FAO/OIE Reference Laboratory Contract Report
January-March 2008

Foot-and-Mouth Disease

FMD Trends

Summary

There were no outbreaks officially reported in FMD-free countries that did not practice vaccination between January and March 2008. Within Europe, the Scientific Commission for Animal Diseases of the OIE recommended reinstatement of FMD-free without vaccination status for the UK and Cyprus starting on the19th and 21st February respectively.

In the Middle East, FMD outbreaks have been reported (February 2008) in cattle in northern **Israel** (due to serotype O) and **Lebanon** (no serotype reported). In Lebanon, movement of infected animals via a local market (in Bekkaa province) has been proposed to be the likely route of infection. An un-expected increase in mortality due to FMD (serotype O) in **Bahrain** has been reported to the OIE and there have also been recent reports of FMD cases in **Kuwait**. Phylogenetic analysis shows a close relationship between FMD viruses recovered from these outbreaks in Bahrain and Kuwait and other members of the PanAsia II lineage (analysis described elsewhere in this report). Elsewhere in Asia, the FMD virus causing outbreaks of FMD affecting cattle in July 2007 in **Kyrgyzstan** have now been serotyped as A. There continue to be further outbreaks of FMD (Serotype Asia 1) in **China**. During this reporting period, three cases have been detected in Ningxia province in north-central China and additional cases in Xinjiang province neighbouring Kyrgyzstan in the far west of the country. In **Vietnam**, new cases of FMD have been reported in March 2008 affecting 2 central provinces (Nghe An and Ha Tinh). In order to attempt to control FMD, 100,000 animals in the central province of Quang Tri province have been recently vaccinated with trivalent (serotype O, A and Asia 1) vaccine.

In Africa, the FMD virus causing outbreaks in northern **Egypt** (Al Iskandariyah and Al Buhayrah) from September 2007 and January 2008 has been characterised as belonging to the new PanAsia II lineage of Serotype O. Introduction of infected animals via legal movement and contact via grazing and watering points has been implicated as the routes by which the virus has spread. To-date, these cases represent the most southerly extension of this new lineage that has recently spread through the Middle East. In January and February 2008, FMD outbreaks have occurred in **Nigeria** affecting cattle in the central Province of Niger. The serotype of the causative virus has not been determined. Many cases of FMD have also been reported in two districts of Isingiro in **Uganda** close to the border with Tanzania, resulting in a ban on livestock movement in the country`s southern and western regions. In the south of the continent, 170 cases of FMD in cattle (no serotype designated) have been reported in the Southern province of **Zambia**. The affected animals were in the Kafue plains, close to a game park where contact with wild animals may have occurred as a result of flooding due to heavy rains in the area. In **Namibia**, further serotype SAT2 serotype outbreaks have been reported in the Caprivi strip close to the area affected by last year's cases. Movement and quarantine restrictions in concert with ring vaccination (with SAT 1-3) have been employed in an attempt to control the spread of the disease. In January 2008, new FMD cases have been reported in Sehithwa area, Botswana. The affected areas are further south of the Habu Extension, where the disease was confirmed in mid October last year. Eleven cases of FMD have also been reported on the southern coast of **Mozambique**. The affected cattle (showing vesicular lesions on their tongues) had been moved from Tete province, in the central part of Mozambique. 5000 susceptible animals have now been vaccinated and quarantine and movement restrictions have been initiated.

Within South America, outbreaks of FMD continue to be reported in **Venezuela** (January 2008). The most recent of these was in the State of Merida in the west of the country. Elsewhere in the continent, vaccination programmes continue to be employed. In particular, in Paraguay more than 360,000 cattle have been vaccinated in the Departments of Amambay and Canindeyu, within the 15-km buffer zone established along the borders with Brazil.

WRL vaccine recommendations are unchanged.

Results from samples received at WRL (status of samples being tested is shown in Table 1)

An up-to-date list and reports of FMD viruses characterised by sequencing can be found at the following website: http://www.wrlfmd.org/fmd_genotyping/2008.htm

Table 1: Status of sequencing of samples received recently to WRLFMD

Batch	Country	Serotype	No. of samples	Status

WRLFMD-2008-00001	Bahrain	O	3	Completed
WRLFMD-2008-00002	Ethiopia	O	1	Completed
WRLFMD-2008-00002	Ethiopia	SAT 2	1	Completed
WRLFMD-2008-00002	Ethiopia	SAT 1	1	Completed
WRLFMD-2008-00002	Ethiopia	A	1	Completed
WRLFMD-2008-00004	Kuwait	O	10	Completed
WRLFMD-2008-00006	Pakistan	O	25	In progress
WRLFMD-2008-00007	Saudi Arabia	O	2	Completed
WRLFMD-2008-00008	Saudi Arabia	O	5	In progress
WRLFMD-2008-00009	Ethiopia	O	3	In progress
WRLFMD-2008-00009	Ethiopia	SAT1	3	In progress

Middle East and Asia

FMDV serotype O

Fifteen recent FMDV isolates from the Middle East (2, 3 and 10 from Saudi Arabia, Bahrain and Kuwait respectively) have been characterised by VP1 sequencing (See Annex 2, Figure 1). All viruses belong to the PanAsia II lineage of serotype O. The majority of these viruses (9/10 of the viruses from Kuwait and all the isolates from Saudi Arabia and Bahrain) were clustered as a single group also containing 3 Iranian viruses from 2007. Within this group, there appear to be 3 separate sub-clusters ([i] SAU and BAH [ii] KUW 3-5/2008 and [iii] KUW 1, 2, 6-7, 8 and 10/200) indicating that although these viruses share a common ancestor, they have different epidemiological histories prior to their detection. Interestingly, the final isolate from Kuwait (KUW 9/2008) appeared to be more distantly related to viruses in this cluster.

