.0
O Pak 2005/24	O Manisa		>1.0
O Pak 2005/25	O Manisa		>1.0
O Phi 2004/4	O Manisa	1	
	3039	1	
	4147	0.61	
	O Phi 95	1	
	O Tai 189/87	1	
	O TNN 24/84	0.86	
O Phi 2004/5	O Manisa		0.26
O Phi 2004/6	O Manisa	1	
	3039	1	
	4147	0.68	
	O Phi 95	1	

	O Tai 189/87	1		
	O TNN 24/84	0.86		
O Phi 2004/7	O Manisa			0.21
	O Taiwan 3/97			0.30
O Phi 2005/1	O Manisa			0.43
O Phi 2005/2	O Manisa			0.35
O Phi 2005/3	O Manisa			0.3
O Sau 2005/4	O Manisa			0.78
O Sau 2005/8	O Manisa			0.68
O Sau 2005/9	O Manisa			0.95
O Sau 2005/10	O Manisa			0.83
O Sau 2005/14	O Manisa			>1.0
O Sud 2005/1	O Manisa			0.97
O Sud 2005/3	O Manisa			0.83
O Rwa 2004/2	O Manisa			0.69
O Rwa 2004/3	O Manisa			0.56
O Tan 2004/1	O Manisa			0.65
O Tan 2004/2	O Manisa			0.21
O Tan 2004/14	O Manisa			0.72
O Tai 2004/6	ASK	0.25		
	118/87	1		
O Tai 2004/8	O Manisa			>1.0
	189/87	1		
O Tai 2004/9	ASK	0.22		
	118/87	0.43		
O Tog 2004/1	O Manisa			0.69
O Tog 2005/1	O Manisa			0.55
O Tur 2000/5	O Manisa			>1.0
O Tur 2002/12	O Manisa			>1.0
O Tur 2003/3	O Manisa			>1.0
O Tur 2003/7	O Manisa			>1.0
O Uga 2004/4	O Manisa			0.43
O Uga 2004/5	O Manisa			0.19
O Uga 2004/6	O Manisa			0.28
O Uga 2004/18	O Manisa			0.3
O Vit 2005/3	O Manisa			0.59
O Zam 2000/2	O Manisa			0.6
O/Eldorado/MS/Bra/05(4523-2)	O1 Campos		0.62	
O/Eldorado/MS/Bra/05(4583-9)*	O1 Campos		0.56	
O/Eldorado/MS/Bra/05(4583-10)	O1 Campos		0.41	
O/Eldorado/MS/Bra/05(4583-11)	O1 Campos		0.48	
O/Eldorado/MS/Bra/05(814-7)	O1 Campos		0.31	
O/Eldorado/MS/Bra/05(837-2)	O1 Campos		0.45	

* Antigenic match of O/Eldorado/MS/Bra/05(4583-9) to vaccine strain O1 Campos studied by r relationship and Expectancy of Protection (EPP) assay.

EPP Value	**By VNT:**	**by ELISA:**
30 days post vaccination	87.96	82.91
30 days post revaccination	98.59	99.29

Serotype A

A Bhu 2003/7	A Irn96		0.24
	A 5925		0.55
	A Sau 95		0.47
	A22 Irq 24/64		0.22
	A Irn 2001		0.41
A Bhu 2003/40	A Irn96		0.31
	A 5925		0.55
	A Sau 95		0.4
	A22 Irq 24/64		0.15
	A Irn 2001		0.25
A Irn 1999/22	A 5925	0.61	
	A Irn 2001	0.61	
A Irn 2001/32	A22 Irq 24/64		0.18
	A24 Cruzeiro		0.05
	A May97		0.06
	A 5925	<0.1	0.45
	A Sau95		0.2
	A Irn 2001	<0.1	0.1
A Irn 2002/6	A Irn96		0.85
	A22 Irq 24/64		>1.0
	A24 Cruzeiro		0.05
	A May97		0.1
	A 5925	0.43	
	A Irn 2001	<0.1	
A Ken 2003/1	A22 Irq 24/64		0.26
	A15 Tai 1/60		0.1
	A24 Cruzeiro		0.07
	A Irn96		0.09
	A May97		0.05
	A Irn87		0.15
A Ken 2003/2	A22 Irq 24/64		0.28
	A15 Tai 1/60		0.15
	A24 Cruzeiro		0.08
	A Irn96		0.09
	A May97		0.07
	A Irn87		0.14
A Irn 2003/5	A22 Irq 24/64		0.13
	A24 Cruzeiro		No neutralisation
	A Irn96		0.14
	A May97		0.12
	A Tur 14/98	>1.0	
	A 5925	0.22	

	A Irn 2001	<0.1	
A Irn 2003/7	A22 Irq 24/64		0.13
	A24 Cruzeiro		0.02
	A Irn96		0.09
	A May97		0.06
	A 5925	0.23	0.12
	A Sau95		0.06
	A Irn 2001	<0.1	0.03
A Irn 2003/10	A22 Irq 24/64		0.18
	A24 Cruzeiro		0.07
	A Irn96		0.39
	A May97		0.14
	A Sau95		0.04
	A 5925	0.5	
	A Irn 2001	0.38	0.17
A Irn 2003/41	A22 Irq 24/64		0.33
	A24 Cruzeiro		0.05
	A Irn96		0.35
	A May97		0.06
	A 5925	0.61	
	A Irn 2001	0.4	
A Irn 2004/7	A22 Irq 24/64		0.67
	A24 Cruzeiro		0.05
	A Irn96		0.11
	A May97		0.09
	A Irn87		0.12
	A 5925	0.61	0.39
	A Sau95		0.13
	A Irn 2001	<0.1	
A Irn 2004/32	A22 Irq 24/64		0.16
	A24 Cruzeiro		No neutralisation
	A Irn96		0.4
	A May97		No neutralisation
	A Irn87		No neutralisation
	A 5925	0.43	0.27
	A Sau95		0.13
	A Irn 2001	0.25	0.1
A Irn 2004/33	A Irn96		>1.0
	A May97		0.16
	A Irn87		0.12
	A 5925		No neutralisation
	A Sau95		0.12
A Irn 2005/1	A24 Cruzeiro		0.08
	A Irn96		0.06
	A May97		0.14
	A Irn87		0.16
	A Irn 2001		0.09

A Irn 2005/4	A22 Irq 24/64		>1.0
	A24 Cruzeiro		0.06
	A Irn96		0.11
	A May97		0.14
	A Irn87		0.16
	A 5925	0.53	0.43
	A Sau95		0.18
	A Irn 2001	<0.2	0.07
A Irn 2005/5	A22 Irq 24/64		0.71
	A24 Cruzeiro		0.08
	A Irn96		0.1
	A May97		0.07
	A Irn87		0.17
	A 5925	0.61	0.51
	A Sau95		0.18
	A Irn 2001	<0.2	
A Irn 2005/7	A22 Irq 24/64		31
	A Irn96		0.05
A Irn 2005/17	A22 Irq 24/64		0.07
	A Irn96		0.19
A Irn 2005/22	A22 Irq 24/64		0.45
	A Irn96		0.05
A Irn 2005/28	A22 Irq 24/64		0.41
	A Irn96		0.05
A Irn 2005/29	A22 Irq 24/64		0.45
A Lao 2003/36	A22 Irq 24/64		0.13
	A15 Tai 1/60		0.26
	A24 Cruzeiro		0.06
	A Irn96		0.2
	A May97		0.36
	A Irn87		0.25
A Mai 2004/4	A22 Irq 24/64		0.55
	A Irn96		0.09
A May 2004/3	A Irn96		0.35
	A May97		0.44
	A Irn87		0.22
	A 5925		0.37
	A Sau95		0.19
A May 2004/4	A Irn96		0.2
	A May97		0.37
	A Irn87		0.17
	A 5925		0.05
	A Sau95		0.09
	A Irn96		0.05
A Pak 2003/9	A22 Irq 24/64		0.1
	A 5925		0.6
	A Sau95		0.31
	A Irn 2001		0.26
A Pak 2003/11	A22 Irq 24/64		0.1
	A 5925		0.51
	A Sau95		0.36

	A Irn 2001		0.23
A Pak 2003/77	A24 Cruzeiro		0.11
	A Irn96		0.18
	A May97		0.11
	A Irn87		0.22
A Syr 2002/5	A Tur 14/98	>1.0	
A Tai 2004/6	A24 Cruzeiro		0.07
	A Irn96		0.17
	A May97		0.26
	A Irn87		0.25
	ASK	0.25	
	118/87	1	
A Tai 2004/9	A24 Cruzeiro		0.05
	A Irn96		0.16
	A May97		0.26
	A Irn87		0.29
	ASK	0.22	
	118/87	0.43	
A Tur 2002/14	A Tur 14/98	>1.0	
A Tur 2003/5	A22 Irq 24/64		0.14
	A Sau95		0.13
	A Irn 2001		0.18
A Tog 2005/9	A22 Irq 24/64		0.21
	A Irn96		0.09
A Vit 2004/4	A24 Cruzeiro		0.1
	A Irn96	0.5	0.16
	A May97	>1.0	0.28
	A Irn87	<0.2	0.23
	A 5925		0.15
	A Sau95		0.11
	Tai ASK S9	0.7	
	A Ind 17/82	0.3	
	A Sau 23/86	0.9	
	A22 Irq 24/64	>1.0	
A Vit 2004/5	A Irn96	0.4	
	A May97	>1.0	
	A Irn87	0.9	
	Tai ASK S9	0.9	
	A Ind 17/82	<0.1	
	A Sau 23/86	0.9	
	A22 Irq 24/64	0.4	

Asia1

Asia1 Hkn 2005/1	As Ind 8/79		0.35
	As Shamir		0.58
Asia1 Hkn 2005/2	As Ind 8/79		0.39
	As Shamir		0.87
Asia1 Ind 1980/10	As Shamir	0.45	
	WBN 117/87	0.48	

Asia1 Ind 1981/15	As Shamir	1	
	WBN 117/87	1	
Asia1 Irn 2004/10	As Ind 8/79		0.13
	As Shamir		0.91
Asia1 Irn 2004/30	As Ind 8/79		0.58
	As Shamir		>1.0
Asia1 Irn 2004/31	As Ind 8/79		0.62
	As Shamir		0.52
Asia1 Pak 2003/67	As Ind 8/79		0.16
	As Shamir		0.55
Asia1 Pak 2003/76	As Ind 8/79		0.11
	As Shamir		0.48
Asia1 Pak 2004/1	As Ind 8/79		0.13
	As Shamir	>1.0	0.74
	WBN 117/87	1	
Asia1 Pak 2004/2	As Ind 8/79	>1.0	0.12
	As Shamir	>1.0	0.39
	WBN 117/87		
Serotype C			
C Ken 2004/1	C Oberbayern		0.28

3.2. Overview and discussion of typing results

3.2.1. FMDV serotype O

From Africa, FMD viruses of serotype O collected in Sudan belonged to the EA-3 topotype and were closely related to those collected in 2004 (Fig 5.1). Isolates of the same serotype collected in Mali and Togo were related and belonged to the West Africa (WA) topotype (Fig 1). Isolates collected in Sudan and in Togo showed a good matching with O Manisa by VNT.

