FAO/OIE Reference Laboratory Report
January - March 2006

Foot-and-Mouth Disease

FMD Trends

Summary

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 March 2006.

A new strain of serotype A FMDV appeared in Turkey late in 2005 and became widespread, entering the European buffer zone of Turkish Thrace in January 2006. The strain involved had been detected earlier in 2005 in Iran and also spread to Saudi Arabia. In vitro vaccine matching by serology suggests that the A Iran 96 type vaccine used in Turkey, including Turkish Thrace, will not offer good protection against the new strain. Emergency vaccination in Thrace has therefore been completed during March using A22 vaccine. Although A22 is not closely related to the new strain genetically, it appears to give a moderate antigenic match to it. So far, there have been no indications of further westward spread of the strain into Greece or Bulgaria, but this possibility remains a serious concern.

Outbreaks of FMDV type A were reported from Egypt in February 2006, a country where previously only type O was sporadically reported. There was suspicion of multiple serotype involvement, but only type A was confirmed at WRL. The origin of the virus appears to be North East Africa and may be related to cattle imports from there. It is not connected to the outbreaks in Turkey and Saudi Arabia. Commercially available vaccines do not seem to offer a good match to the Egyptian strains, although A Eritrea 98 from Merial may prove to be appropriate once post-vaccination antisera are available for testing. Monovalent antisera to A Eritrea 98 are being prepared at WRL to enable the vaccine to be matched to the Egyptian isolates.

Recent outbreaks of FMDV from Israel and the Palestine Autonomous Authority have been of type O.

WRLFMD received 75 FMDV isolates and samples for vesicular virus isolation from Africa and the Middle East during the period January to March 2006 (Annex 1, Table A and B). These specimens originated from Egypt, Israel, Kenya, Rwanda, Saudi Arabia, Senegal and Turkey. No FMDV was detected in 24 of these samples.

Among 51 field isolates and clinical samples, FMD virus serotypes O, A, SAT 1 and SAT 2 were detected (Annex 1; Table A, B). From the Middle-East, FMDV serotype O was detected in clinical samples collected in Israel and Turkey, while serotype A was detected in Saudi Arabia and Turkey (including Turkish Thrace). African samples collected in Kenya belonged to FMDV serotypes O, A, SAT 1 and SAT 2. A single isolation of serotype O was made from samples from Senegal. Serotype A was found in Egypt.

Four partial VP1 sequences (152 nt at the 3' end of VP1) of FMDV A were submitted by the SAP Institute, Ankara, Turkey. Complete VP1 sequences for three FMDV O and four FMDV A isolates from Thailand were submitted by the Regional Reference Laboratory, Pakchong, Thailand. This laboratory also submitted two complete VP1 sequences of FMDV Asia 1 viruses from Vietnam. Three complete VP1 sequences of FMDV Asia 1 were submitted by the All-Russian Research Institute for Animal Health, Vladimir, Russian Federation, from outbreaks in Amursky (December 2005), Khabarovsk (December 2005) and Chita (January 2006).

Middle East/southern Asia

FMDV serotype A

The complete VP1 sequences of A/SAU/15 & 16/2005 were determined and were shown to be closely related to a new strain recently found in Iran (Annex 2; Fig. 1). Similarly, complete VP1 sequences of three FMDV A isolates from Turkish Thrace were determined (A/TUR/1 to 3/2006). These were closely related to recent Iranian isolates and to the two isolates from Saudi Arabia (Annex 2; Fig. 1). Partial VP1 sequences sent from the SAP Institute, Turkey, indicate that this lineage was found in various parts of Turkey during 2005 (Annex 2; Fig. 2). Thus it appears that a new strain, first seen in Iran in 2003, has swept across Turkey reaching Thrace early in 2006. Work on complete VP1 sequencing of further isolates collected in Anatolia during 2005 is on-going.

Asia

FMDV serotype Asia 1

FMDV Asia 1 VP1 sequences received from ARRIAH (from Amursky, Khabarovsk and Chita) were compared to the database and found to be closely related to previous outbreak viruses in the region (Annex 2; Fig. 3). The sequences of two isolates from Vietnam (received from the Thailand RRL) were most closely related to viruses from Southeast Asia (from Thailand and Myanmar) but not to the virus circulating in the China/Russia/Mongolia region (Annex 2; Fig. 4).

Africa

Egypt - Serotype A

Complete VP1 sequences from various provinces in Egypt were determined. They were all closely related to each other and most closely related to older viruses from East Africa (e.g. Kenya/98) (Annex 2; Fig. 5). They were not closely related to the recent type A viruses from the Middle East (Iran, Saudi Arabia and Turkey).

Senegal - Serotype O

The complete VP1 sequence of a single isolate of type O (O/SEN/8/2006) was obtained and compared to the WRLFMD database. It was most closely related to other isolates from West Africa indicating that it is probably a virus indigenous to the region (Annex 2; Fig. 6).

Work on the complete VP1 sequencing of type O isolates from Israel, Turkey and Kenya is on-going.

The follow are preliminary analyses of large batches of samples received during this or the last reporting period and which work is still on-going.

Ethiopia

Serotype O: Preliminary VP1 sequence analysis was performed on 15 type O viruses from Ethiopia. These sequences fell into three genetic groups which correlated with place of isolation (Arsi, Robe - O/ETH/54, 56, 57, 63, 64, 65, 66 & 67/2005; Gubalafto, North Wello - O/ETH/48, 49, 51, 52, 53, 61 & 62/2005; Mizan Terefi, Maji - O/ETH/58, 59 & 60/2005 (data not shown). The relationship of these viruses to other type O's remains to be determined.