FMDV serotype A

Two sequences obtained from viruses recovered from Tajikistan (3003) and Kyrgyzstan (2007) have been sent to IAH for analysis from ARRIAH (Russia).

Africa

Material received to the WRL from Ethiopia has been characterised as belonging to 4 different FMDV serotypes: ***FMDV serotype O*** (See Annex 2, Figure 2):The serotype O isolate was characterised as belonging to the EA-3 topotype, distantly related to earlier viruses from 2005 and 2006 collected from Ethiopia; ***FMDV serotype A*** (See Annex 2, Figure 3) Characterised as belonging to the Africa topotype; ***FMDV serotype SAT1*** (See Annex 2, Figure 4); ***FMDV serotype SAT2*** (See Annex 2, Figure 5) In general these viruses (of all 4 serotypes) are not clustered closely with any other previously analysed strains indicating that there is a considerable amount of uncharacterised FMDV circulating in the region.

Vaccine matching

Six FMDV type O isolates (O IRN 26/2007; O IRN 30/2007; O BAR 2/2008; O KUW 4/2008; O YEM 4/2006 and O YEM 29/2006) from Iran, Bahrain, Kuwait and Yemen collected in 2006, 2007 and 2008 were further characterised by two dimensional virus neutralisation test (VNT: see Annex 1; TABLE C). These results showed that most of these isolates were antigenically matched with O1 Manisa vaccine strains. Four of these field isolates (O YEM 4/2006 and 29/2006; O BAR 2/2008 and O KUW 4/2008) were also closely matched with O BFS 1860 and O Ind R2/75 indicating that these serotype O viruses can be covered by a vaccine present in many vaccine banks.

Five FMDV type A isolates (A ETH 4/2007; A IRN 36/2007; A IRN 39/2007; A MAY 1/2007 and A MAY 3/2007) from Ethiopia, Iran and Malaysia have been analysed by two dimensional VNT. The results showed that both of the isolates from Malaysia were matched with A May 97 (one isolate was also matched withA22 and A Turkey/06). The 2 isolates from Iran showed antigenic matching with A Turkey/06 vaccine strain (and not A22). Finally, isolate A ETH 4/2007 from Ethiopia showed no matching with either A22 or A Eritrea vaccine strains. (Annex 1; TABLE C).

Two FMD type Asia 1 isolates (Asia 1 KRG 1/2004 and Asia 1 NKR 2/2007) from North Korea and Kyrgyzstan have been characterised by two dimensional VNT and the results showed they were antigenically matched with both of Asia 1 India and Asia 1 Shamir vaccine strains.

Publication of data to the scientific community and the industry

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

1. Rweyemamu M, Roeder P, Mackay D, Sumption K, Brownlie J, Leforban Y, Valarcher JF, Knowles NJ, Saraiva V. Epidemiological Patterns of Foot-and-Mouth Disease Worldwide. Transbound Emerg Dis. 2008 Feb;55(1):57-72.
2. De Clercq K, Goris N, Barnett PV, Mackay DK. FMD vaccines: reflections on quality aspects for applicability in European disease control policy. Transbound Emerg Dis. 2008 Feb;55(1):46-56.
3. De Clercq K, Goris N, Barnett PV, Mackay DK. The Importance of Quality Assurance/Quality Control of Diagnostics to Increase the Confidence in Global Foot-and-Mouth Disease Control. Transbound Emerg Dis. 2008 Feb;55(1):35-45.
4. Valarcher JF, Leforban Y, Rweyemamu M, Roeder PL, Gerbier G, Mackay DK, Sumption KJ, Paton DJ, Knowles NJ. Incursions of Foot-and-Mouth Disease Virus into Europe between 1985 and 2006. Transbound Emerg Dis. 2008 Feb;55(1):14-34.
5. Ryan E, Mackay D, Donaldson A. Foot-and-Mouth Disease Virus Concentrations in Products of Animal Origin. Transbound Emerg Dis. 2008 Mar;55(2):89-98.
6. Bronsvoort BM, Parida S, Handel I, McFarland S, Fleming L, Hamblin P, Kock R. Serological survey for foot-and-mouth disease in wildlife in East Africa and parameter estimation of the Cedi test NSP ELISA for buffalo. Clin Vaccine Immunol. 2008 Apr 2; [Epub ahead of print]
7. Fowler VL, Paton DJ, Rieder E, Barnett PV. Chimeric foot-and-mouth disease viruses: Evaluation of their efficacy as potential marker vaccines in cattle. Vaccine. 2008 Apr 7;26(16):1982-9. Epub 2008 Feb 22.
8. King DP, Dukes JP, Reid SM, Ebert K, Shaw AE, Mills CE, Boswell L, Ferris NP. Prospects for rapid diagnosis of foot-and-mouth disease in the field using reverse transcriptase-PCR. Vet Rec. 2008 Mar 8;162(10):315-6. No abstract available.
9. Li Y, Stirling CM, Denyer MS, Hamblin P, Hutchings G, Takamatsu HH, Barnett PV. Dramatic improvement in FMD DNA vaccine efficacy and cross-serotype antibody induction in pigs following a protein boost. Vaccine. 2008 Feb 12; [Epub ahead of print]
10. Ryan E, Horsington J, Brownlie J, Zhang Z. Foot-and-Mouth Disease Virus Infection in Fetal Lambs: Tissue Tropism and Cytokine Response. J Comp Pathol. 2008 Feb-Apr;138(2-3):108-20. Epub 2008 Feb 25.
11. Zhang Z, Bashiruddin JB. Quantitative analysis of foot-and-mouth disease virus RNA duration in tissues of experimentally infected pigs. Vet J. 2008 Feb 20; [Epub ahead of print]
12. Schumann KR, Knowles NJ, Davies PR, Midgley RJ, Valarcher JF, Raoufi AQ, McKenna TS, Hurtle W, Burans JP, Martin BM, Rodriguez LL, Beckham TR. Genetic characterization and molecular epidemiology of foot-and-mouth disease viruses isolated from Afghanistan in 2003-2005. Virus Genes. 2008 Apr;36(2):401-413. Epub 2008 Feb 16.
13. Guzman E, Taylor G, Charleston B, Skinner MA, Ellis SA. An MHC-restricted CD8+ T-cell response is induced in cattle by foot-and-mouth disease virus (FMDV) infection and also following vaccination with inactivated FMDV. J Gen Virol. 2008 Mar;89(Pt 3):667-75.
14. Knowles NJ, Wadsworth J, Reid SM, Swabey KG, El-Kholy AA, Abd El-Rahman AO, Soliman HM, Ebert K, Ferris NP, Hutchings GH, Statham RJ, King DP, Paton DJ. Foot-and-Mouth Disease Virus Serotype A in Egypt. Emerg Infect Dis. 2007 Oct;13(10):1593-6.
15. Cottam EM, Thébaud G, Wadsworth J, Gloster J, Mansley L, Paton DJ, King DP, Haydon DT. Integrating genetic and epidemiological data to determine transmission pathways of foot-and-mouth disease virus. Proc Biol Sci. 2008 Apr 22;275(1637):887-95.
16. Hindson BJ, Reid SM, Baker BR, Ebert K, Ferris NP, Tammero LF, Lenhoff RJ, Naraghi-Arani P, Vitalis EA, Slezak TR, Hullinger PJ, King DP. Diagnostic evaluation of multiplexed reverse transcription-PCR microsphere array assay for detection of foot-and-mouth and look-alike disease viruses.J Clin Microbiol. 2008 Mar;46(3):1081-9. Epub 2008 Jan 23.
17. Hollister JR, Vagnozzi A, Knowles NJ, Rieder E. Molecular and phylogenetic analyses of bovine rhinovirus type 2 shows it is closely related to foot-and-mouth disease virus. Virology. 2008 Apr 10;373(2):411-25. Epub 2008 Jan 16.