From Southern Asia, FMD viruses of serotype O were collected in Iran, Pakistan and Saudi Arabia. Isolates collected in Iran and Pakistan belonged to the PanAsia strain (ME-SA topotype) and were closely related to those collected in Nepal and Bhutan in 2004 (Fig. 5.2 and 5.3). Isolates of serotype O collected in Saudi Arabia belonged to the PanAsia strain and were closely related to those collected in Iran in 2004 (Fig 5.4). Isolates from these countries were shown to have a very good matching with O Manisa by VNT.

From East Asia, FMD viruses of serotype O collected in Hong Kong and the Philippines belonged to the Cathay topotype (Fig 5.5 and Fig 5.6). Some of the isolates collected in Vietnam also belonged to this topotype. Genetic differences could be observed between isolates collected in different countries. However genetic relationships were demonstrated between isolates collected in each country and those collected in 2003 and 2004 in the same place (Fig. 5.7).
Other isolates of serotype O collected in Myanmar, Thailand and Vietnam belonged to various topotypes and sub-lineages (Fig 5.7). Isolates collected in Myanmar in 2004 belonged exclusively to the SEA topotype (Mya98 strain) and were closely related to isolates collected in 1999, 2000 and 2002 in the same country. Vietnamese viruses collected in the same year belonged either to the ME-SA topotype (PanAsia strain) or to the SEA topotype (Mya98

strain). These isolates were very closely related to isolates collected in 2004 and 2005 in Thailand.
Isolates belonging to the Cathay topotype collected in Philippines were shown to have a good match to O Manisa, 3039, 4147, Phi 95, Tai 189/87and O TNN 24/84 by ELISA and those collected in Hong Kong had a moderate match to O Manisa and 3039 by VNT. Other isolates of serotype O collected in Myanmar, Thailand and Vietnam had a good matching by ELISA and /or VNT to O Manisa, 189/87 and moderate to O ASK.

From South America, The type O isolate responsible for the outbreaks recorded in the FMD-free with vaccination area in Mato Grosso do Sul, Brazil belonged to the Euro-SA topotype, being endogenous from 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 (Fig 5.17). It was subtyped as O1 (Fig 6). Vaccine matching gave satisfactory results by r relationships and Expectancy of Protection (EPP) (by VNT and ELISA), with vaccines containing strain O1 Campos.
The other FMD viruses of type O characterized in the continent were from episodes in still endemic countries (Ecuador and Venezuela), all belonging to the Euro-SA topotype, although from different lineage than that causing the emergence in the Southern Cone (Fig 5.17)

3.2.2. FMDV serotype A

From Africa, Kenyan isolates of serotype A were identical to each other and very closely related to one of the Kenyan vaccine strains, K5/80, with percentage identity values of 99.69% (2 nucleotide difference) (Fig. 5.8). FMDV isolates collected in Mali and Togo were related to isolates collected in Cameroon in 2000 (Fig 5.9). By VNT, Isolates collected in Kenya had a moderate match to A22 IrQ 24/64 and poor to A15 Tai 1/60, A24 Cruzeiro, A Irn 96, A May 97 and A Irn 87. Isolates collected In Mali and Togo had a good and poor match to A22 Irq 24/64, respectively. Both of these isolates had a poor match to A Irn96.

From Southern Asia, FMD viruses collected in Iran belonged to the Asia topotype (Irn 96 strain or unnamed sublineages) (Fig 5.10). All these isolates were closely related to those collected in the same country in 2003 and 2004. By VNT and for most of the isolates, isolates collected in Iran in 2005 had a good match to A22 Irq 24/64 and A5925 but a poor match to A Irn 96, A May 97, A Irn 87 and A Irn 2001.

From East Asia, isolates were collected in Lao PDR and Thailand in 2003 and 2004, respectively. These viruses were closely related to those collected in Southeast Asia (Fig 5.11). The FMDV isolate of serotype A from Lao PDR was closely related to isolates collected in Malaysia and Thailand in 2003 and 2004, respectively. All isolates of type A collected in Thailand in 2004, except one, were closely related to each other and to some collected in the same country in 2003. By Elisa, isolates collected in Vietnam had a very good matching to A May 97, A Irn 87, ASK, A Ind 17/82, A Sau 23/86 and A22 Irq 24/64. By VNT, isolates collected in Malaysia, Thailand and Vietnam good to poor matching to A May 97, A Irn 96 and A5925.

From South America, occurrence of FMDV Type A was recorded in Colombia, specifically in Bogotá, Department of Cundinamarca. No outbreaks have been confirmed in this area since September 2002 (twenty-nine months). A precise characterization of the agent was undertaken and it was found to have a high level of homology with the A24 Cruzeiro reference strain, Fig. 5.18, matching at 638 out of the 639 nucleotides. As a result of laboratory testing and

epidemiological investigations carried out around the outbreak and in in-contact farms, the likelihood of a field origin has been ruled out and it was assumed that the outbreak was caused by a laboratory virus strain.

The other FMDV type A characterized in the continent were from episodes in a still endemic country (Venezuela), and all isolates were placed within the Euro-SA cluster (Fig 5.18)

3.2.3. FMDV serotype C

FMDV of serotype C was collected in Kenya in 2004. This isolate appeared to be very closely related (99.84%; 1 nucleotide difference) to the Kenyan vaccine strain, K267/67 and to previous outbreaks that country in 1983 and 1996 (Fig. 5.12). By VNT a weak match was shown to C Oberbayern.

3.2.3. FMDV serotype SAT1 and SAT2

SAT1 isolates collected in Zambia in 2005 were very closely related to isolates collected in the same country in 2004 (Fig 5.13). This shows that this outbreak is not yet under control. A SAT1 virus collected in Kenya, was not closely related to any other SAT 1 virus (Fig. 5.13).

SAT 2 isolates collected in Kenya belonged to two different sublineages (Fig. 5.14). Two FMDV isolates were very closely related to the Kenya vaccine strain, K65/82 (99.54 and 99.69 % nt identity, respectively). The others were closely related to viruses isolated from outbreaks of FMDV in Tanzania and Malawi in 2004. SAT2 viruses collected in Botswana were closely related (Fig 5.14) to an FMDV isolate collected in African buffalo in the same country in 1998 (not shown on phylogenetic tree) supporting the supposition that this outbreak has probably an origin in wildlife.

3.2.4. FMDV serotype Asia1

Asia1 serotype remained restricted to Asia.
Viruses belonging to five different sublineages are circulating in Asia (Fig 5.15):
-One FMDV isolate of serotype Asia 1 collected in Iran was closely related to those collected in Iran and Afghanistan in 2001
-Other FMDV of serotype Asia 1 collected in Iran were closely related to viruses collected in Pakistan between 2002 and 2005, Tajikistan in 2004 and Hong Kong in 2005.
- FMD viruses collected in India in 2004 belonged to a unique sub-lineage.
- Finally, FMDV isolates collected in Myanmar were related to viruses collected in Myanmar or Thailand a few years earlier.
The Asia 1 virus responsible for outbreaks in China and Russia were also closely related to each other (less than 0.79% difference) and to viruses from India (Tamil Nadu) isolated in 1980-81 (1.42-1.74%). It can be suspected that these outbreaks are vaccine related, although Indian viruses from 1980-81 do not match with any known vaccine strains of Asia 1.
FMDV isolates collected in Mongolia were closely related to isolates collected in China and Russia between May and July 2005. By VNT and/or ELISA it appears that Asia 1 Shamir should provide a good coverage. Some isolates collected in Pakistan, Iran and Hong Kong showed a good match by ELISA to Asia 1 Shamir and A Ind 8/79. However by VNT, isolates from these countries have shown a better match to Asia 1 Shamir than to Asia 1 Ind 8/79. Isolates collected in India in 1980 and 1981 that are closely related to viruses responsible the outbreaks in Russia and China had a good match to Asia 1 Shamir and WBN 117/87.

4. Overall conclusions

FMDV is still active in many parts of the world. An improvement of the global surveillance for FMD has occurred this year. Different reasons can explain this observation such as the existence of projects on FMD funded by FAO or other organisations in different parts of the world and also by the good collaborations between several FMD laboratories (WRL FMD, FGI ARRIAH, BVI, Pakchong RRL, Lanzhou, VRI). However, the situation in the Middle East remains a concern because a very low number of clinical samples were submitted in 2005 from this area.

Serotype O remains the most prevalent serotype. FMDV of serotypes A and SAT show the highest degree of genetic and antigenic variability. In 2005, the spread of Asia 1 in Asia and the confirmation of serotype C in Africa were the two main novelties.

The epidemic of FMD serotype Asia 1 was in reality caused by viruses that belong to five different sublineages. It has become increasingly clear that China has a key role in the control of the spread in Asia.

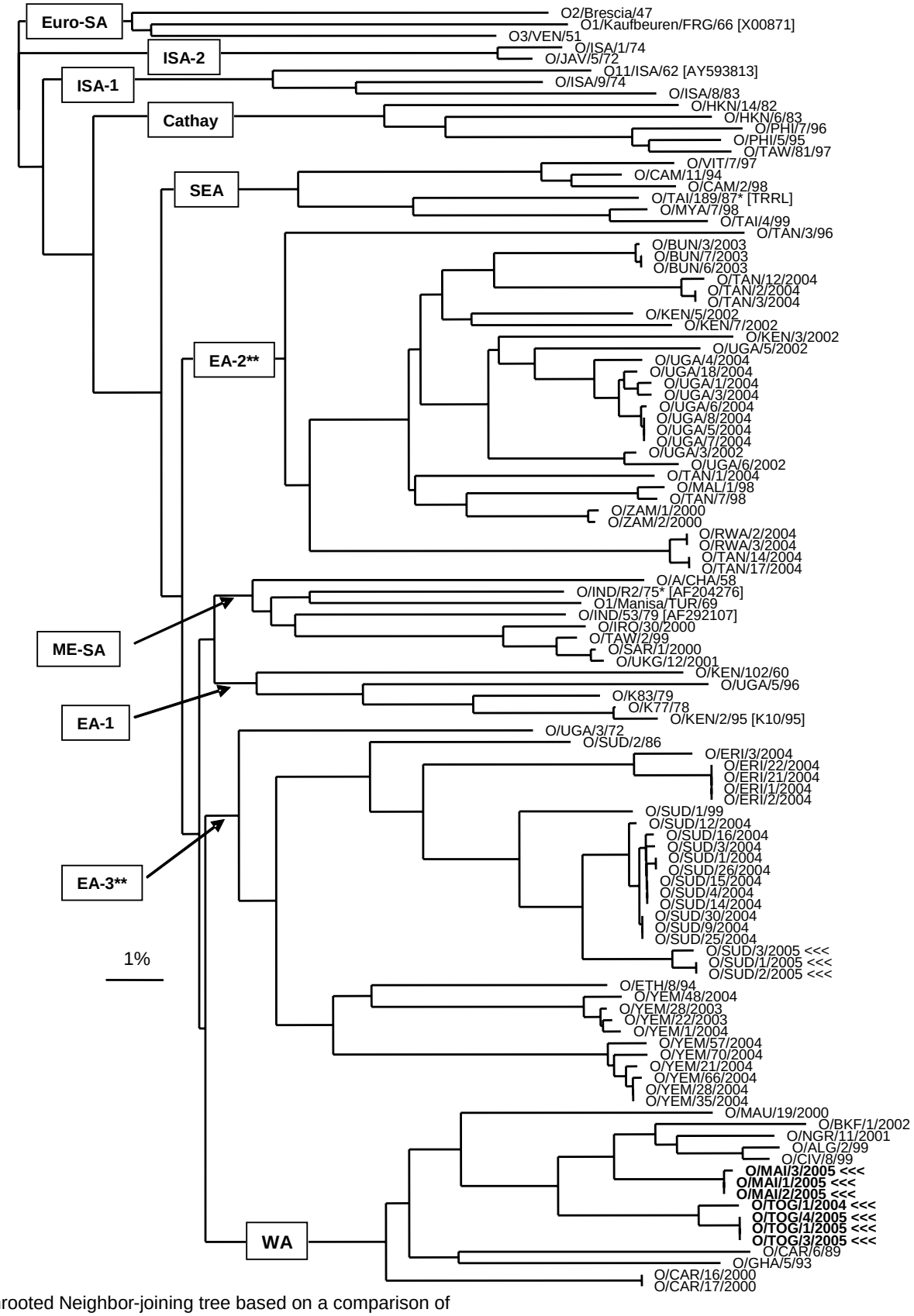
The occurrence of serotype C in Kenya in 2004 was confirmed and the isolate was closely related to a vaccine strain. The report of type C in Pakistan in 2004 was not confirmed by analysing samples detected positive in this country. The infrequent occurrence of serotype C and the relatedness of the Kenyan isolate to a vaccine strain raises the question of whether it would be pertinent to globally cease vaccination against this serotype (except in areas where wild-type viruses are proved to be circulating, e.g. Brazil).