Serotype C: The complete VP1 sequences of two isolates were determined. One was said to originate from 1983, but no collection date was specified for the other. 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).

Cameroon

Serotype O: Preliminary VP1 sequence analysis was performed on seven type O viruses from the Cameroon. All were closely related differing by no more than 5% (data not shown). Relationships to other type O's in Africa remain to be determined.

Serotype SAT 2: 19 VP1 sequences were obtained and all found to be closely related to each other; they differed by no more than 4% (data not shown).

Kenya

Serotype A: The VP1 sequence of a single isolate, A/KEN/12/2005, from Nakuru, Rift Valley province was not closely related to any other type A sequence held on our database; the closest match was A/K49/84 at over 13% different.

Serotype SAT 1: Seven VP1 sequences were obtained (data not shown). Preliminary analysis shows that they fall into three groups which correlate with geographic location: Nairobi - SAT1/KEN/11/2005; Meru South (Eastern Province) - SAT1/KEN/21/2004; and Rift Valley - SAT1/KEN/13, 15, 16 & 17/2005.

Serotype SAT 2: Five VP1 sequences were obtained (data not shown). They fell into two groups, i) Central Province - SAT2/KEN/7/2005 and ii) Central Province - SAT2/KEN/13/2005, Eastern Province – SAT2/ETH/17/2004 and Rift Valley Province – SAT2/KEN/22/2004 & SAT2/KEN/8/2005.

Vaccine matching

FMD isolates of serotype A or O collected in Asia (Israel, Malaysia, Saudi Arabia, Turkey) or Africa (Cameroon, Egypt, Ethiopia, Kenya) between 2005 and 2006 were further characterized by VNT and/or ELISA (Annex 1; TABLE C). This confirmed the utility of O_1 Manisa to all serotype O isolates tested (Israel and Malaysia), except for an isolate from Israel (ISR/1/2005). Preliminary sequence analysis of this isolate, both at Pirbright and in Israel, suggests a relatively close relationship with other isolates circulating in the Middle East (Turkey/Lebanon/Israel) in 2003 and 2004; further investigations are necessary to resolve this antigenic anomaly.

The best match, by VNT, for the type A viruses from the 2006 outbreak in Egypt was an antiserum to a bivalent vaccine containing A/Eri/98 and A/Irn/99. However, by ELISA, a good match against A/Irn/2001 was also observed. A/MAY/5/2005 reacted well with antiserum to A/May/97 by VNT. The A/SAU/2005 and A/TUR/2006 isolates could possibly be covered by A22 or A 5925 as judged by VNT and ELISA.

Publication of data to the scientific community and the industry

FMD papers published in the reporting period from the Pirbright Laboratory (Pirbright authors underlined):

Bordeleau ME, Mori A, Oberer M, Lindqvist L, Chard LS, Higa T, Belsham GJ, Wagner G, Tanaka J, Pelletier J. (2006). Functional characterization of IRESes by an inhibitor of the RNA helicase eIF4A. Nat Chem Biol. 2(4):213-20.

Chard LS, Bordeleau ME, Pelletier J, Tanaka J, Belsham GJ. (2006). Hepatitis C virus-related internal ribosome entry sites are found in multiple genera of the family Picornaviridae. J Gen Virol. 87(Pt 4):927-36.

Chard LS, Kaku Y, Jones B, Nayak A, Belsham GJ. (2006). Functional analyses of RNA structures shared between the internal ribosome entry sites of hepatitis C virus and the picornavirus porcine teschovirus 1 Talfan. J Virol. 80(3):1271-9.

Cox SJ, Voyce C, Parida S, Reid SM, Hamblin PA, Hutchings G, Paton DJ, Barnett PV. (2006). Effect of emergency FMD vaccine antigen payload on protection, sub-clinical infection and persistence following direct contact challenge of cattle. Vaccine. [Epub ahead of print]

King DP, Ferris NP, Shaw AE, Reid SM, Hutchings GH, Giuffre AC, Robida JM, Callahan JD, Nelson WM, Beckham TR (2006) Detection of foot-and-mouth disease virus: comparative diagnostic sensitivity of two independent real-time reverse transcription-polymerase chain reaction assays. *Journal of Veterinary Diagnostic Investigation* 18: 93-97.

Ko Y-J, Choi K-S, Nah J-J, Paton DJ, Oem J-K, Wilsden G, Kang S-Y, Jo N-I, Kim J-H, Lee H-W, Park J-M. (2005). Noninfectious virus-like particle antigen for detection of swine vesicular disease virus antibodies in pigs by enzyme linked immunosorbent assay. Clinical and Diagnostic Laboratory Immunology 12 (8), 922-929.

Parida S, Oh Y, Reid SM, Cox SJ, Statham RJ, Mahapatra M, Anderson J, Barnett PV, Charleston B, Paton, D.J. (2006). Interferon-γ production in vitro from whole blood of foot-and-mouth disease virus (FMDV) vaccinated and infected cattle after incubation with inactivated FMDV. Vaccine 24, 964-9.

Parida S, Anderson J, Cox SJ, Barnett PV, Paton DJ. (2006). Secretory IgA as an indicator of oro-pharyngeal foot-and-mouth disease virus replication and as a tool for post vaccination surveillance. Vaccine 24, 1107-1116.

Paton DJ, Valarcher J-F, Bergmann I, Matlho OG, Zakharov VM, Palma EL, Thomson GR. (2005). Selection of foot-and-mouth disease vaccine strains – a review. OIE Sci et Tech Rev. 24 (3), 981-993.