Annex 1.

Table A: Summary of clinical sample diagnostics made by the WRL between January - March 2008

Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
BAHRAIN	BAR 1/2008	Cattle	08.01.08	O	Positive	O
	BAR 2/2008	Cattle	08.01.08	O	Positive	O
	BAR 3/2008	Cattle	08.01.08	O	Positive	O
BOTSWANA	BOT 1/2008	Pig	00.02.08	NVD	Negative	NVD
	BOT 2/2008	Pig	00.02.08	NVD	Negative	NVD
	BOT 3/2008	Pig	00.02.08	NVD	Negative	NVD
	BOT 4/2008	Pig	00.02.08	NVD	Negative	NVD
	BOT 5/2008	Pig	00.02.08	NVD	Negative	NVD
ETHIOPIA	ETH 1/2007	Cattle	08.02.07	O	Positive	O
	ETH 2/2007	Cattle	07.09.07	SAT 2	Positive	SAT 2
	ETH 3/2007	Cattle	10.11.07	SAT 1	Positive	SAT 1
	ETH 4/2007	Cattle	07.12.07	A	Positive	A
	ETH 5/2007	Cattle	10.11.07	NVD	Negative	NVD
	ETH 6/2007	Sheep	10.11.07	NVD	Negative	NVD
	ETH 7/2007	Cattle	11.11.07	NVD	Negative	NVD
	ETH 8/2007	Cattle	11.11.07	NVD	Negative	NVD
	ETH 9/2007	Cattle	11.11.07	NVD	Negative	NVD
	ETH 10/2007	Sheep	11.11.07	NVD	Negative	NVD
	ETH 11/2007	Sheep	11.11.07	NVD	Negative	NVD
	ETH 12/2007	Goat	11.11.07	NVD	Negative	NVD
	ETH 13/2007	Cattle	12.11.07	NVD	Negative	NVD
	ETH 14/2007	Sheep	12.11.07	NVD	Negative	NVD
	ETH 15/2007	Goat	12.11.07	NVD	Negative	NVD
	ETH 16/2007	Goat	05.12.07	NVD	Negative	NVD
	ETH 17/2007	Goat	06.12.07	NVD	Negative	NVD
	ETH 18/2007	Goat	06.12.07	SAT 1	Negative	SAT 1
	ETH 19/2007	Sheep	07.12.07	SAT 1	Negative	SAT 1
	ETH 20/2007	Goat	07.12.07	NVD	Negative	NVD
	ETH 21/2007	Cattle	07.12.07	SAT 1	Positive	SAT 1
	ETH 22/2007	Cattle	22.12.07	NVD	Negative	NVD
	ETH 23/2007	Sheep	22.12.07	NVD	Negative	NVD
	ETH 24/2007	Goat	22.12.07	NVD	Negative	NVD
	ETH 25/2007	Cattle	00.12.07	NVD	Negative	NVD
	ETH 26/2007	Cattle	00.12.07	O	Positive	O
	ETH 27/2007	Cattle	00.12.07	O	Positive	O
	ETH 28/2007	Cattle	00.12.07	O	Positive	O
KUWAIT	KUW 1/2008	Cattle	03.01.08	O	Positive	O
	KUW 2/2008	Cattle	03.01.08	O	Positive	O
	KUW 3/2008	Cattle	20.01.08	O	Positive	O
	KUW 4/2008	Cattle	20.01.08	O	Positive	O
	KUW 5/2008	Cattle	20.01.08	O	Positive	O
	KUW 6/2008	Cattle	24.01.08	O	Positive	O
	KUW 7/2008	Cattle	24.01.08	O	Positive	O