Based on VNT and ELISA assays, O Manisa and Asia1 Shamir remain very appropriate as vaccine strains to protect against most field isolates. For serotype A, different vaccine strains are necessary to provide a full coverage. It is noticeable that some recent isolates collected in Iran gave a good matching to A22 Iraq 24/64. Vaccine matching studies carried out with FMDV strains circulating in South America indicated that strains O1 Campos, A24 Cruzeiro and C3 Indiana l remain appropriate as vaccine strains to protect against field isolates.

Global surveillance will be improved by continuing efforts to solicit sample submissions, however, the cost and difficulties of sending infectious goods by air remains a considerable constraint. Efforts to improve the global surveillance must be pursued by supporting financially the coordination of reference laboratories for FMD such as the OIE/FAO network of reference laboratories for FMD.

5. Appendix of dendrograms

Fig. 5.1. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Africa (Mali, Sudan and Togo)



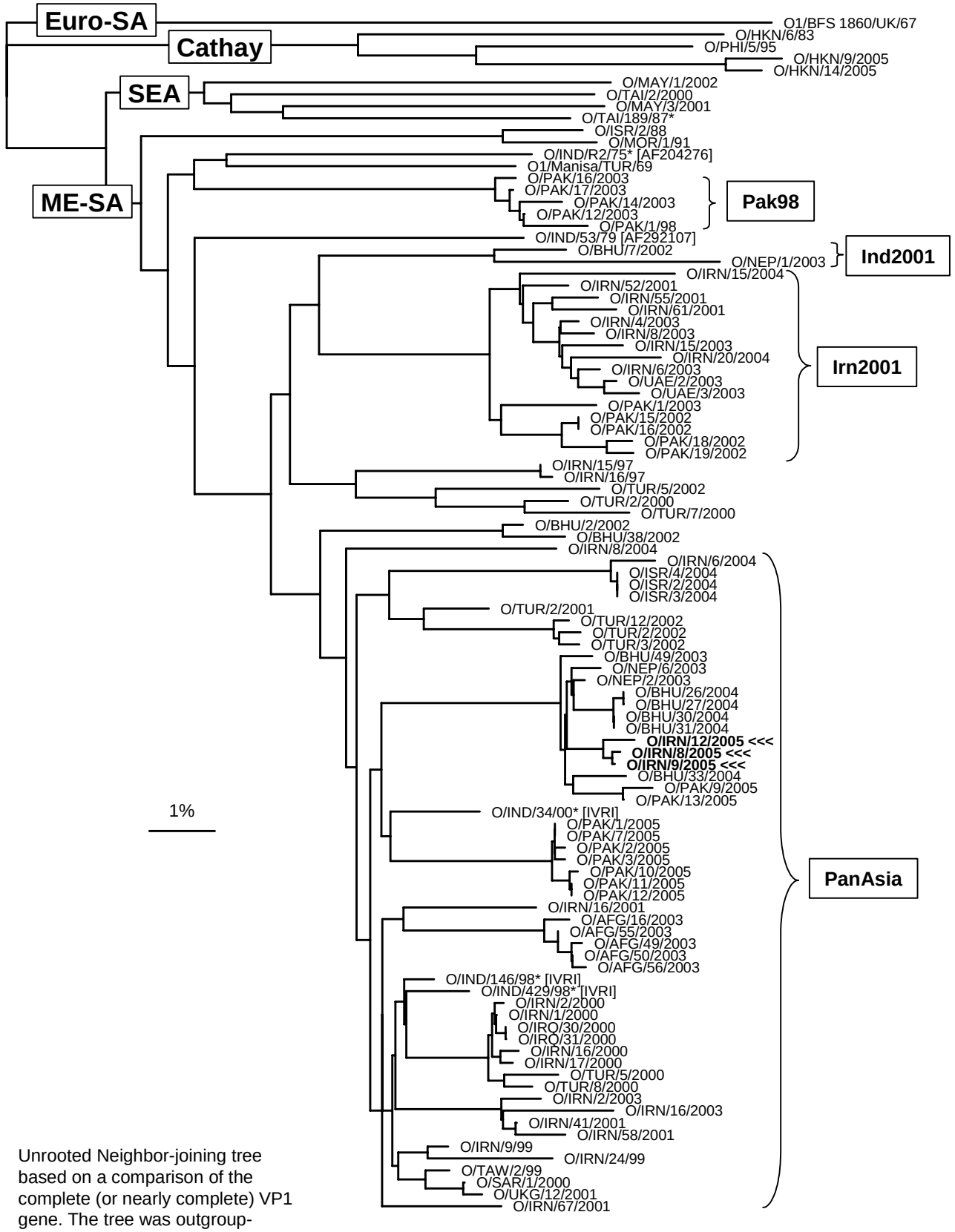
Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (~639 nt). The tree was outgroup-rooted using the Euro-SA topotype sequences.

* Not a WRLFMD Ref. No.

** proposed new topotypes

N.J. Knowles R. J. Midgley & J.-F. Valarcher, 10 October 2005

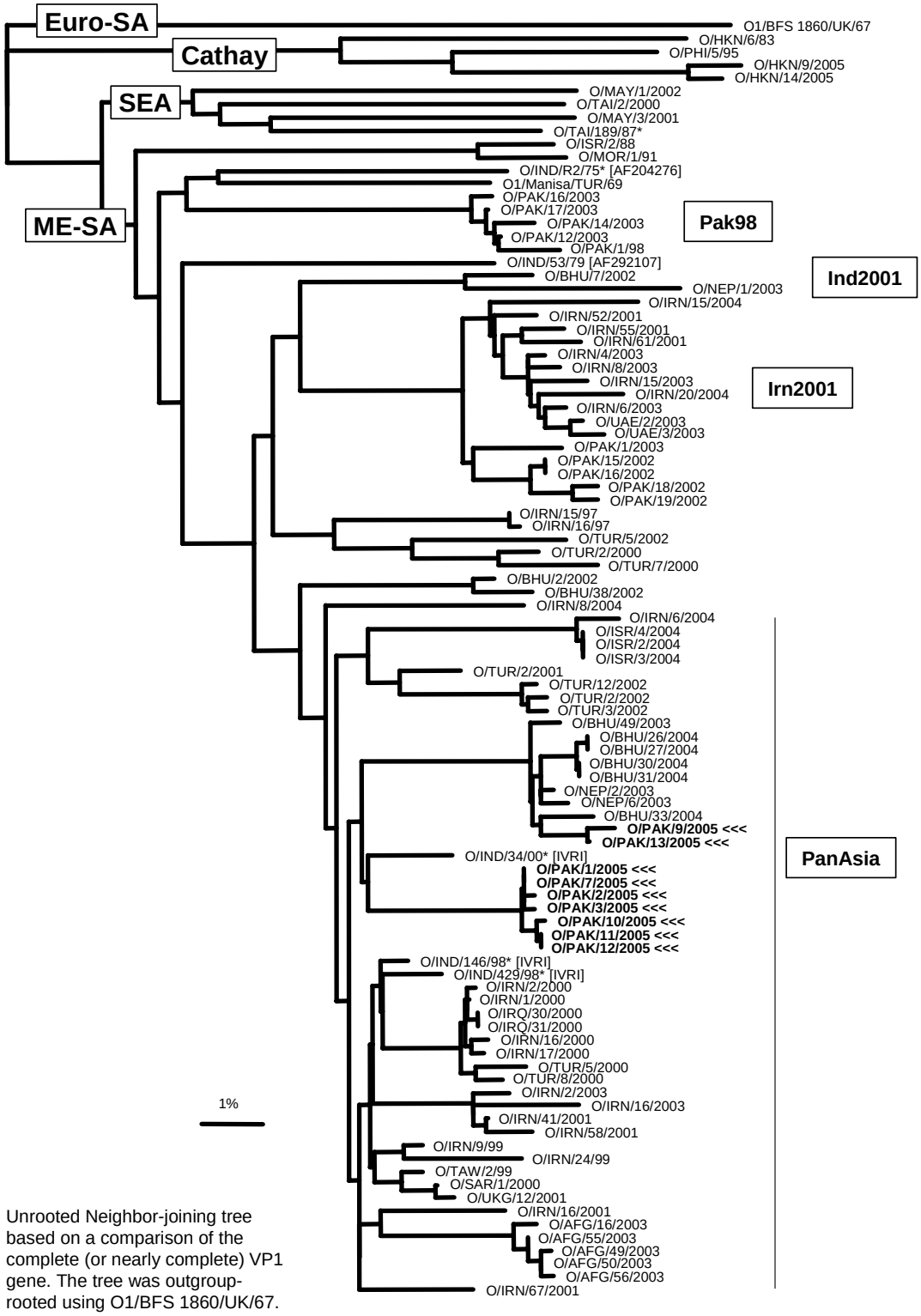
Fig. 5.2. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Iran