Reid SM, Parida S, King DP, Hutchings GH, Shaw AE, Ferris NP, Zhang Z, Hillerton JE, Paton DJ. (2006). Utility of automated real-time RT-PCR for the detection of foot-and-mouth disease virus excreted in milk. Veterinary Research 37, 121-132

Wernery U, Nagy P, Amaral-Doel CM, Zhang Z, Alexandersen S. (2006). Lack of susceptibility of the dromedary camel (Camelus dromedarius) to foot-and-mouth disease virus serotype O. Vet Rec., 158(6):201-3.

Zhang Z., J. Bashiruddin, C. Doel, J. Horsington, S. Durand and S. Alexandersen (2006) Cytokine and Toll-like receptor mRNAs in the nasal-associated lymphoid tissues of cattle during foot-and-mouth disease virus infection. J. Comp. Path. 134:60-6.

Annex 1.

Table A: Summary of clinical sample diagnostics made by the WRL Between January to March 2006

Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
ISRAEL	ISR 7/2004	Cattle	17.01.04	O	Positive	O
	ISR 8/2004	Cattle	26.01.04	O	Positive	O
	ISR 9/2004	NK	08.02.04	O	Positive	O
	ISR 10/2004	Sheep	11.02.04	O	Positive	O
	ISR 11/2004	Cattle	18.03.04	O	Positive	O
	ISR 1/2005	Cattle	19.12.05	O	Positive	O
	ISR 2/2005	Cattle	22.12.05	O	Positive	O
KENYA	KEN 13/2004	Cattle	13.01.04	SAT 2	Positive	SAT 2
	KEN 14/2004	Cattle	20.01.04	NVD	Positive	FMDV GD
	KEN 15/2004	Cattle	06.02.04	NVD	Positive	FMDV GD
	KEN 16/2004	Cattle	18.02.04	NVD	Negative	NVD
	KEN 17/2004	Cattle	16.03.04	SAT 2	Positive	SAT 2
	KEN 18/2004	Cattle	22.03.04	NVD	Positive	FMDV GD
	KEN 19/2004	Cattle	25.05.04	NVD	Positive	FMDV GD
	KEN 20/2004	Cattle	26.05.04	NVD	Positive	FMDV GD
	KEN 21/2004	Cattle	11.06.04	SAT 1	Positive	SAT 1
	KEN 22/2004	Cattle	18.06.04	SAT 2	Positive	SAT 2
	KEN 23/2004	Cattle	08.07.04	O	Positive	O
	KEN 24/2004	Cattle	30.07.04	O	Positive	O
	KEN 25/2004	Cattle	18.08.04	NVD	Negative	NVD
	KEN 26/2004	Cattle	23.08.04	NVD	Positive	FMDV GD
	KEN 27/2004	Cattle	09.09.04	NVD	Positive	FMDV GD
	KEN 28/2004	Cattle	19.10.04	NVD	Negative	NVD
	KEN 29/2004	Cattle	21.10.04	O	Positive	O
	KEN 30/3004	Cattle	24.12.04	O	Positive	O
	KEN 2/2005	Cattle	11.01.05	NVD	Positive	FMDV GD
	KEN 3/2005	Cattle	20.01.05	NVD	Positive	FMDV GD
	KEN 4/2005	Cattle	26.01.05	O	Positive	O
	KEN 5/2005	Cattle	22.02.05	NVD	Positive	FMDV GD
	KEN 6/2005	Cattle	01.03.05	O	Positive	O
	KEN 7/2005	Cattle	22.03.05	SAT 2	Positive	SAT 2
	KEN 8/2005	Cattle	19.04.05	SAT 2	Positive	SAT 2
	KEN 9/2005	Cattle	NK	NVD	Positive	FMDV GD
	KEN 10/2005	Cattle	13.06.05	O	Positive	O
	KEN 11/2005	Cattle	15.07.05	SAT 1	Positive	SAT 1
	KEN 12/2005	Cattle	15.07.05	A	Positive	A
	KEN 13/2005	Cattle	19.07.05	SAT 1	Positive	SAT 1
	KEN 14/2005	Cattle	21.07.05	O	Positive	O
	KEN 15/2005	Cattle	28.07.05	NVD	Positive	FMDV GD
	KEN 16/2005	Cattle	25.11.05	SAT 1	Positive	SAT 1
	KEN 17/2005	Cattle	11.12.05	SAT 1	Positive	SAT 1
	KEN 18/2005	Cattle	13.12.05	SAT 1	Positive	SAT 1
	KEN 19/2005	Cattle	15.12.05	SAT 1	Positive	SAT 1

RWANDA	RWA 1/2005	Cattle	26.10.05	NVD	Negative	NVD
SAUDI ARABIA	SAU 15/2005	Cattle	27.12.05	A	Positive	A
	SAU 16/2005	Cattle	27.12.05	A	Positive	A
EGYPT	EGY 1/2006	Cattle	09.02.06	A	Positive	A
	EGY 2/2006	Cattle	09.02.06	A	Positive	A
	EGY 3/2006	Cattle	09.02.06	A	Positive	A
	EGY 4/2006	NK	00.02.06	A	Positive	A
	EGY 5/2006	NK	00.02.06	A	Positive	A
SENEGAL	SEN 1/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 2/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 3/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 4/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 5/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 6/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 7/2006	Cattle	00.01.06	NVD	Negative	NVD
	SEN 8/2006	Cattle	00.01.06	O	Negative	O
	SEN 9/2006	Cattle	23.01.06	NVD	Negative	NVD
TURKEY	TUR 1/2005	Cattle	15.07.05	O	Positive	O
	TUR 2/2005	Cattle	11.08.05	O	Positive	O
	TUR 3/2005	Cattle	15.09.05	O	Positive	O
	TUR 4/2005	Cattle	16.09.05	O	Positive	O
	TUR 5/2005	Cattle	25.09.05	O	Positive	O
	TUR 6/2005	Cattle	18.11.05	A	Positive	A
	TUR 7/2005	Cattle	26.11.05	A	Positive	A
	TUR 8/2005	Cattle	07.12.05	A	Positive	A
	TUR 9/2005	Cattle	13.12.05	A	Positive	A
	TUR 10/2005	Cattle	20.12.05	A	Positive	A
	TUR 11/2005	Cattle	23.12.05	A	Positive	A
	TUR 12/2005	Cattle	27.12.05	A	Positive	A
	TUR 1/2006	Cattle	31.01.06	A	Positive	A
	TUR 2/2006	Cattle	01.02.06	A	Positive	A
	TUR 3/2006	Cattle	05.02.06	A	Positive	A