	KUW 8/2008	Cattle	24.01.08	O	Positive	O
	KUW 9/2008	Cattle	24.01.08	O	Positive	O
	KUW 10/2008	Cattle	24.01.08	O	Positive	O
SENEGAL	SEN 1/2008	Cattle	25.01.08	NVD	Negative	NVD
	SEN 2/2008	Cattle	25.01.08	NVD	Negative	NVD
	SEN 3/2008	Cattle	25.01.08	NVD	Positive	FMDV GD
	SEN 4/2008	Cattle	25.01.08	NVD	Negative	NVD
	SEN 5/2008	Cattle	25.01.08	NVD	Negative	NVD
	SEN 6/2008	Cattle	25.01.08	NVD	Negative	NVD
	SEN 7/2008	Cattle	25.01.08	NVD	Positive	FMDV GD
	SEN 8/2008	Cattle	25.01.08	NVD	Negative	NVD
PAKISTAN	PAK 27/2005	Cattle	00.01-03.05	NVD	Negative	NVD
	PAK 28/2005	Buffalo	00.01-03.05	NVD	Negative	NVD
	PAK 29/2005	Cattle	00.01-03.05	NVD	Negative	NVD
	PAK 30/2005	Cattle	00.01-03.05	NVD	Positive	FMDV GD
	PAK 31/2005	Cattle	00.01-03.05	O	Positive	O
	PAK 32/2005	Cattle	00.01-03.05	O	Positive	O
	PAK 33/2005	Cattle	00.01-03.05	O	Positive	O
	PAK 34/2005	Cattle	00.01-03.05	O	Positive	O
	PAK 35/2005	Buffalo	00.01-03.05	O	Positive	O
	PAK 36/2005	Cattle	00.01-03.05	NVD	Negative	NVD
	PAK 37/2005	Cattle	00.01-03.05	NVD	Positive	FMDV GD
	PAK 38/2005	Cattle	00.02.05	O	Positive	O
	PAK 39/2005	Cattle	00.02.05	NVD	Positive	FMDV GD
	PAK 40/2005	Buffalo	00.02.05	NVD	Positive	FMDV GD
	PAK 41/2005	Cattle	00.02.05	NVD	Negative	NVD
	PAK 42/2005	Cattle	00.00.05	NVD	Negative	NVD
	PAK 60/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 61/2006	Cattle	00.01-03.06	O	Positive	O
	PAK 62/2006	Cattle	00.01-03.06	NVD	Positive	FMDV GD
	PAK 63/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 64/2006	Cattle	00.01-03.06	NVD	Negative	NVD
	PAK 65/2006	Cattle	00.01-03.06	NVD	Positive	FMDV GD
	PAK 66/2006	Cattle	00.01-03.06	O	Negative	O
	PAK 67/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 68/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 69/2006	Cattle	00.01-03.06	NVD	Negative	NVD
	PAK 70/2006	Cattle	00.01-03.06	O	Positive	O
	PAK 71/2006	Cattle	00.01-03.06	O	Positive	O
	PAK 72/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 73/2006	Buffalo	00.01-03.06	O	Positive	O
	PAK 74/2006	Cattle	00.01-03.06	O	Negative	O
	PAK 53/2007	Cattle	00.01-03.07	O	Positive	O
	PAK 54/2007	Buffalo	00.01-03.07	NVD	Negative	NVD
	PAK 55/2007	Buffalo	00.01-03.07	NVD	Positive	FMDV GD
	PAK 56/2007	Buffalo	00.01-03.07	O	Positive	O
	PAK 57/2007	Buffalo	00.01-03.07	NVD	Negative	NVD
	PAK 58/2007	Cattle	00.01-03.07	NVD	Negative	NVD
	PAK 59/2007	Cattle	00.01-03.07	NVD	Positive	FMDV GD
	PAK 60/2007	Cattle	00.01-03.07	O	Positive	O
	PAK 61/2007	Cattle	00.01-03.07	O	Positive	O
	PAK 62/2007	Cattle	00.01-03.07	NVD	Positive	FMDV GD
	PAK 63/2007	Cattle	00.01-03.07	O	Positive	O

	PAK 64/2007	Cattle	00.01-03.07	NVD	Negative	NVD
	PAK 65/2007	Cattle	00.03.07	NVD	Positive	FMDV GD
	PAK 66/2007	Buffalo	00.12.07	O	Positive	O
	PAK 67/2007	Buffalo	00.12.07	NVD	Positive	FMDV GD
	PAK 1/2008	Cattle	00.01.08	O	Positive	O
	PAK 2/2008	Buffalo	00.01.08	O	Positive	O
SAUDI ARABIA	SAU 1/2008	Cattle	01.03.08	O	Positive	O
	SAU 2/2008	Cattle	01.03.08	O	Positive	O
	SAU 3/2008	Cattle	15.01.08	O	Positive	O
	SAU 4/2008	Cattle	12.01.08	O	Positive	O
	SAU 5/2008	Cattle	03.03.08	O	Positive	O
	SAU 6/2008	Cattle	28.10.07	O	Positive	O
	SAU 7/2008	Sheep	01.01.08	O	Positive	O
	SAU 8/2008	Sheep	03.03.08	NVD	Positive	FMDV GD
	SAU 9/2008	Cattle	08.03.08	NVD	Positive	FMDV GD
	SAU 10/2008	Cattle	05.01.08	NVD	Positive	FMDV GD
	TOTAL : 112					

*	Institute for Animal Health, Pirbright Laboratory, Woking, Surrey GU24 0NF
FMD(V)	foot-and-mouth disease (virus)
GD	genome detected
VI/ELISA	FMDV serotype identified following virus isolation in cell culture and antigen ELISA
RT-PCR	reverse transcription polymerase chain reaction on epithelial suspension for FMD (or SVD) viral genome
NVD	no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected

TABLE B: Summary of samples collected and received to IAH-Pirbright (January – March 2008)