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

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 10 October 2005

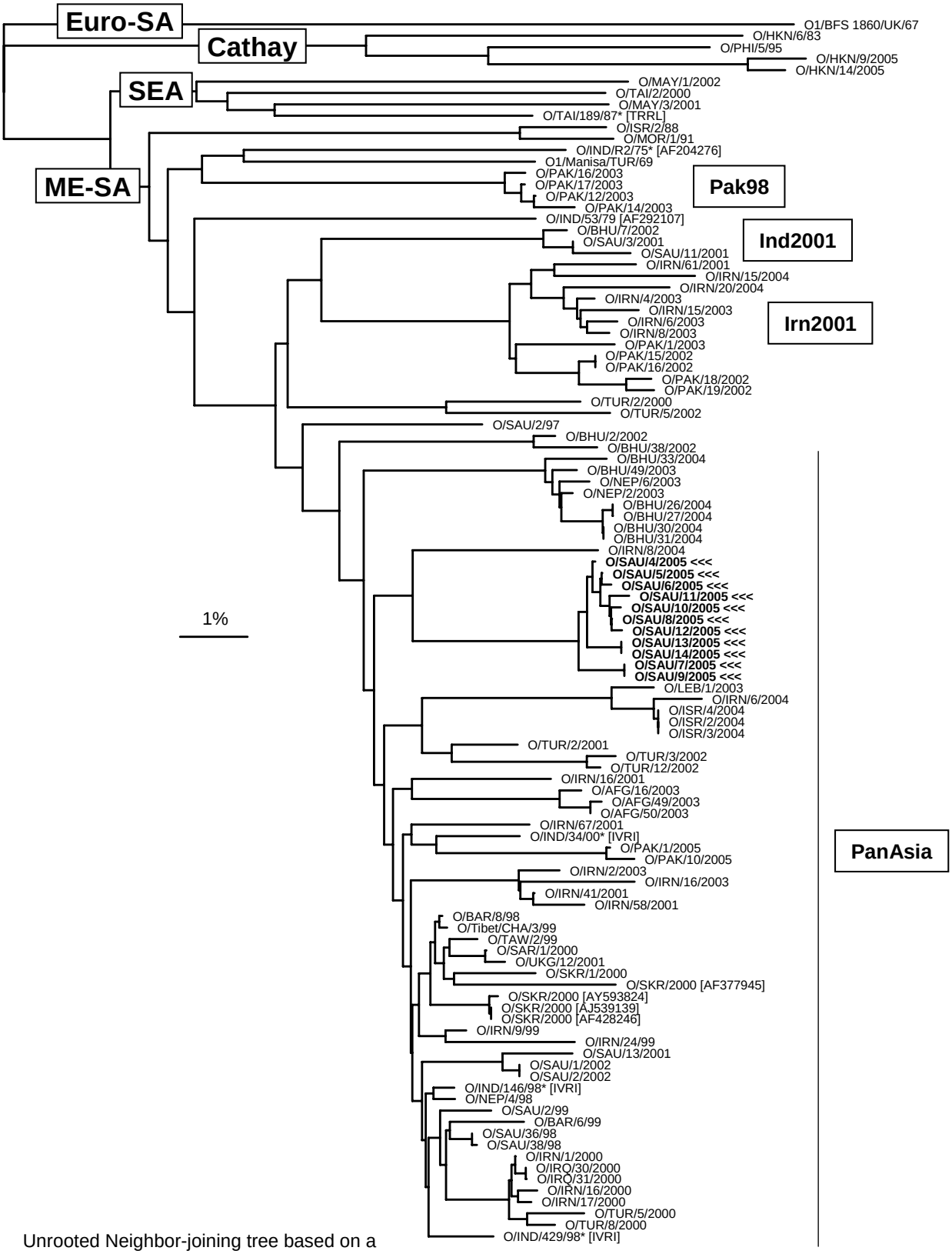
Fig. 5.3. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Pakistan



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

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 22 June 2005

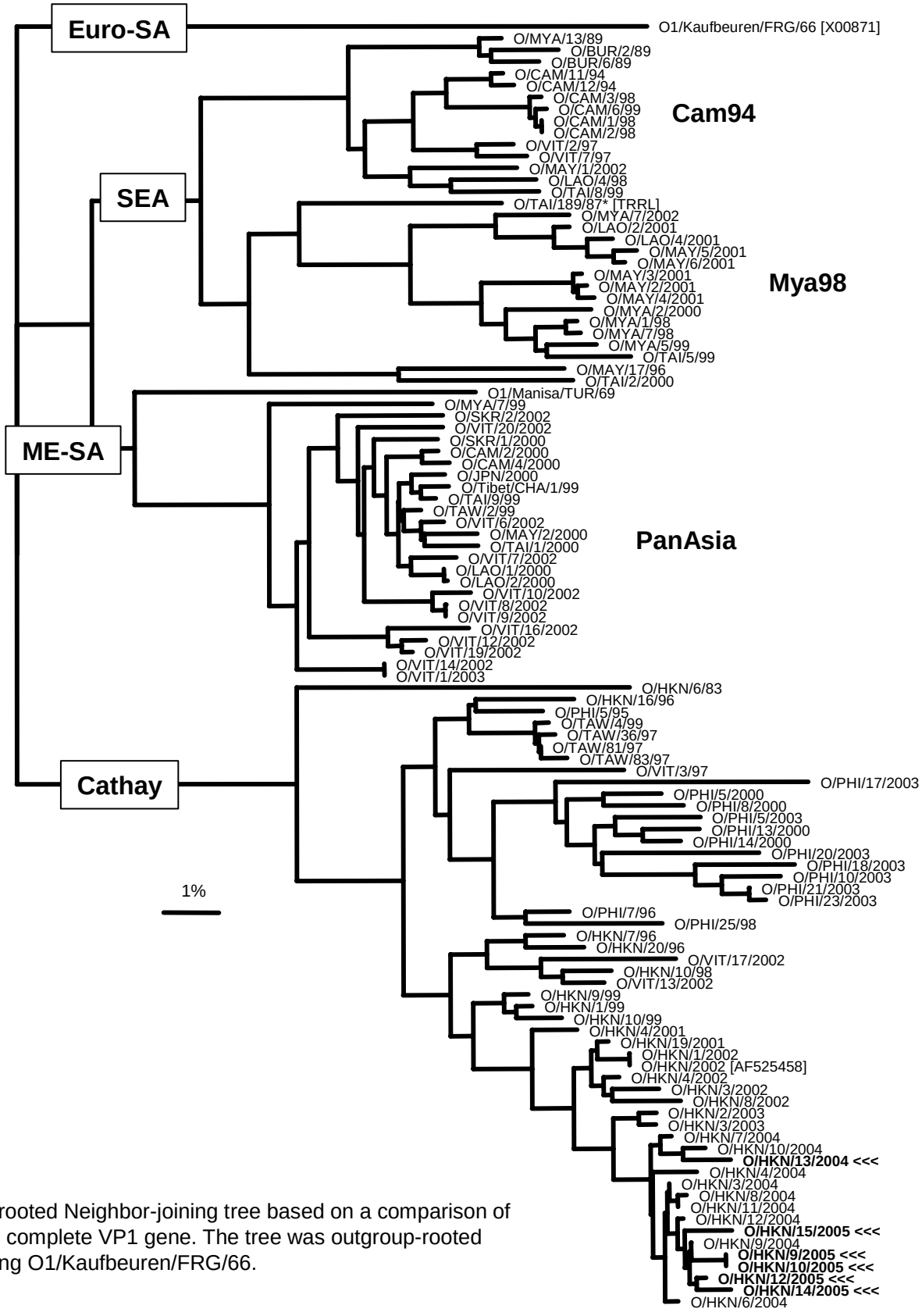
Fig. 5.4. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Saudi Arabia.



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.

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 5 September 2005

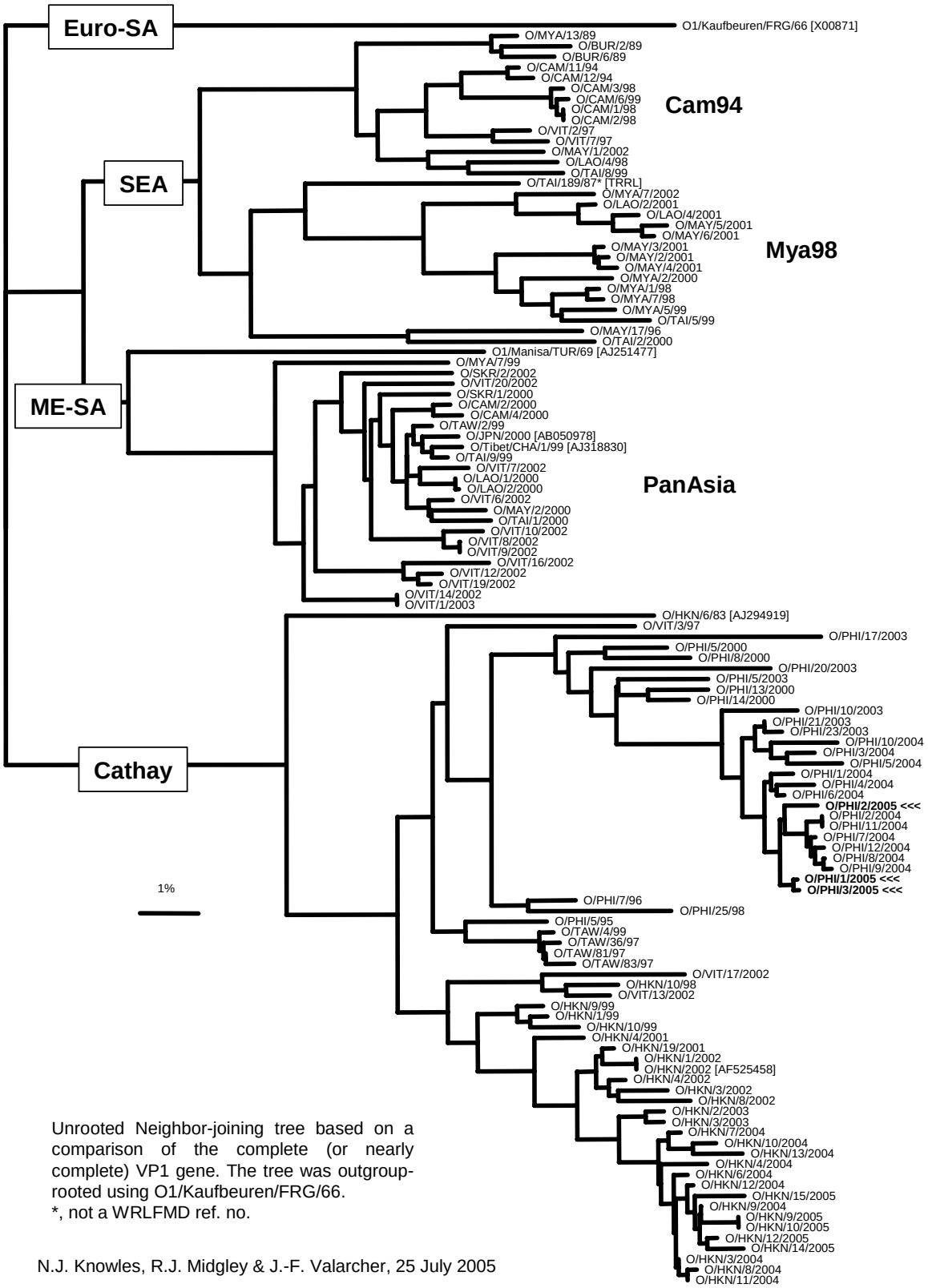
Fig. 5.5. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Hong Kong.



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using O1/Kaufbeuren/FRG/66.