TOTAL: 318

*	Institute for Animal Health, Pirbright Laboratory, Woking, Surrey GU24 0NF
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 or SVD viral genome
NVD	no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected
GD	genome detected

TABLE B: Samples received in 2005

Country	No. of samples	Virus isolation in cell culture/ELISA									RT-PCR for FMD (or SVD) virus	
		FMD virus serotypes							SVD	NVD		
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1	virus		Positive	Negative
BOTSWANA	8	-	-	-	-	8	-	-	-	-	8	-
BURKINA FASO	10	-	-	-	-	-	-	-	-	10	-	10
CAMEROON	119[a]	25	3	-	-	54	-	-	-	38	19	100
CHINA (HONG KONG)	16	7	-	-	-	-	-	8	-	1	16	-
COTE D'IVOIRE	6	-	-	-	-	-	-	-	-	6	-	6
ETHIOPIA	68[b]	22	9	4	-	-	-	-	-	36	45	23
GAMBIA	5	-	-	-	-	-	-	-	-	5	1	4
GHANA	4	-	-	-	-	-	-	-	-	4	-	4
IRAN	55	20	20	-	-	-	-	-	-	15	42	13
IRELAND	11	-	-	-	-	-	-	-	-	11	-	11[d]
ITALY	4	-	-	-	-	-	-	-	4	-	4[e]	-
KENYA	1	-	-	-	1	-	-	-	-	-	1	-
MALAYSIA	8	7	1	-	-	-	-	-	-	-	8	-
MALI	4	3	-	-	-	-	-	-	-	1	4	-
PAKISTAN	26[c]	19	-	-	-	-	-	2	-	7	25	1
PHILIPPINES	10	3	-	-	-	-	-	-	-	7	3	7
SAUDI ARABIA	14	11	-	-	-	-	-	-	-	3	10	4
SENEGAL	3	-	-	-	-	-	-	-	-	3	-	3
SUDAN	3	3	-	-	-	-	-	-	-	-	2	1
TOGO	16	4	1	-	-	-	-	-	-	11	3	13
VIETNAM	5	5	-	-	-	-	-	-	-	-	5	-
ZAMBIA	2	-	-	-	2	-	-	-	-	-	2	-
TOTAL	**398**	**129**	**34**	**4**	**3**	**62**	**-**	**10**	**4**	**158**	**198**	**200**

*	Institute for Animal Health, Pirbright Laboratory, Woking, Surrey GU24 0NF
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 FMD, SVD or vesicular stomatitis virus detected
RT-PCR	reverse transcription polymerase chain reaction for FMD (or SVD) viral genome
[a]	one sample from Cameroon contained a mixture of FMD virus serotypes O and SAT 2
[b]	two samples from Ethiopia contained a mixture of FMD virus serotypes - one of A and C and one of O, A and C
[c]	two samples from Pakistan contained a mixture of FMD virus serotypes O and Asia 1
[d]	negative by RT-PCR for both FMD and SVD viral genome
[e]	positive by RT-PCR for SVD viral genome

NPF, 23 January 2006

The following samples were additionally received by the OIE/FAO World Reference Laboratory for Foot and Mouth Disease in 2005 :

Country	Sample year	No. of samples	ELISA/Virus isolation in cell culture									RT-PCR for FMD (or SVD) virus	
			FMD virus serotypes							SVD	NVD		
			O	A	C	SAT 1	SAT 2	SAT 3	Asia 1	virus		Positive	Negative
CHINA (HONG KONG)	2004	1	1	-	-	-	-	-	-	-	-	1	-
IRAN	2004	12	-	2	-	-	-	-	3	-	7	4	8
ITALY	2004	6	-	-	-	-	-	-	-	6	-	6[a]	-
KENYA	2003	2	-	2	-	-	-	-	-	-	-	2	-
	2004	12	-	-	1	-	7	-	-	-	4	12	-
LAOS	2003	1	-	1	-	-	-	-	-	-	-	1	-
MALI	2004	16	-	1	-	-	-	-	-	-	15	-	16
MYANMAR	2004	4	4	-	-	-	-	-	-	-	-	4	-
PAKISTAN	2004	2	-	-	-	-	-	-	-	-	2	2	-
THAILAND	2004	9	1	2	-	-	-	-	-	-	6	9	-
TOGO	2004	1	1	-	-	-	-	-	-	-	-	-	1
ZAMBIA	2004	16	-	-	-	6	-	-	-	-	10	7	9
TOTAL		**82**	**7**	**8**	**1**	**6**	**7**	**-**	**3**	**6**	**44**	**48**	**34**