Country	No. of samples	Virus isolation in cell culture/ELISA									RT-PCR for FMD (or SVD) virus (where appropriate)	
		FMD virus serotypes							SVD virus	NVD		
		O	A	C	SAT 1	SAT 2	SAT 3	Asia 1			Positive	Negative
BAHRAIN	3	3	-	-	-	-	-	-	-	-	3	-
BOTSWANA	5	-	-	-	-	-	-	-	-	5	-	5
ETHIOPIA	28	4	1	-	4	1	-	-	-	18	8	20
KUWAIT	10	10	-	-	-	-	-	-	-	-	10	-
PAKISTAN	48	25	-	-	-	-	-	-	-	23	34	14
SAUDI ARABIA	10	7	-	-	-	-	-	-	-	3	10	-
SENEGAL	8	-	-	-	-	-	-	-	-	8	2	6
TOTAL	**112**	**49**	**1**	**-**	**4**	**1**	**-**	**-**	**-**	**57**	**67**	**45**

*	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

NPF, 18 April 2008

TABLE C: Antigenic characterisation of FMD field isolates by matching with vaccine strains by VNT – r1 value data from 1st January to 31st March 2008

Field isolates	TEST	r1 values for type A vaccine strains						
		A22	A Ind 17/82	A Irn 96	A May 97	A Eritrea	A Irn 99	A Turkey/06
A ETH 4/2007	VNT	0.14				0.09		
A IRN 36/2007	VNT	0.20	0.19	0.19	0.17		0.11	0.36
A IRN 39/2007	VNT	0.12		0.11	0.29		0.34	0.46
A MAY 1/2007	VNT	0.33	0.06		0.36			0.36
A MAY 3/2007	VNT	0.05	0.09		0.44			0.15

Field isolates	TEST	r1 values for type O vaccine strains		
		O Manisa	BFS1860	O Ind R2/75
O BAR 2/2008	VNT	0.30	0.30	0.60
O IRN 26/2007	VNT	<1.0		
O IRN 30/2007	VNT	0.15		
O KUW 4/2008	VNT	0.87	0.44	>1.0
O YEM 29/2006	VNT	0.29	0.25	>1.0
O YEM 4/2006	VNT	0.36	0.47	

Field isolates	TEST	r1 value for type Asia 1 vaccine strains	
		Asia1 India	Asia1 Shamir
Asia1 KRG 1/2004	VNT	0.32	0.59
Asia1 NKR 2/2007	VNT	0.31	0.52

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 protec

In the case of ELISA:

$r_1 = 0.4\text{-}1.0$. 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.
$r_1 = 0.2\text{-}0.39$, 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

Annex 2: Phylogenetic analysis of characterised FMDV isolates:

Fig 1 FMDV serotype O viruses characterised from Saudi Arabia, Bahrain and Kuwait

Report on FMD type O viruses from the Middle East in 2008 (Saudi Arabia, Bahrain and Kuwait)

No. of Taxa : 161
Data File : n:\evd\meg\db\fmdv\o\SAU2008a.meg
Data Title : Saudi Arabia 2008
Data Type : Nucleotide (Coding)
Analysis : Phylogeny reconstruction
Tree Inference : ==========
->Method : Neighbor-Joining
->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
Include Sites : ==========
->Gaps/Missing Data : Pairwise Deletion
->Codon Positions : 1st+2nd+3rd+Noncoding
Substitution Model : ==========
->Model : Nucleotide: Kimura 2-parameter
->Substitutions to Include : d: Transitions + Transversions
->Pattern among Lineages : Same (Homogeneous)
->Rates among sites : Uniform rates
No. of Sites : 639
No Of Bootstrap Reps = 1000
Only bootstrap values of 70% and less are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 28 March 2008