N.J. Knowles, P.R. Davies, R.J. Midgley & J.-F. Valarcher, 7 June 2005

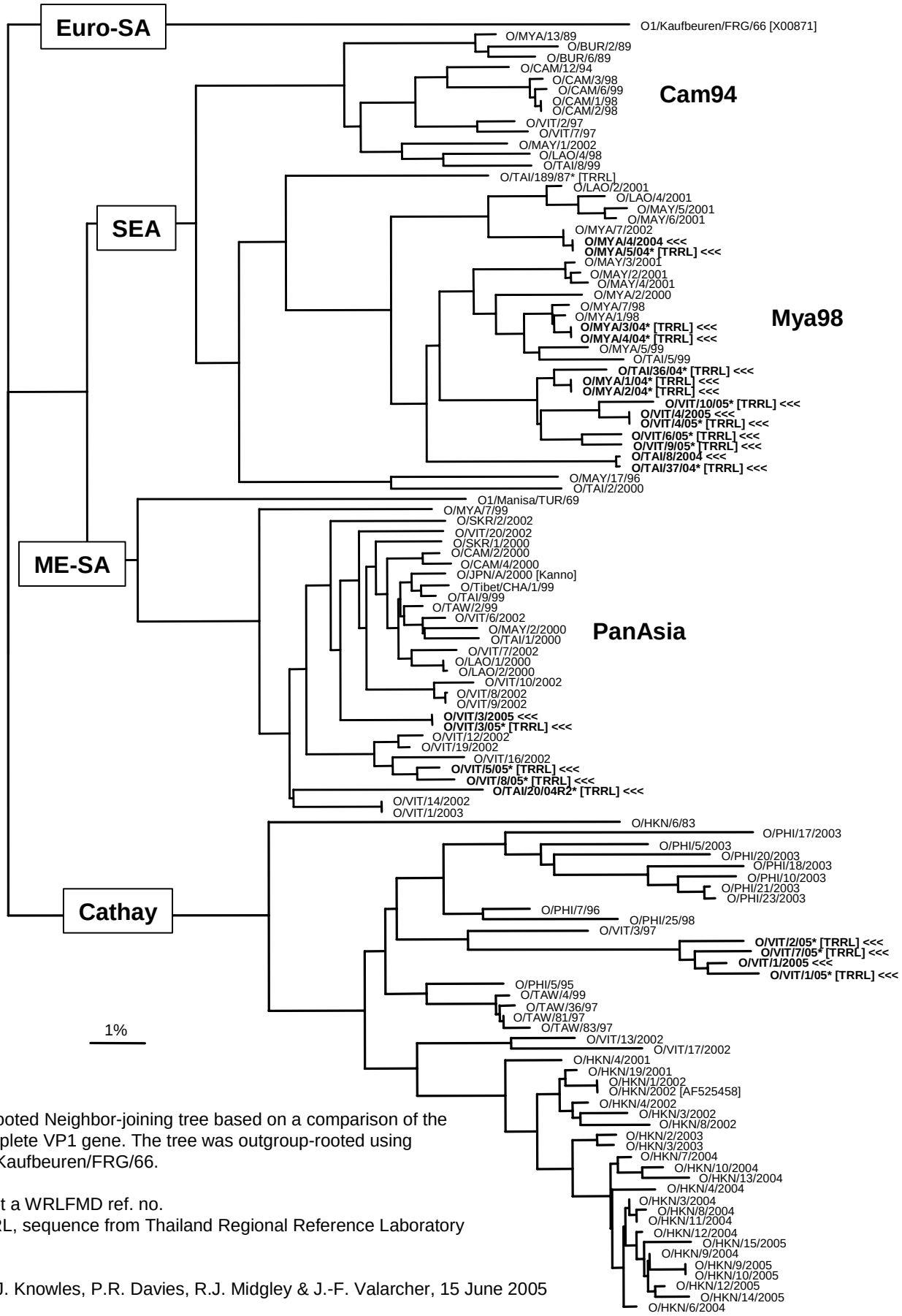
Fig. 5.6. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Philippines.



Unrooted Neighbor-joining tree based on a comparison of the complete (or nearly complete) VP1 gene. The tree was outgroup-rooted using O1/Kaufbeuren/FRG/66.
*, not a WRLFMD ref. no.

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 25 July 2005

Fig. 5.7 Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in Thailand, Myanmar and Vietnam. Some of these sequences have been supplied by Pakchong RRL for FMD.

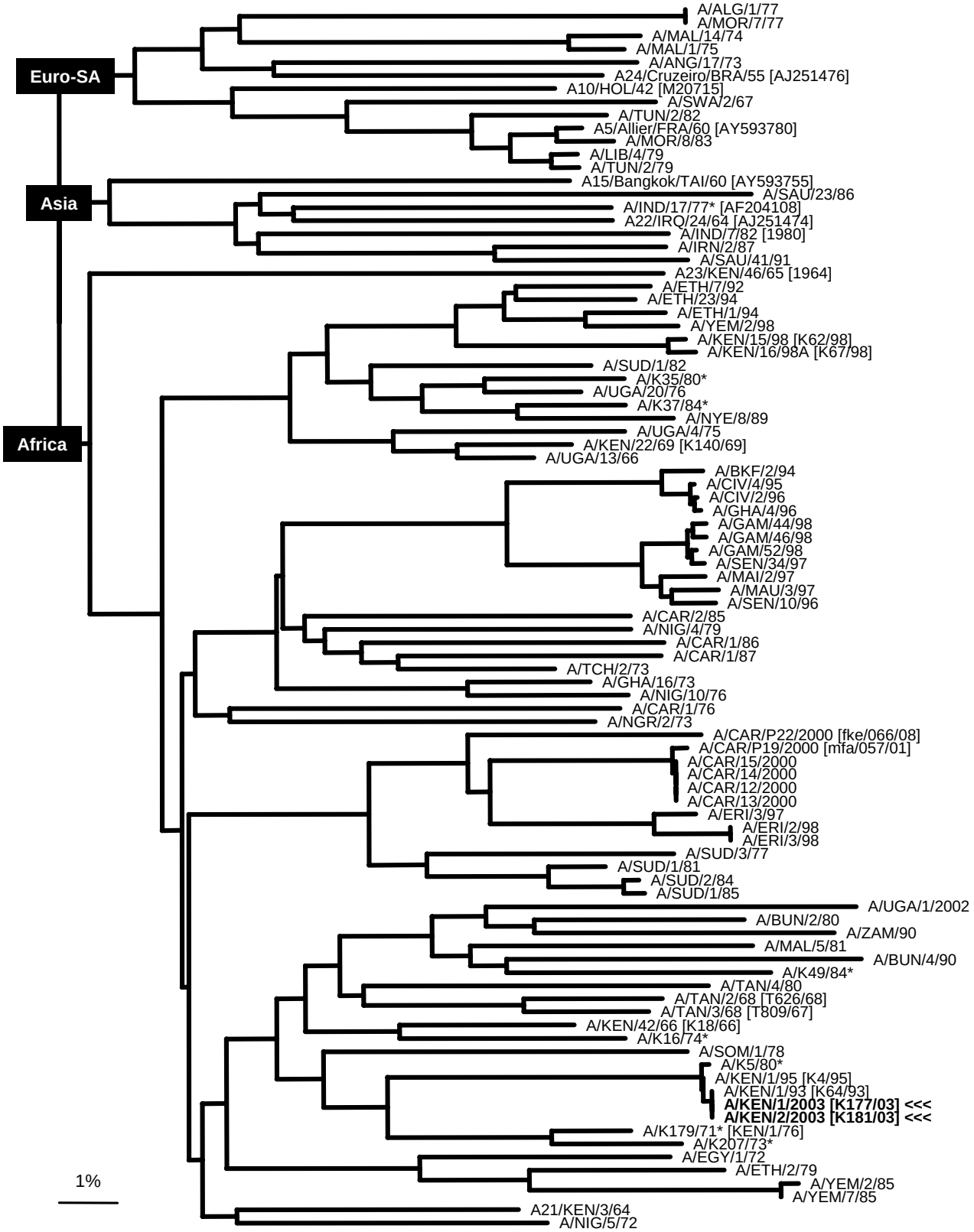


Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene. The tree was outgroup-rooted using O1/Kaufbeuren/FRG/66.

* Not a WRLFMD ref. no.
TRRL, sequence from Thailand Regional Reference Laboratory

N.J. Knowles, P.R. Davies, R.J. Midgley & J.-F. Valarcher, 15 June 2005

Fig. 5.8. Neighbor-joining tree comparing the complete VP1-coding sequences of type A FMDV collected in Kenya.



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

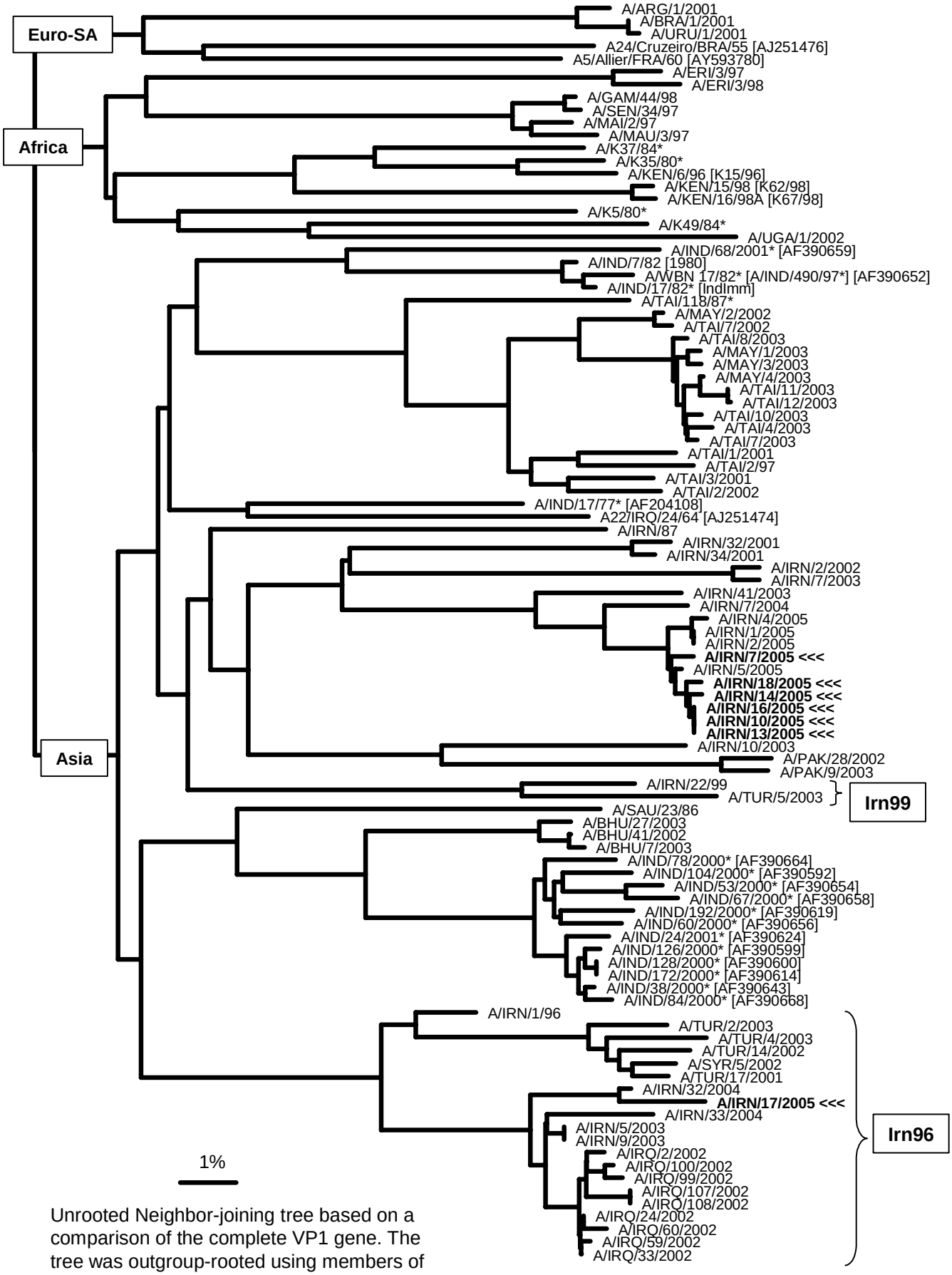
N.J. Knowles, P.R. Davies, R.J. Midgley & J.-F. Valarcher, 15 February 2005

Fig. 5.9. Neighbor-joining tree comparing the complete VP1-coding sequences of type A FMDV collected in Togo and Mali.