*	Institute for Animal Health, Pirbright Laboratory, Woking, Surrey GU24 0NF
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
[a]	positive by RT-PCR for SVD viral genome

NPF, 23 January 2006

TABLE C: Antigenic characterisation of FMD field isolates by matching with vaccine strains. rValues were obtained by VNT or ELISA

FMD 'r' values Jan-Mar 06

Strain	A22		A Irn96	A May97		A 5925		A Sau95		A Irn 01		A Eri98/ Irn99	A 4164	A Irn99	A Irn87	A Ken 35/80
	vnt	elisa	vnt	vnt	elisa	vnt	elisa	vnt	elisa	vnt	elisa	vnt	elisa	elisa	elisa	elisa
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 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 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 Eth 16/05	0.13		0.21	0.22												
A Ken 12/05	0.13		0.30	0.33												
A May 5/05	0.12		0.19	0.58												
A Sau 15/05	0.29	>0.88	0.12	0.16	0.17		0.50	0.35	>1.0				>0.89			
A Sau 16/05	0.25	>0.88	0.12	0.17	0.15		0.58	0.39	>1.0				>1.0			
A Tur 01/06	0.42	0.21	0.08	0.11		0.41	0.32	0.21	0.26				0.29			
A Tur 2/06	0.36	0.29	0.07	0.18		0.48	0.56	0.20	0.50				0.30			
A Tur 3/06	0.39		0.09	0.13		0.48										

	O Manisa
	vnt
O Isr 01/05	0.07
O Isr 11/04	>1.0
O May 04/06	>1.0
O May 06/06	>1.0

	C Ober		C Ken 267/67	C Noville	C Phi 7/84
	vnt	elisa	elisa	elisa	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

Interpretation of r_1 values

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

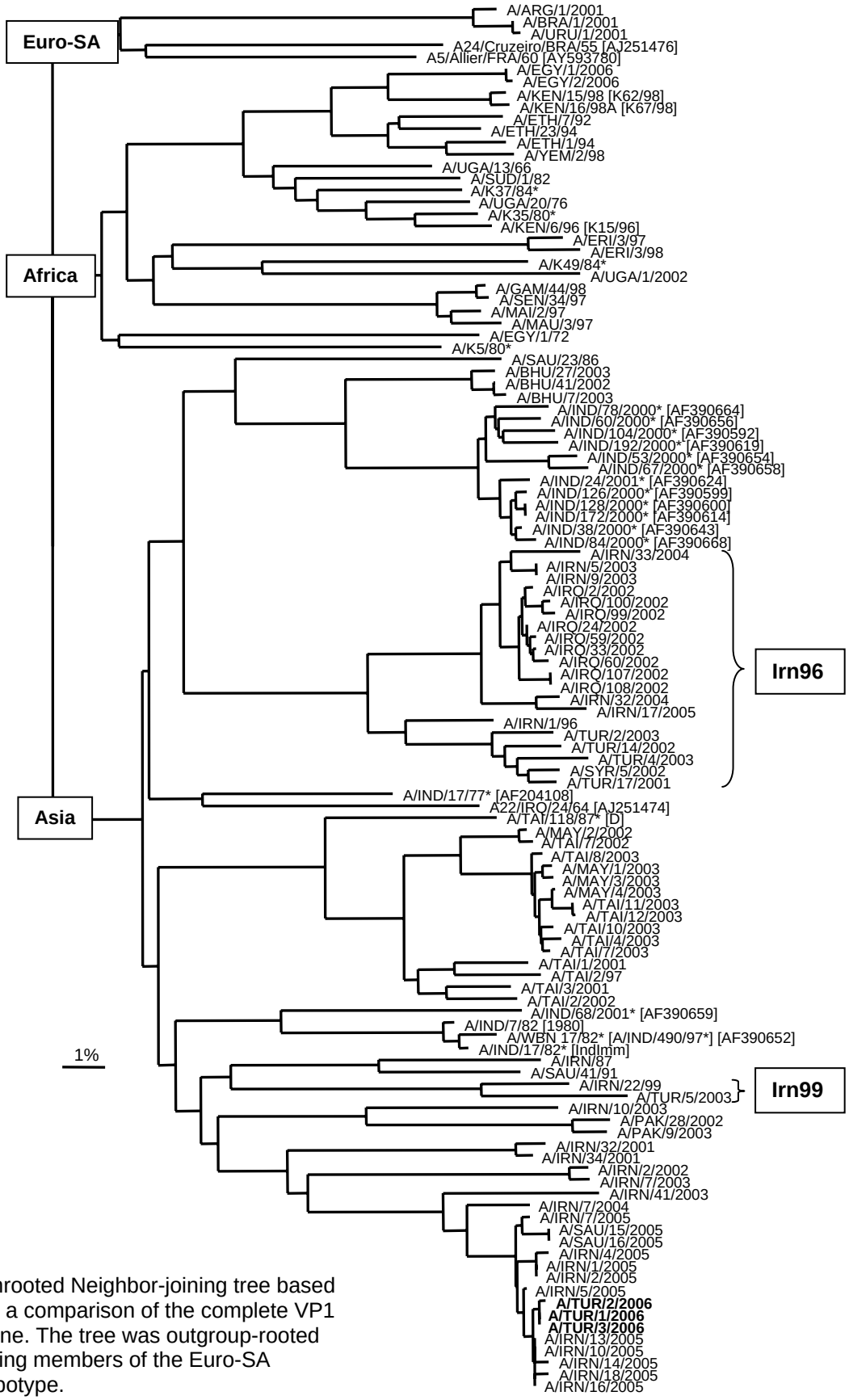
In the case of neutralisation:

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.