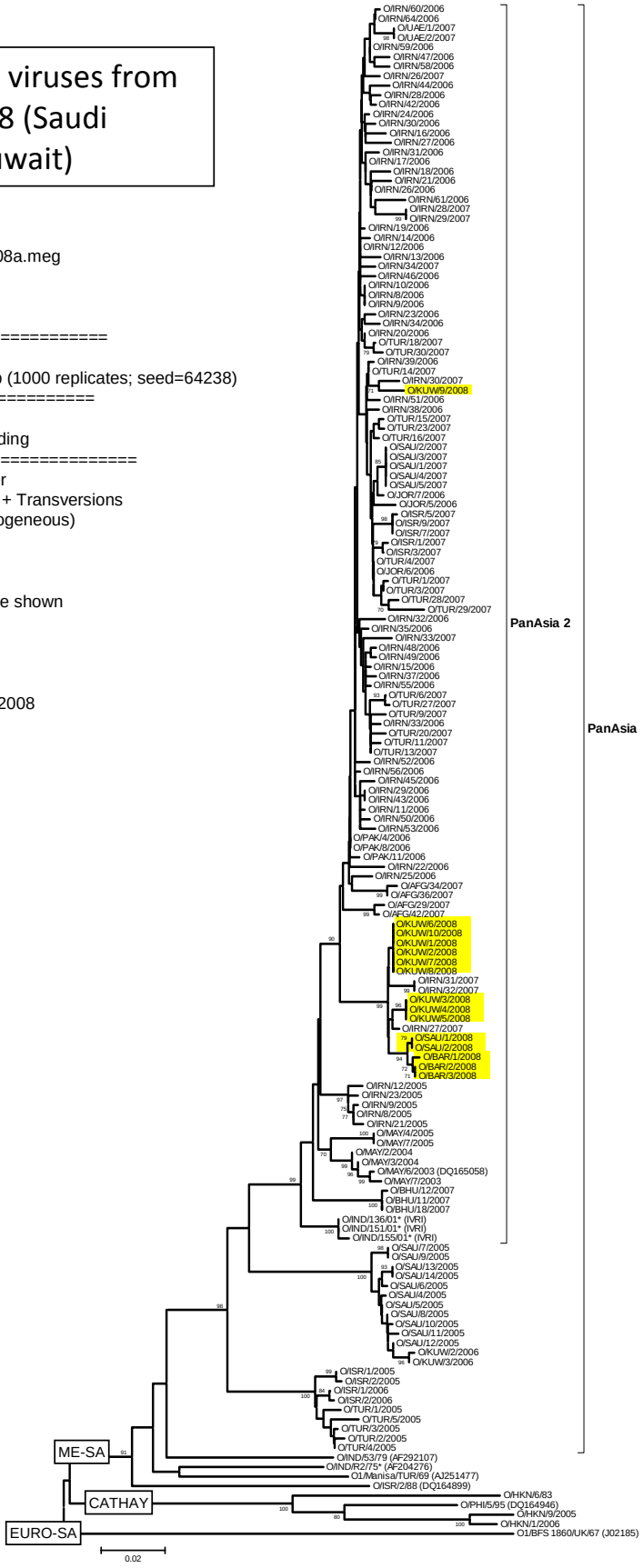


Fig 2: Recent serotype O virus characterised from Ethiopia

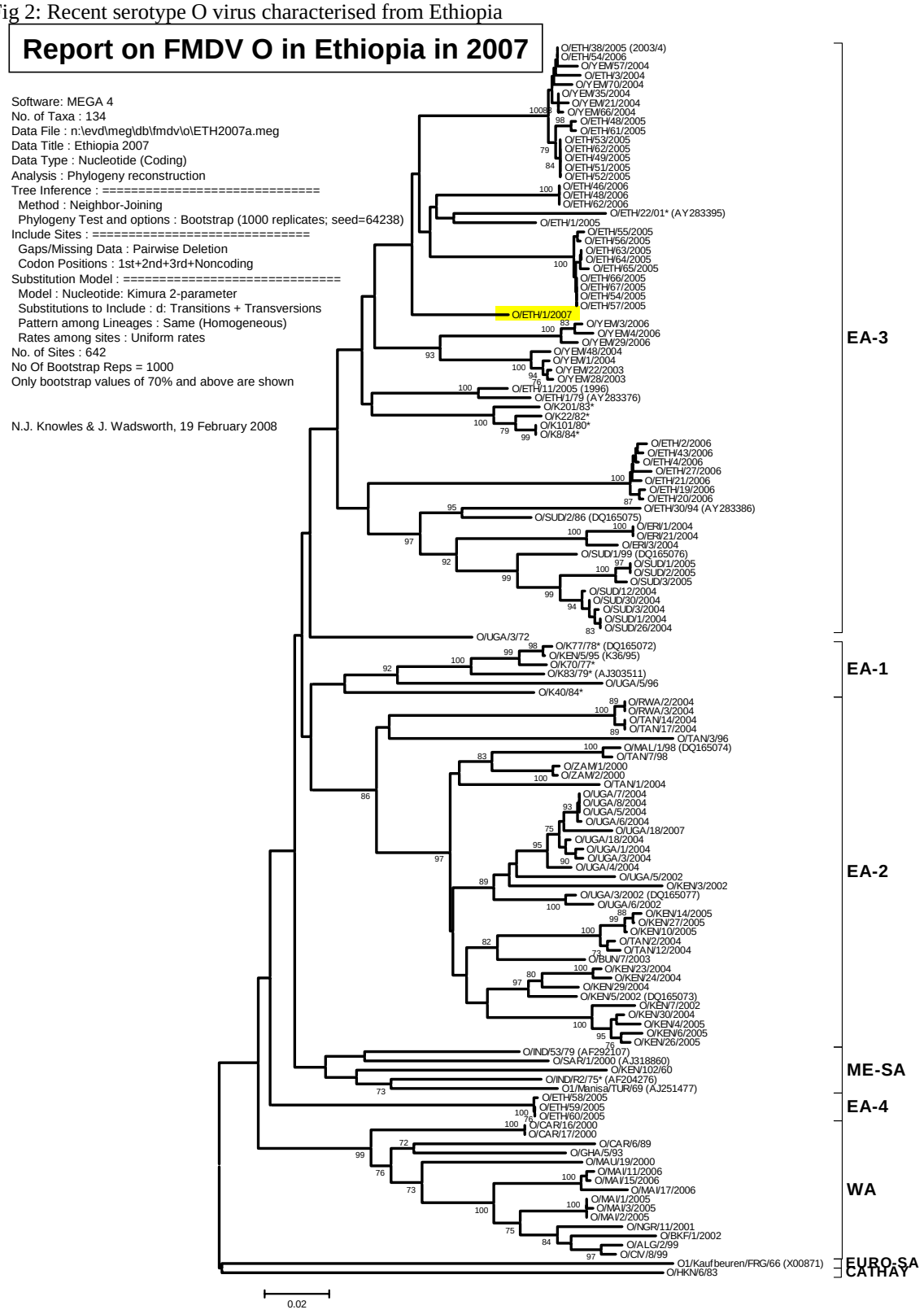


Fig 3: Recent serotype A virus characterised from Ethiopia

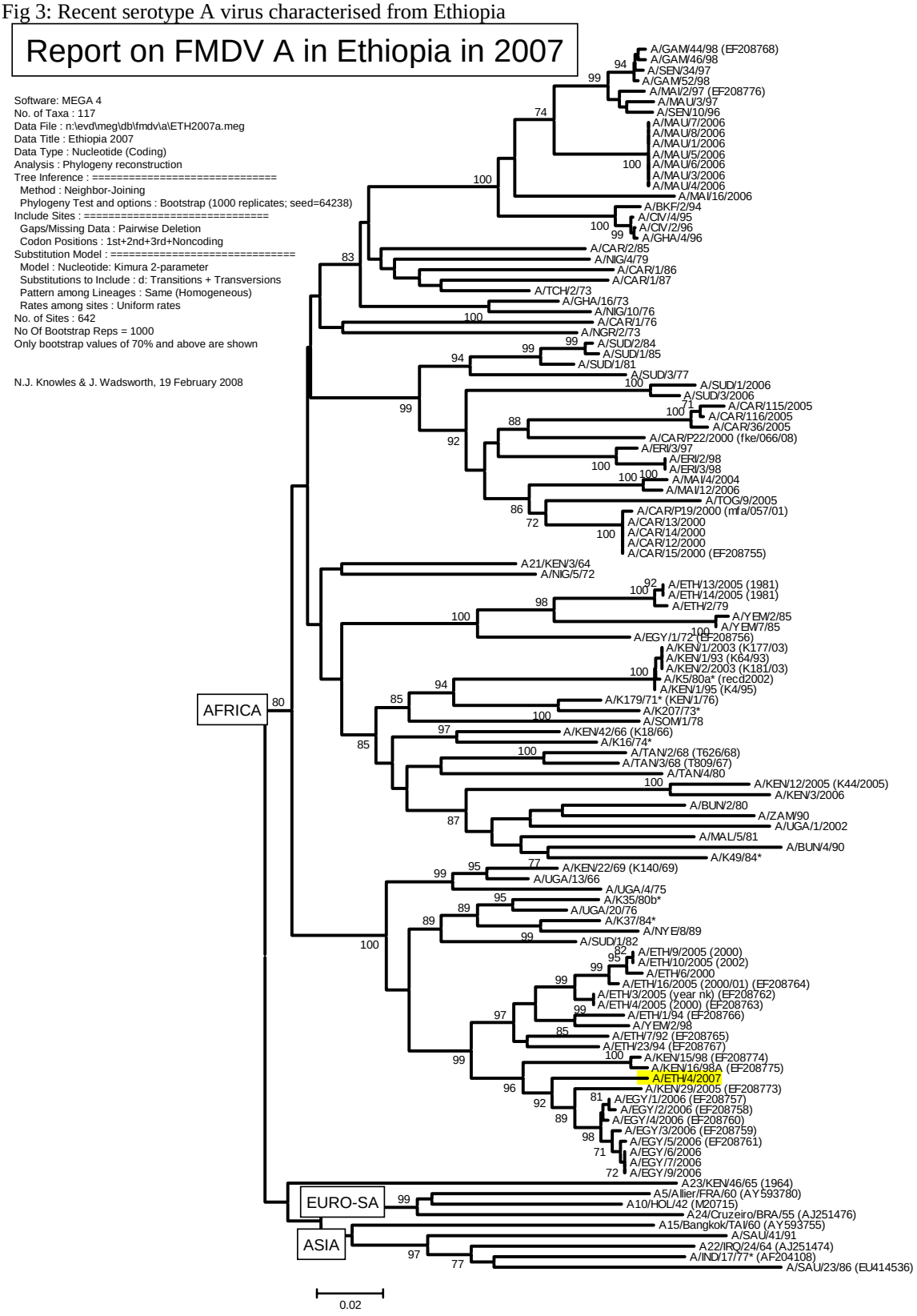


Fig 4: Recent serotype SAT1 virus characterised from Ethiopia

Report on FMDV SAT 1 from Ethiopia in 2007

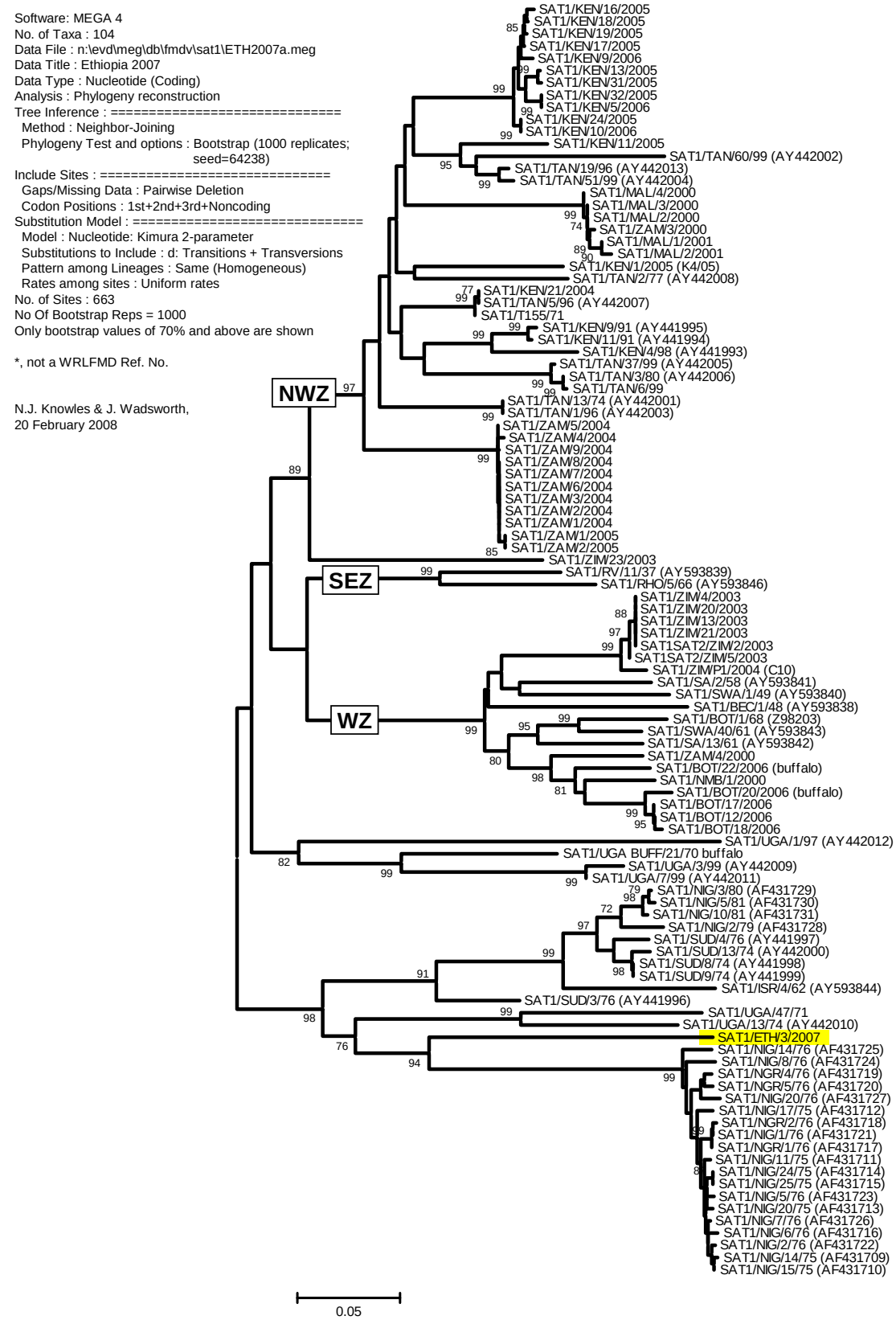
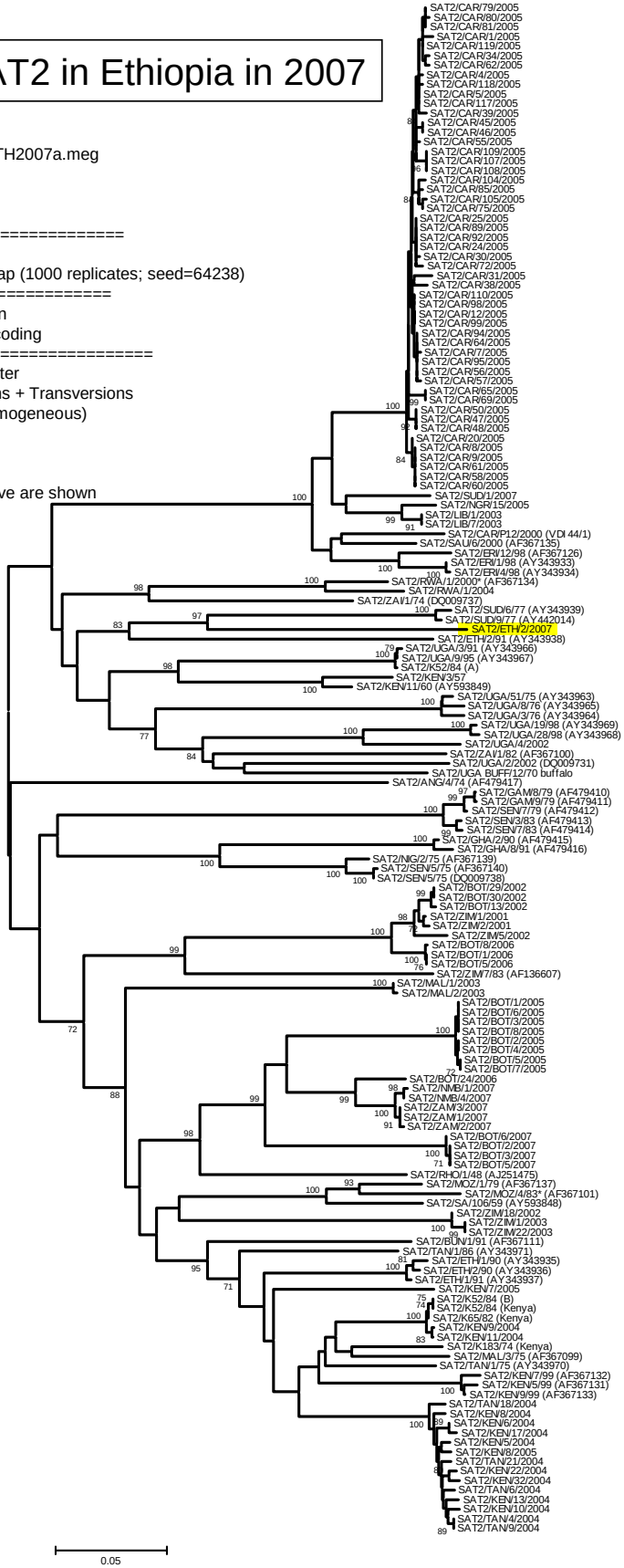


Fig 5: Recent serotype SAT2 virus characterised from Ethiopia

Report on FMDV SAT2 in Ethiopia in 2007

Software: MEGA 4
No. of Taxa : 160
Data File : n:\evd\meg\db\fmdv\sat2\ETH2007a.meg