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

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 10 October 2005

Fig. 5.10. Neighbor-joining tree comparing the complete VP1-coding sequences of FMDV serotype A collected in Iran



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

N.J. Knowles, R.J. Midgley & J.-F. Valarcher, 10 October 2005

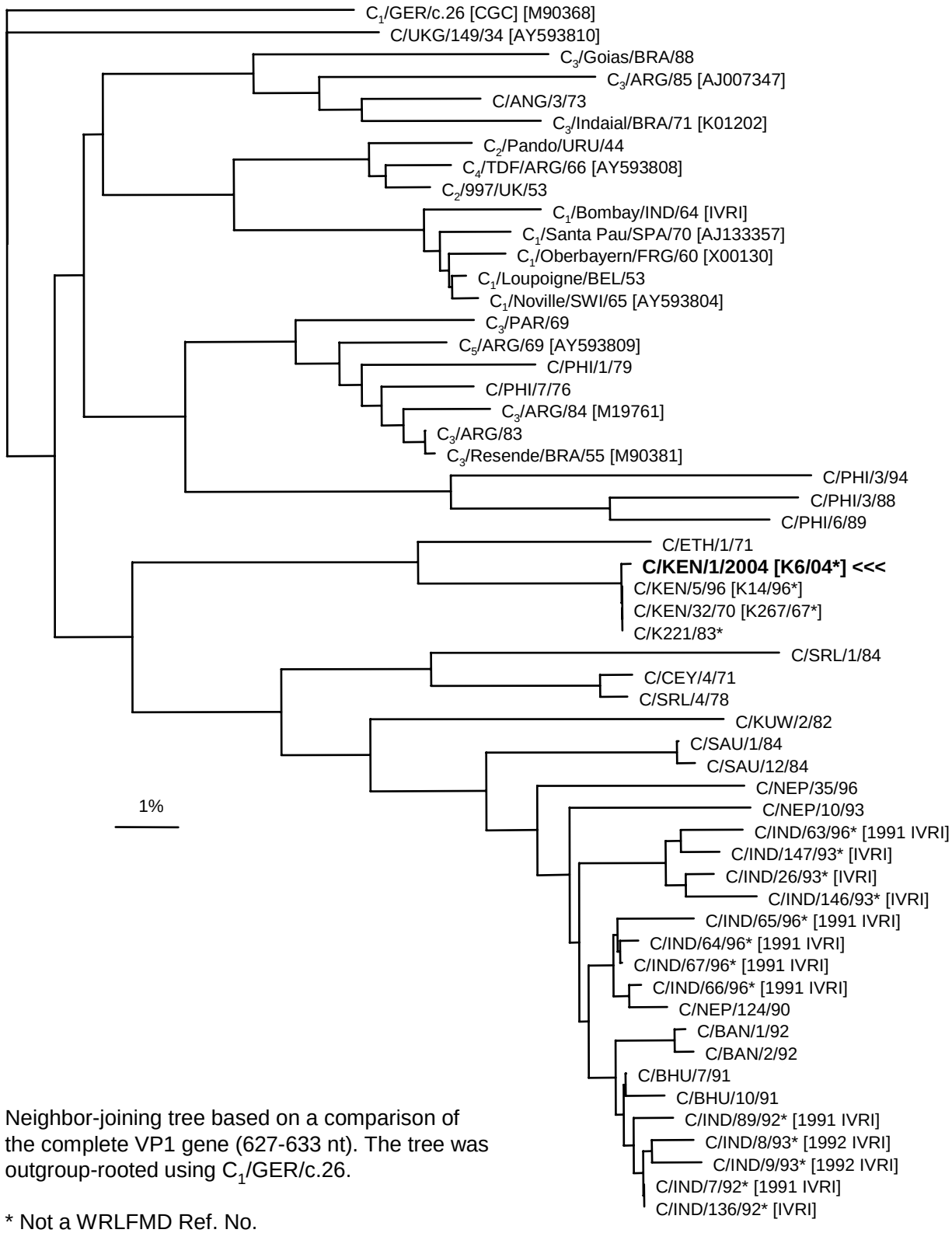
Fig. 5.11. Neighbor-joining tree comparing the complete VP1-coding sequences of type A FMDV collected in Lao PDR and Thailand.

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

* Not a WRLFMD ref. no.
TRRL, sequence from Thailand Regional Reference Laboratory

N.J. Knowles, P.R. Davies, R.J. Midgley & J.-F. Valarcher, 15/06/2005

Fig. 5.12. Neighbor-joining tree comparing the complete VP1-coding sequences of type C FMDV collected in Kenya.

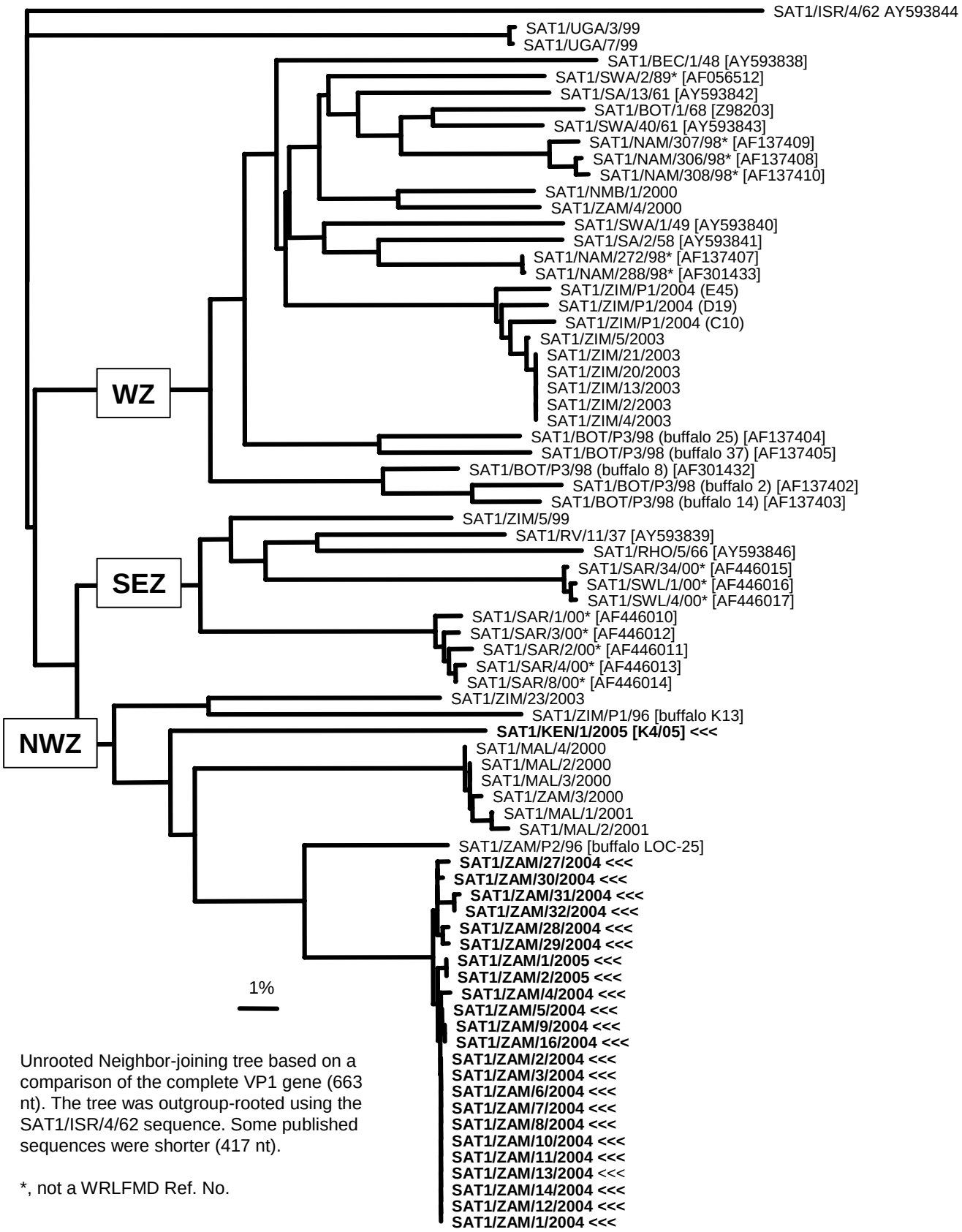


Neighbor-joining tree based on a comparison of the complete VP1 gene (627-633 nt). The tree was outgroup-rooted using C_1/GER/c.26.

* Not a WRLFMD Ref. No.

N.J. Knowles, R.J. Midgley, P.R. Davies and J.-F. Valarcher, 22 March 2005

Fig. 5.13. Neighbor-joining tree comparing the complete VP1-coding sequences of type SAT1 FMDV collected in Kenya and Zambia.

