WRLFMD

WRLFMD Quarterly Report July-September 2009

Reference Laboratory Contract Report

10/20/2009
WRLFMD

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OIE/FAO World Reference Laboratory Report[1]
July-September 2009

Foot-and-Mouth Disease

[1] N.B. Copies of all the individual reports cited herein can be obtained from Dr. Jef Hammond, IAH-Pirbright, jef.hammond@bbsrc.ac.uk

Summary

There were no outbreaks officially reported in FMD-free countries that did not practice vaccination between July and September 2009.

FMD type A in the Middle East
In the Middle East the A-Iran-05 strain continues to evolve. During the past two years four distinct sub-lineages have been recognised and named A-Iran-05^{ARD-07}, A-Iran-05^{EZM-07}, A-Iran-05^{AFG-07} and A-Iran-05^{BAR-08}. A new sub-lineage has appeared in Pakistan and we will maintain a watching brief on its progress. It will be named if it becomes more widespread.

FMD type O in Nepal and Sri Lanka
Samples received from these two countries demonstrate that there are type O viruses circulating in southern Asia which are not part of the PanAsia-2 lineage.

FMD type O in Taiwan
In Taiwan FMDV O (CATHAY topotype) continues to occur sporadically in pigs.

FMD type SAT 2 in Botswana
SAT 2 continues to cause sporadic problems in the north-west of the country.

Uncharacterised FMD viruses
A number of other outbreaks have occurred where samples have not been sent to the WRLFMD. It is probable that the countries involved have performed their own genetic characterisation; however, through the OIE/FAO laboratory network we would also like to encourage the submission of samples (or complete VP1 sequences) to the WRLFMD.

WRL vaccine recommendations have not changed from the previous report (Annex 3) where the availability of new vaccines against the FMDV serotype A Iran-05 strain was highlighted.

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/2009.htm.

Results from samples received at WRL (status of samples being tested) are shown in Table 1 and a complete list of clinical sample diagnostics made by the WRL between July and September 2009 is shown in annex 1 Table A. A record of all samples received to IAH-Pirbright (July-September 2009) is shown in annex 1 Table B.

Table 1: Status of sequencing of samples received by the WRLFMD from July-September 2009.