Annex 2

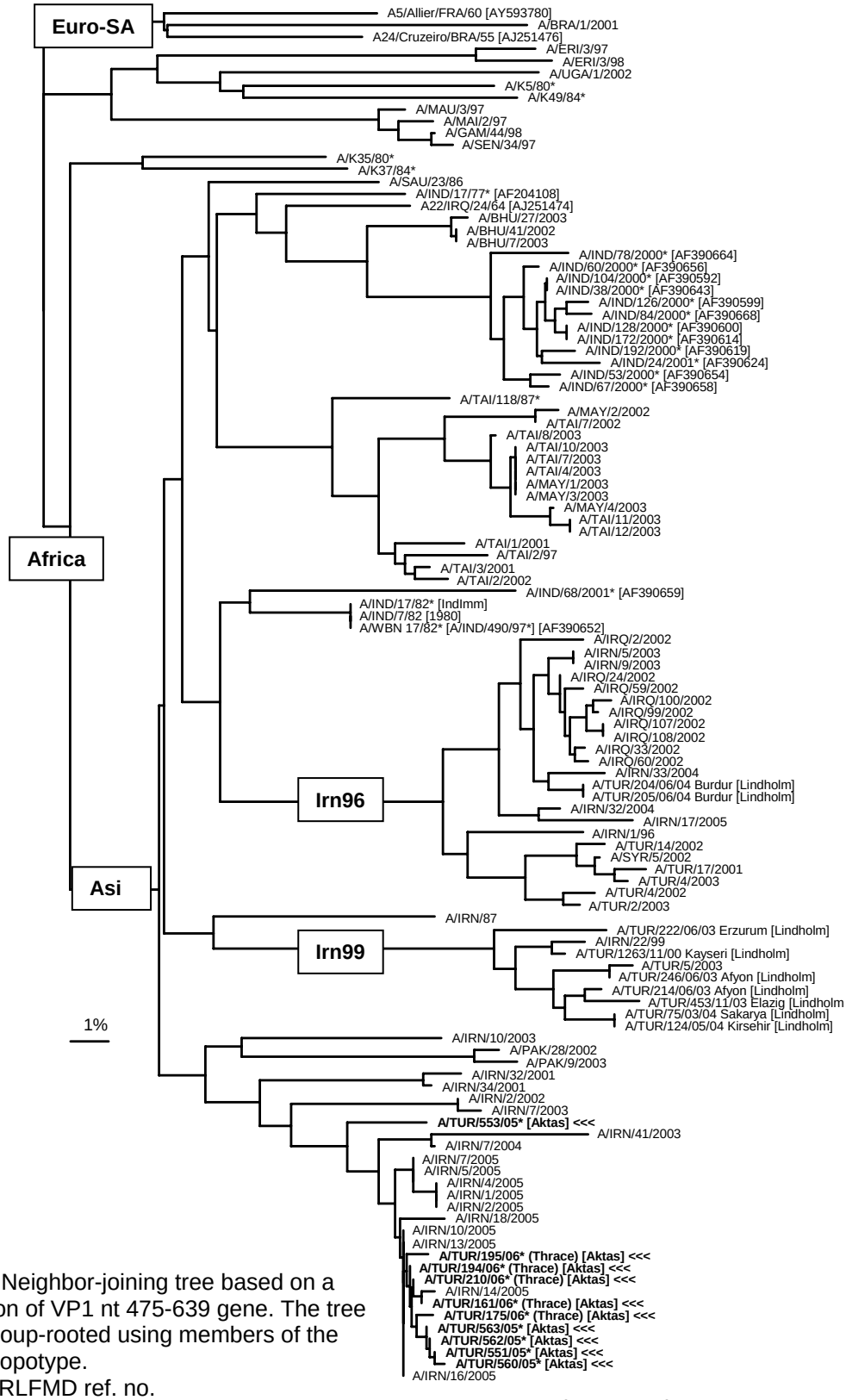
Fig. 1: Report on FMD serotype A collected in Turkey in 2006.



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, J. Smith & K. Swabey, 23 February 2006