Data Title : Ethiopia 2007
Data Type : Nucleotide (Coding)
Analysis : Phylogeny reconstruction
Tree Inference : ==========
  Method : Neighbor-Joining
  Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
Include Sites : ==========
  Gaps/Missing Data : Pairwise Deletion
  Codon Positions : 1st+2nd+3rd+Noncoding
Substitution Model : ==========
  Model : Nucleotide: Kimura 2-parameter
  Substitutions to Include : d: Transitions + Transversions
  Pattern among Lineages : Same (Homogeneous)
  Rates among sites : Uniform rates
No. of Sites : 651
No Of Bootstrap Reps = 1000
Only bootstrap values of 70% and above are shown

N.J. Knowles & J. Wadsworth
20 February 2008



Annex 4. RECOMMENDATIONS FROM THE WRL ON FMD VIRUS STRAINS INCLUDED IN FMDV ANTIGEN BANKS – December 2007

High Priority

O Manisa (*covers panasian topotype)*
O BFS or Campos
A24 Cruzeiro
Asia 1 Shamir
A Iran ’96
A22 Iraq
SAT 2 Saudi Arabia *(or equivalent)*
(not in order of importance)

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 (not in order of importance)

Low Priority

A15 Bangkok related strain
A87 Argentina related strain
C Noville
SAT 2 Kenya
SAT 1 Kenya
SAT 3 Zimbabwe
A Kenya (not in order of importance)