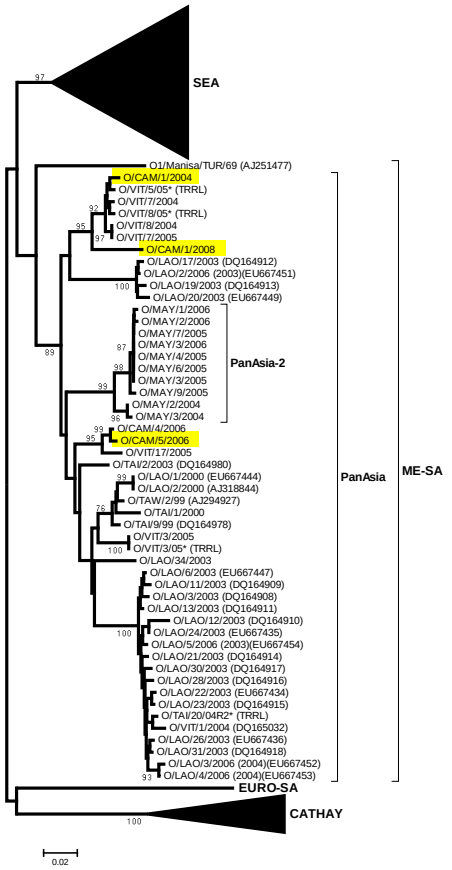
Batch	Date Recd.	Country	Serotype	No. of isolates	Status
WRLFMD/2009/00022	30/04/2009	Kenya	A	2	Completed
WRLFMD/2009/00022	30/04/2009	Kenya	O	5	Completed
WRLFMD/2009/00022	30/04/2009	Kenya	O + SAT 1	1	SIP
WRLFMD/2009/00022	30/04/2009	Kenya	SAT 1	13	Completed
WRLFMD/2009/00022	30/04/2009	Kenya	SAT 2	6	Completed
WRLFMD/2009/00025	01/05/2009	Thailand	O	10	Completed
WRLFMD/2009/00025	01/05/2009	Thailand	A	12	Completed
WRLFMD/2009/00026	01/05/2009	Cambodia	O	3	Completed
WRLFMD/2009/00026	01/05/2009	Cambodia	A	1	Completed
WRLFMD/2009/00027	01/05/2009	Myanmar	O	2	Completed
WRLFMD/2009/00029	02/06/2009	Israel	O	26	Completed
WRLFMD/2009/00029	02/06/2009	Israel	A	18	Completed
WRLFMD/2009/00032	02/06/2009	Palestinian A.T.	O	17	Completed
WRLFMD/2009/00033	22/06/2009	Nepal	O	12	Completed
WRLFMD/2009/00035	22/06/2009	Taiwan	O	1	Completed
WRLFMD/2009/00036	15/06/2009	Pakistan	A	9	Completed
WRLFMD/2009/00037	13/07/2009	Israel	A	1	Completed
WRLFMD/2009/00038	27/07/2009	Israel	A	1	Completed
WRLFMD/2009/00039	31/07/2009	Botswana	SAT2	4	Completed
WRLFMD/2009/00040	19/08/2009	Saudi Arabia	O	2	Completed
WRLFMD/2009/00041	24/08/2009	Sri Lanka	O	1	Completed
WRLFMD/2009/00042	03/09/2009	Yemen	O	5	Completed
WRLFMD/2009/00043	03/09/2009	Ethiopia	O	6	Completed
WRLFMD/2009/00043	03/09/2009	Ethiopia	SAT2	2	Completed
WRLFMD/2009/00044	18/09/2009	South Africa	SAT3*	2	Completed
WRLFMD/2009/00045	18/09/2009	Swaziland	SAT1*	2	Completed
WRLFMD/2009/00046	18/09/2009	Mozambique	SAT1*	1	Completed
WRLFMD/2009/00047	18/09/2009	Malawi	SAT2*	1	Completed
WRLFMD/2009/00048	18/09/2009	Uganda	SAT3*	1	SIP
WRLFMD/2009/00049	28/08/2009	Pakistan	A	4	Completed
WRLFMD/2009/00049	28/09/2009	Pakistan	Asia 1	3	Completed
Total				174	

SIP, sequencing in progress.
*, historical samples requested from the OVI for sequencing studies.

Detailed Analysis: ASIA

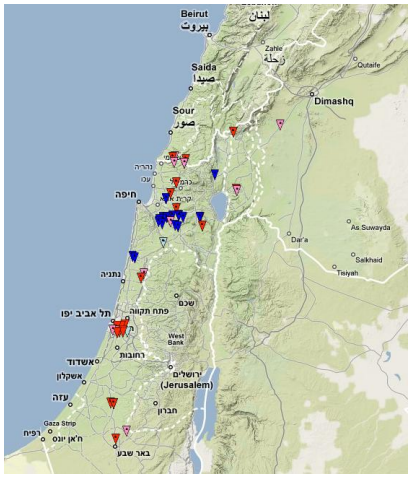
Cambodia: Three type O (collected in 2004, 2006 and 2008) and one type A (collected in 2008) FMD viruses were isolated during the last reporting period and the genotyping results for the type A virus was reported. VP1 sequencing has now been completed for the type O's. All three viruses belong to the ME-SA topotype, PanAsia strain and were most closely related to viruses from Vietnam.

FMD viruses isolated from Cambodia. Red circles are type O and the blue circle is type A.