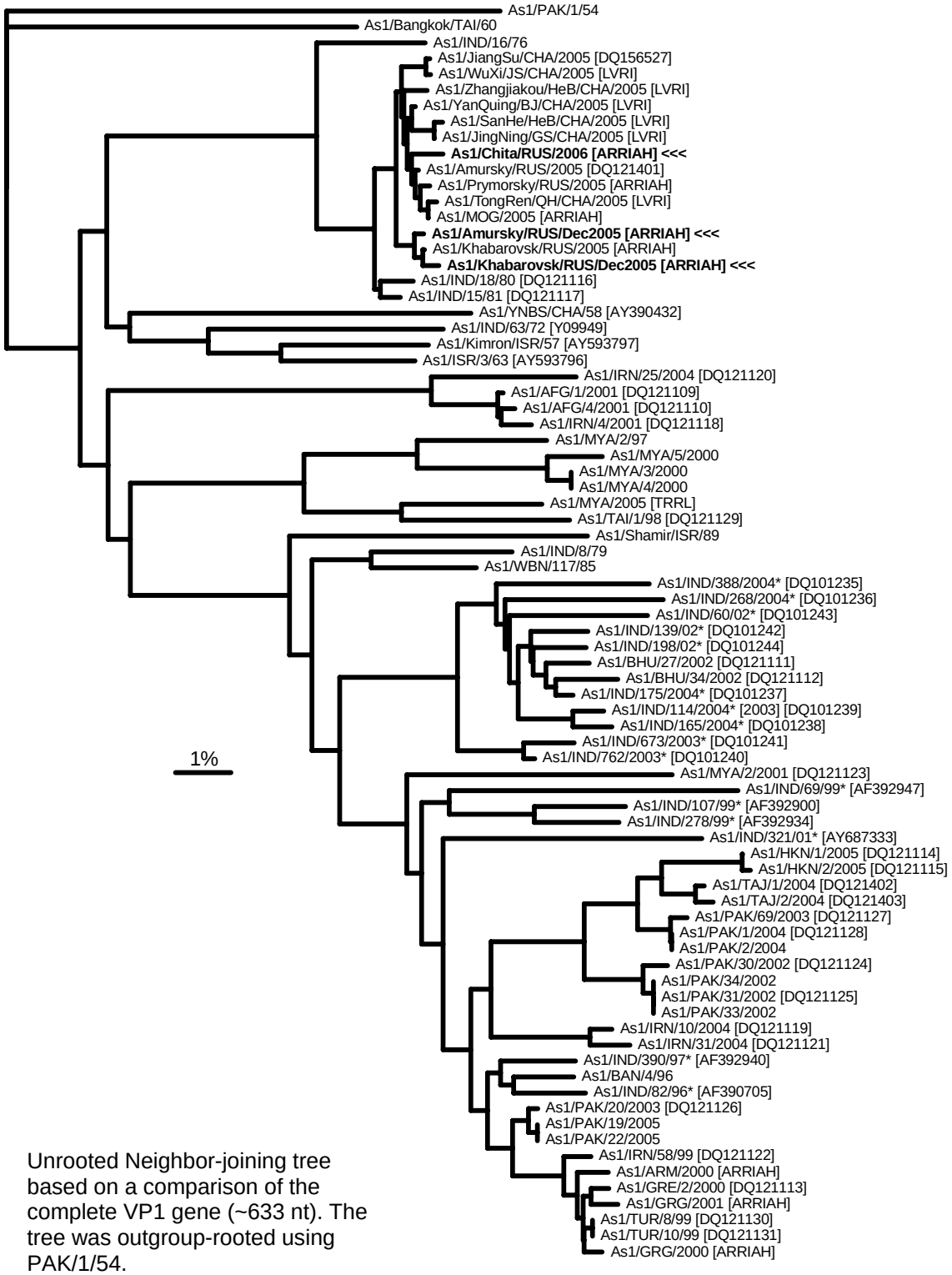
Fig. 2: Report on FMD serotype A collected in Turkey, 2005-6 (partial VP1 sequences).



Unrooted Neighbor-joining tree based on a comparison of VP1 nt 475-639 gene. The tree was outgroup-rooted using members of the Euro-SA topotype.
* Not a WRLFMD ref. no.

N.J. Knowles, 13 February 2006

Fig. 3: Report on FMD serotype Asia 1 collected in the Russian Federation in 2005-06.