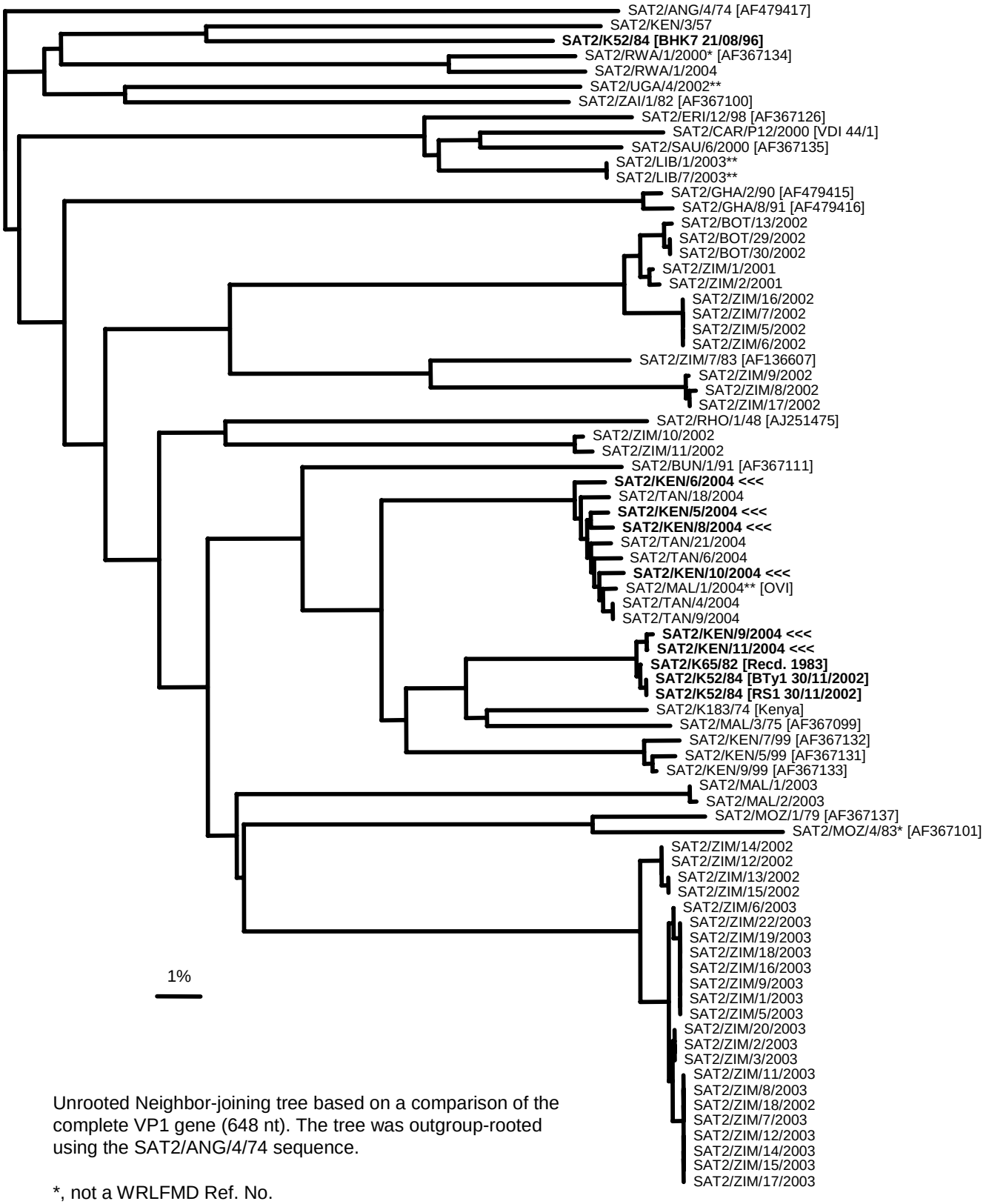


Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (663 nt). The tree was outgroup-rooted using the SAT1/ISR/4/62 sequence. Some published sequences were shorter (417 nt).

*, not a WRLFMD Ref. No.

N.J. Knowles, R.J. Midgley and J.-F. Valarcher, 13 September 2005

Fig. 5.14. Neighbor-joining tree comparing the complete VP1-coding sequences of type SAT2 FMDV collected in Kenya.

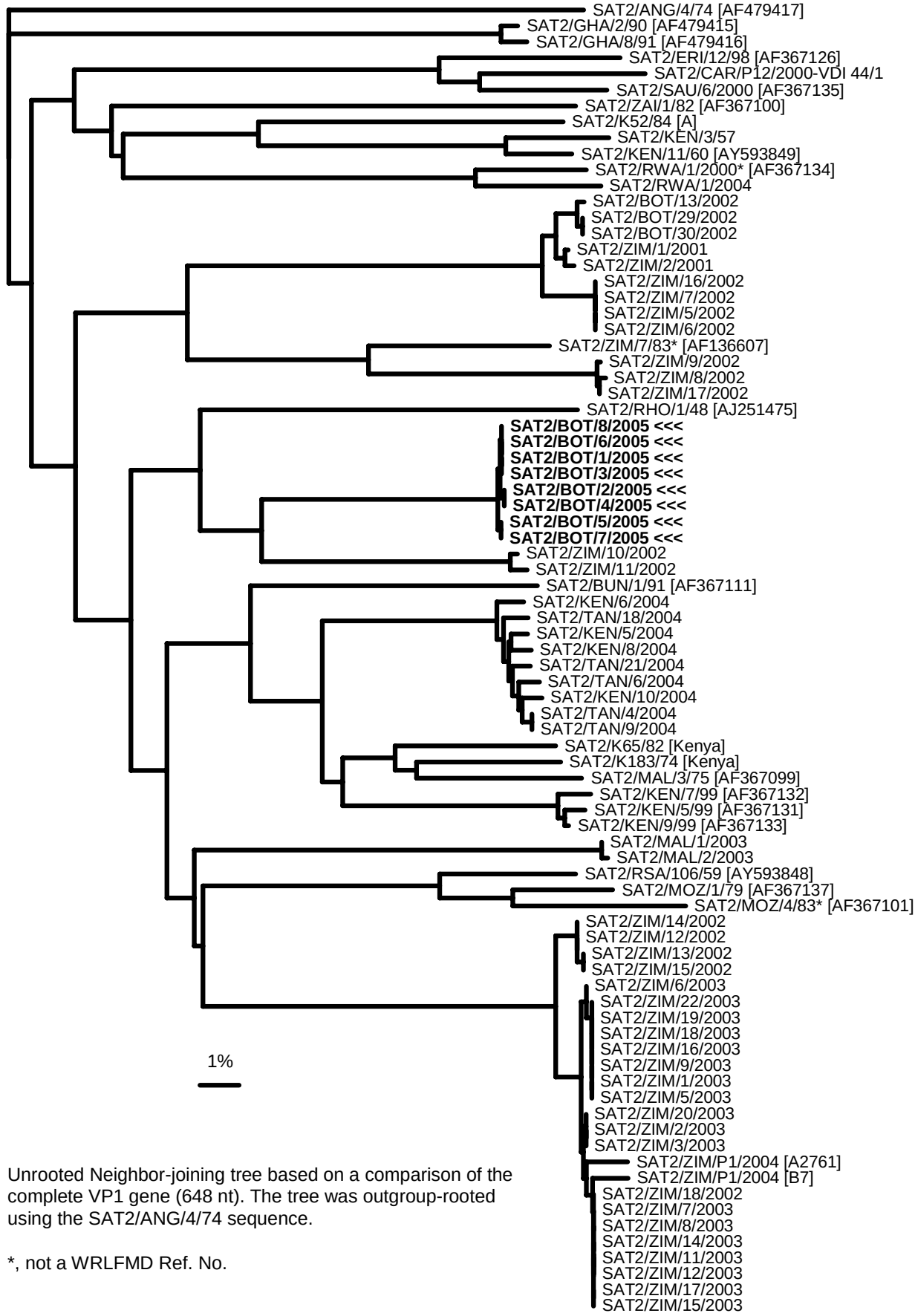


Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (648 nt). The tree was outgroup-rooted using the SAT2/ANG/4/74 sequence.

*, not a WRLFMD Ref. No.
**, Some sequences were shorter (384 to 418 nt).

N.J. Knowles, P.R. Davies, R.J. Midgley and J.-F. Valarcher, 22 March 2005

Fig. 5.15. Neighbor-joining tree comparing the complete VP1-coding sequences of type SAT2 FMDV collected in Botswana.

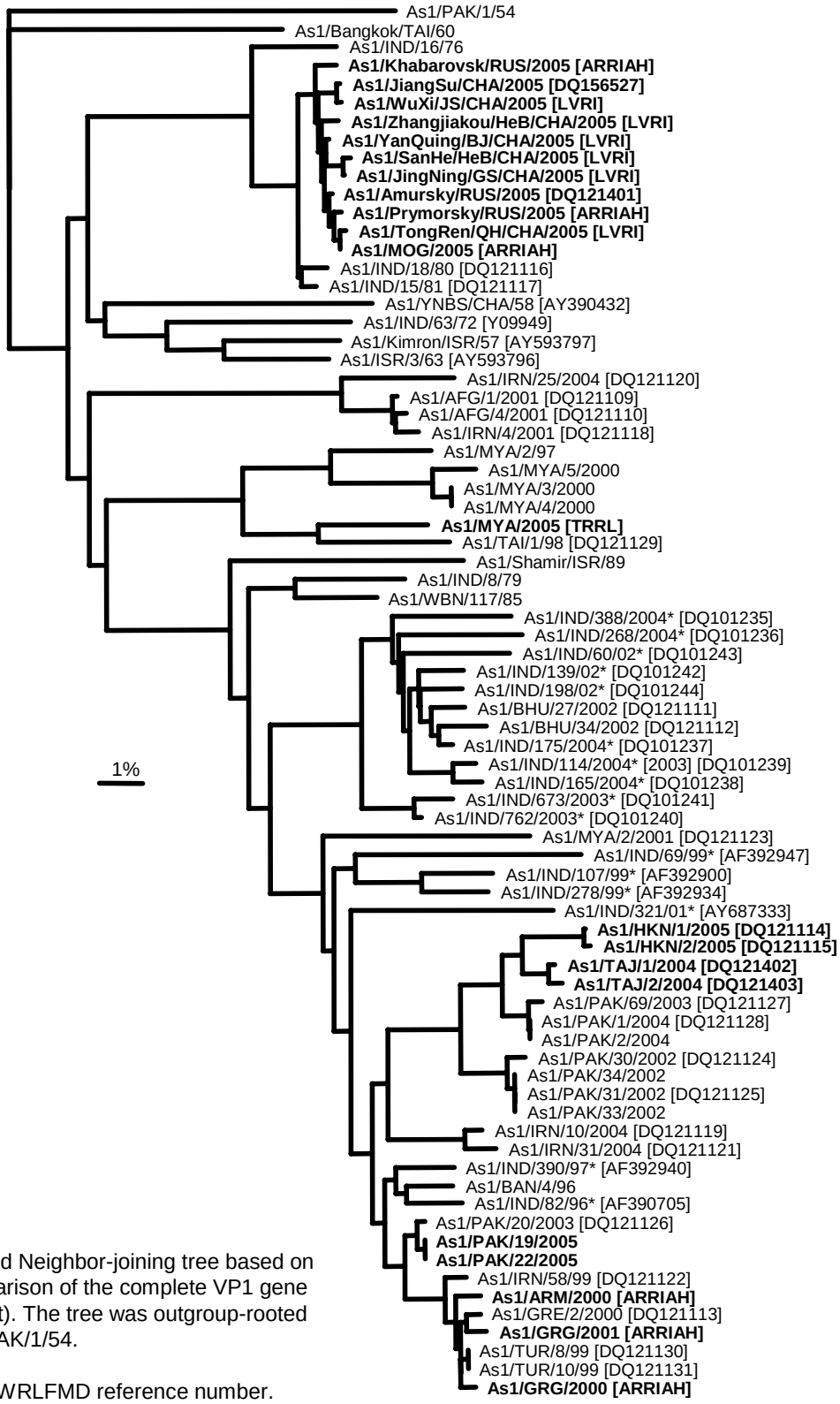


Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (648 nt). The tree was outgroup-rooted using the SAT2/ANG/4/74 sequence.

*, not a WRLFMD Ref. No.

N.J. Knowles, R.J. Midgley and J.-F. Valarcher, 12 September 2005

Fig. 5.16. Neighbor-joining tree comparing the complete VP1-coding sequences of type Asia1 FMDV collected in Afghanistan, China, Hong Kong, India, Iran, Myanmar Pakistan and Russia. Some of Sequence have been provided by FG ARRIAH (Mongolia and Russia), LVI (China), Pakchong RRL (Myanmar), Plum Island Animal Disease Center (Afghanistan) and PDFMD (India)



Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (~633 nt). The tree was outgroup-rooted using PAK/1/54.

* Not a WRLFMD reference number.

N.J. Knowles & J.-F. Valarcher, 28 October 2005

Fig. 5.17. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in South America.