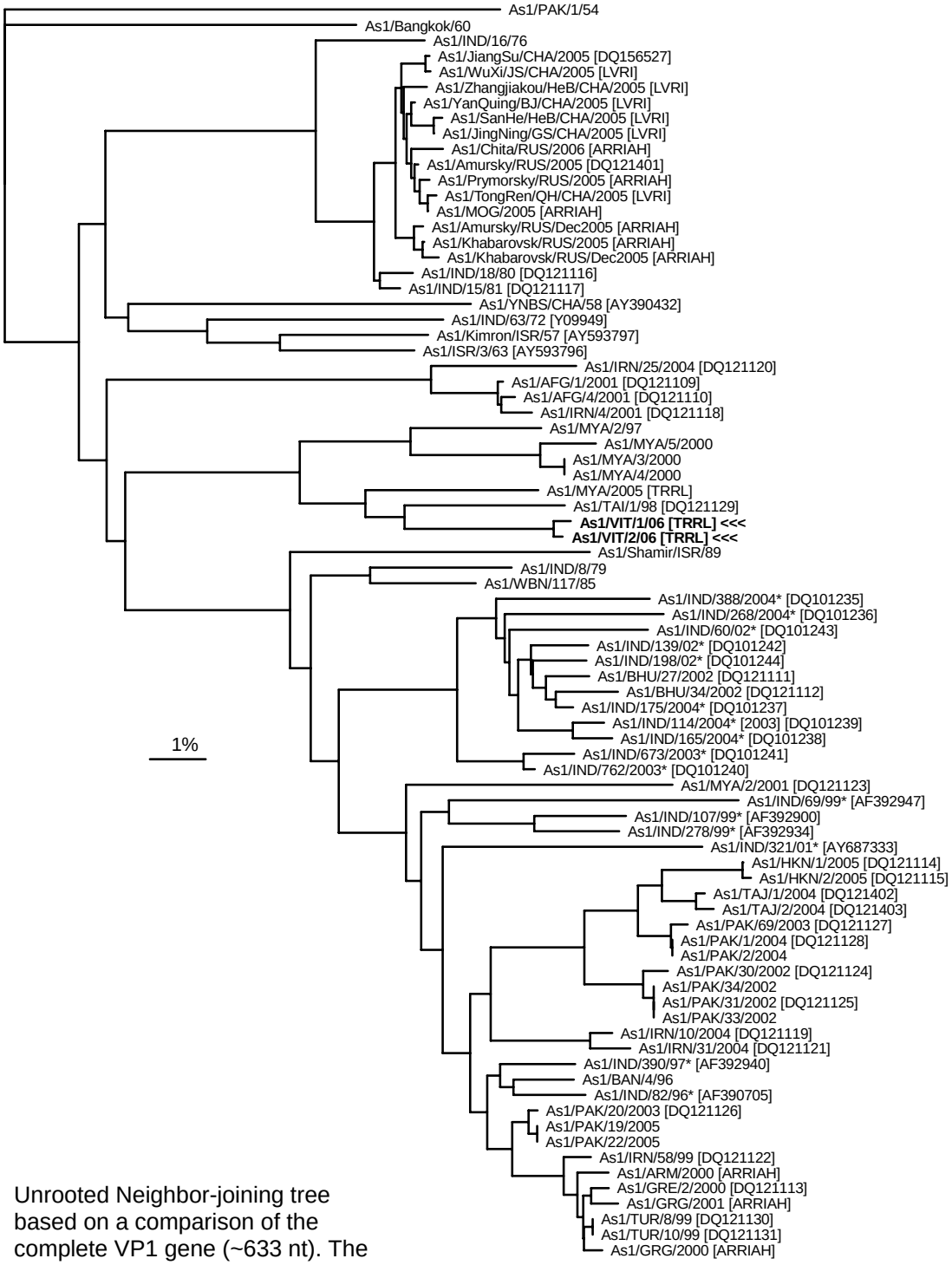


Unrooted Neighbor-joining tree based on a comparison of the complete VP1 gene (~633 nt). The tree was outgroup-rooted using PAK/1/54.

* Not a WRLFMD reference number.

N.J. Knowles, 31 January 2006

Fig. 4: Report on FMD serotype Asia 1 collected in the Vietnam in 2006.



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, 6 February 2006

Fig. 5: Report on FMD serotype A collected in Egypt in 2006.

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.

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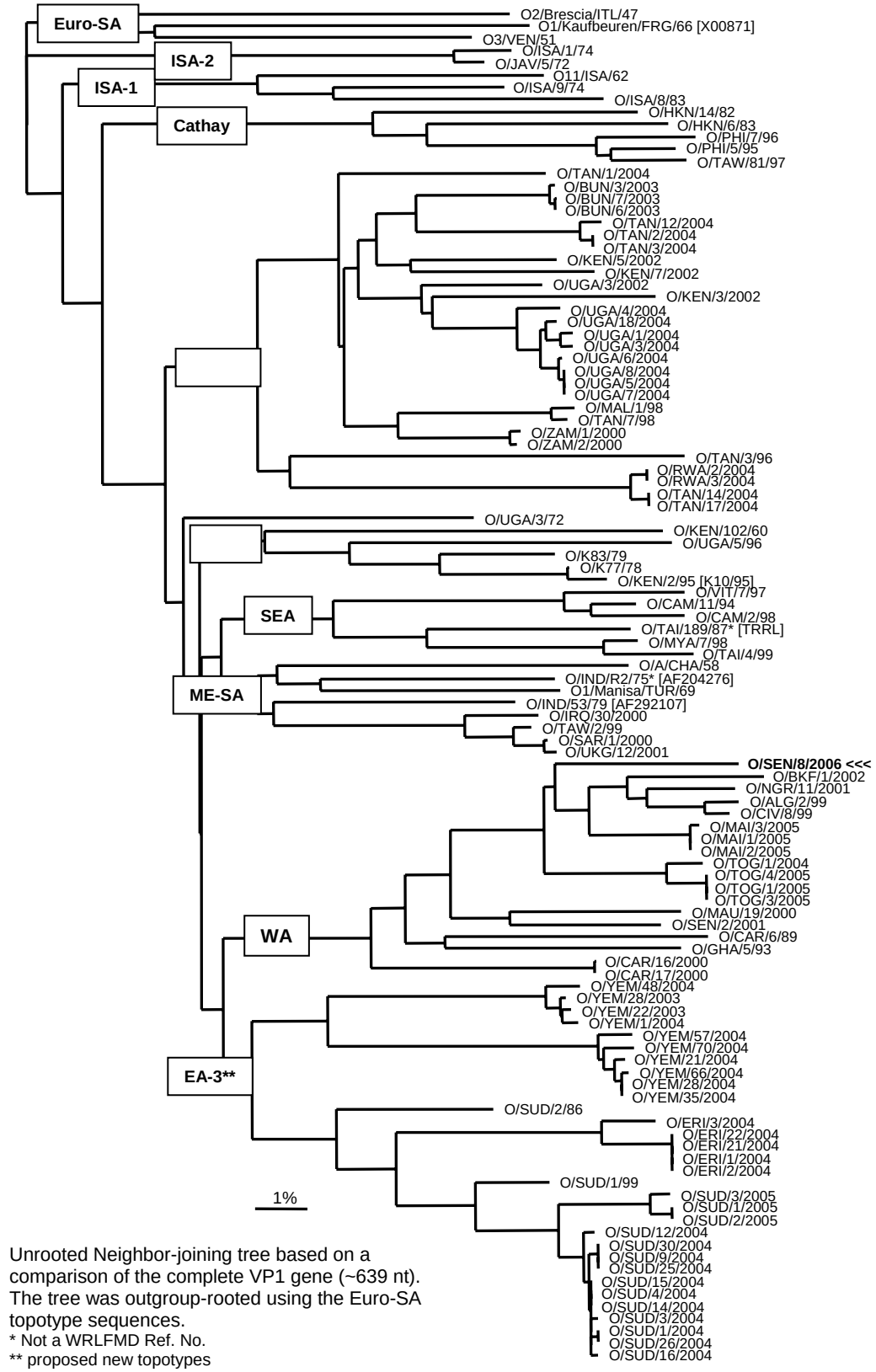
Fig. 6: Report on FMD serotype O collected in Senegal in 2006.



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

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