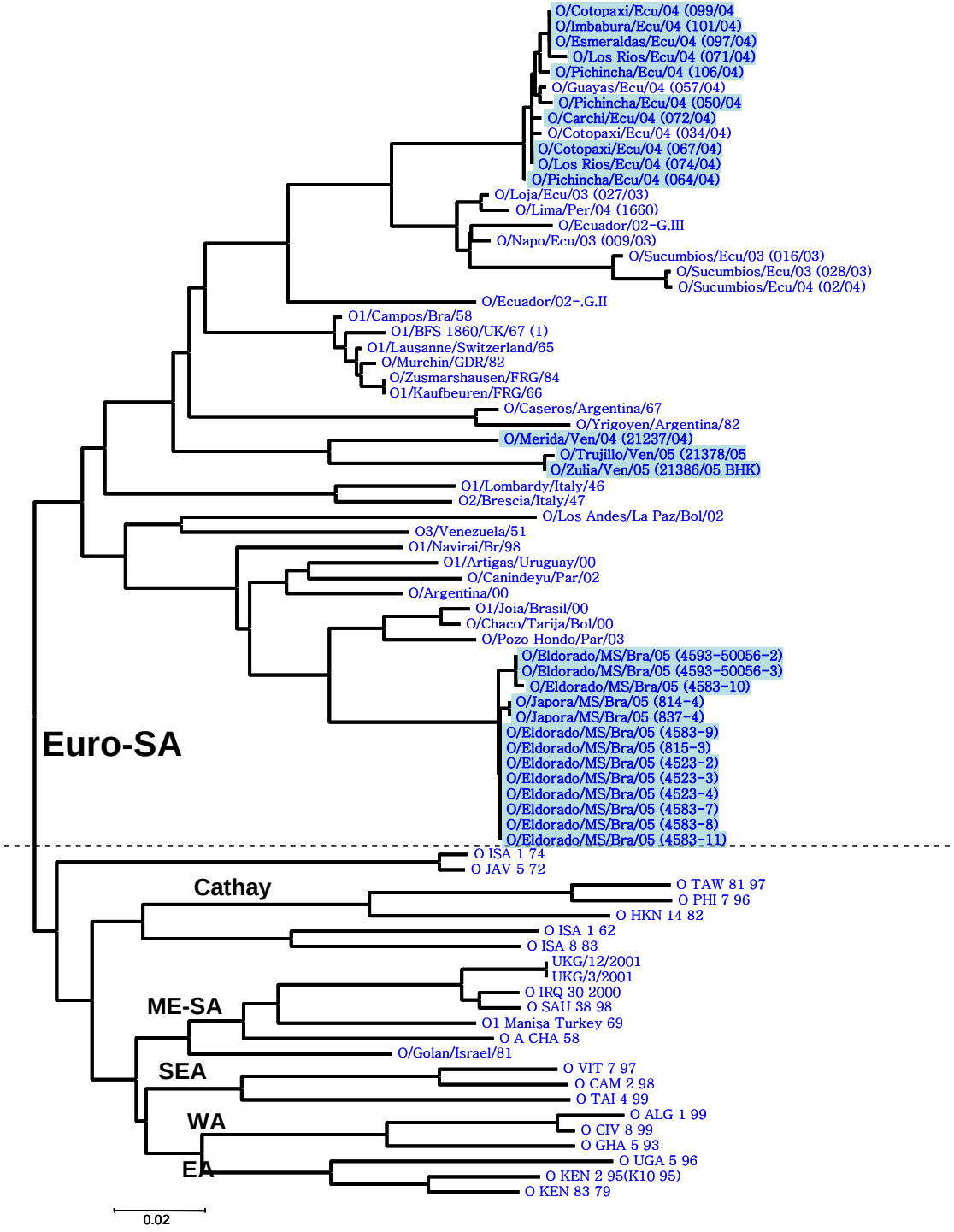


Fig. 5.18. Neighbor-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in South America.

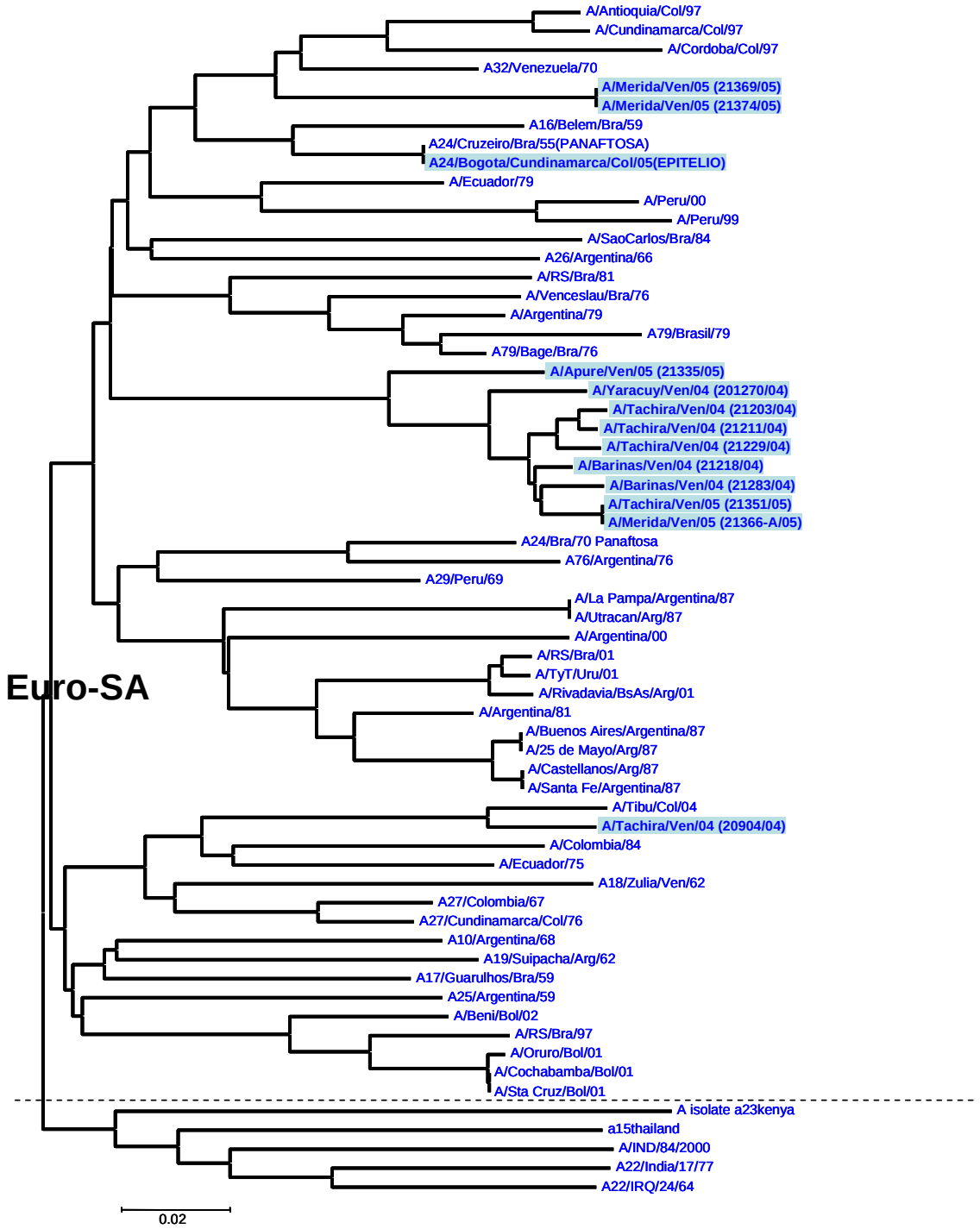
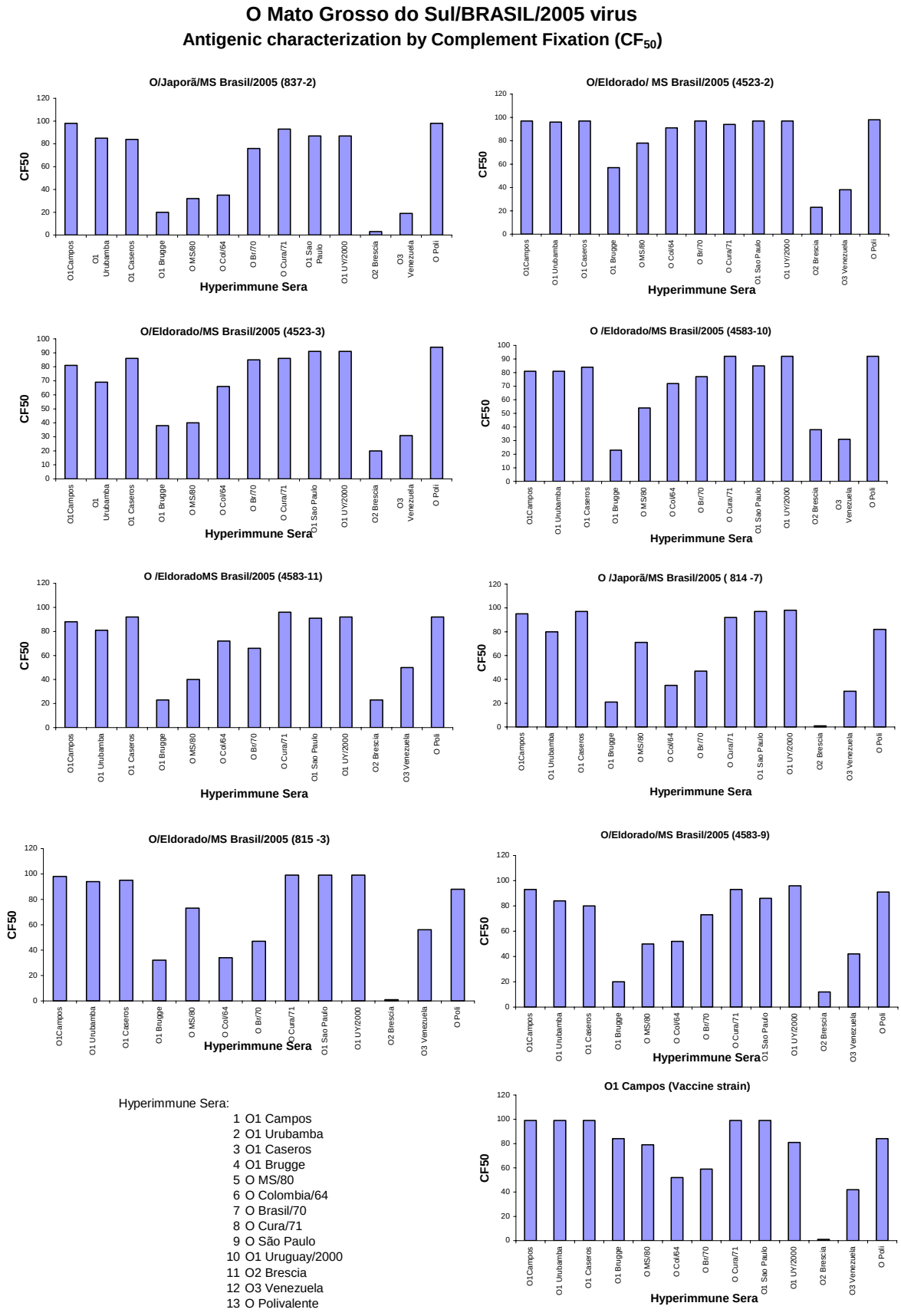


Figure 6. Antigenic characterization of FMDV strains type O collected in Brazil



Hyperimmune Sera:

1 O1 Campos
2 O1 Urubamba
3 O1 Caseros
4 O1 Brugge
5 O MS/80
6 O Colombia/64
7 O Brasil/70
8 O Cura/71
9 O São Paulo
10 O1 Uruguay/2000
11 O2 Brescia
12 O3 Venezuela
13 O Polivalente