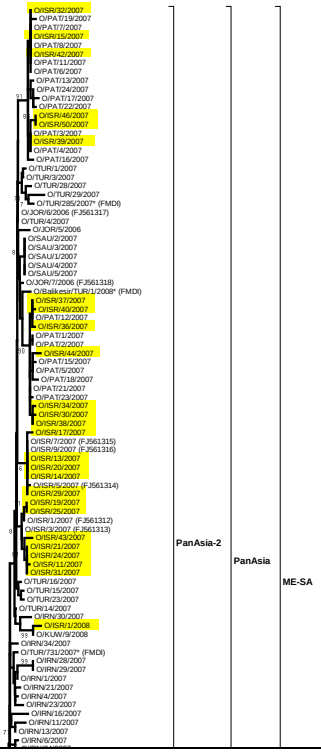
Batch: WRLFMD/2009/00026; received: 01/05/2009

Israel: 26 FMD type O viruses were isolated (25 from 2007 and one from 2008) during the previous reporting period. Phylogenetic analyses showed all the viruses to be closely related and to belong to the ME-SA topotype, PanAsia-2 lineage.

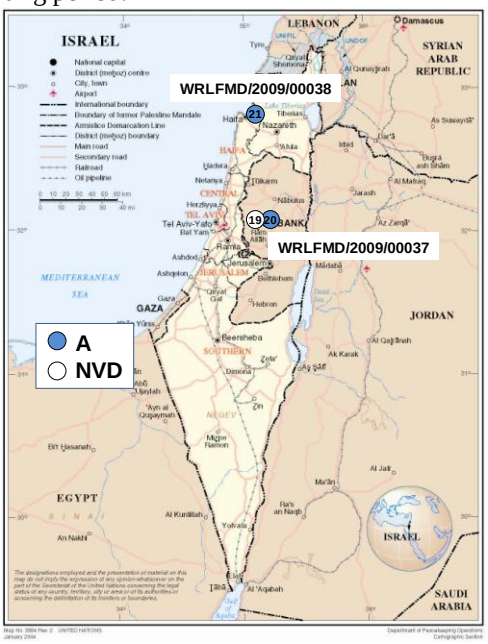


Dark blue – type A; red – type O; light blue – FMDV-GD; pink – NVD.

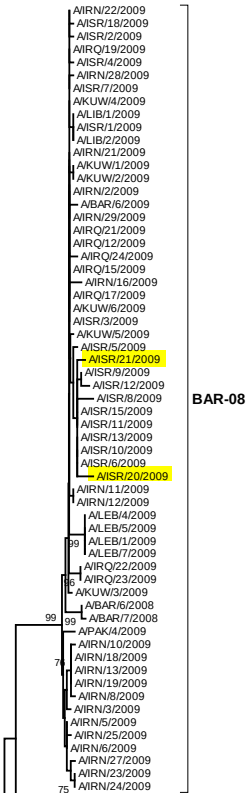
Batch: WRLFMD/2009/00029; received: 02/06/2009



Israel: 12/07/2009: 14 outbreaks of FMDV A were reported to the OIE. They occurred between March and July 2009. Two FMDV A viruses were isolated from three samples received in July 2009. Both belonged to the ASIA topotype, A-Iran-05^{BAR-08} lineage, as were Israeli viruses isolated during the last reporting period.

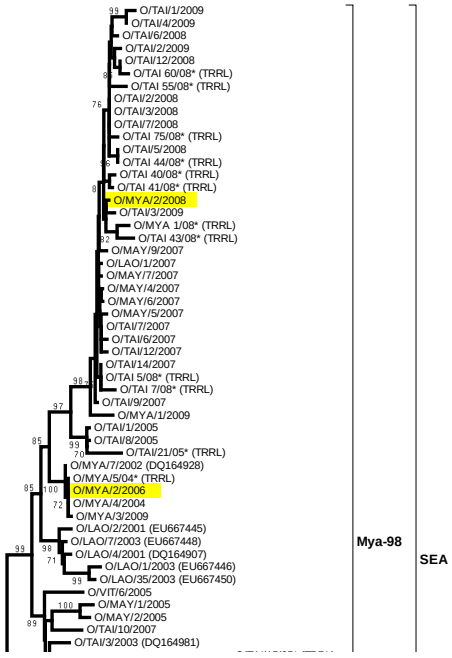


Batch: WRLFMD/2009/00037; received: 27/07/2009
Batch: WRLFMD/2009/00038; received: 31/07/2009

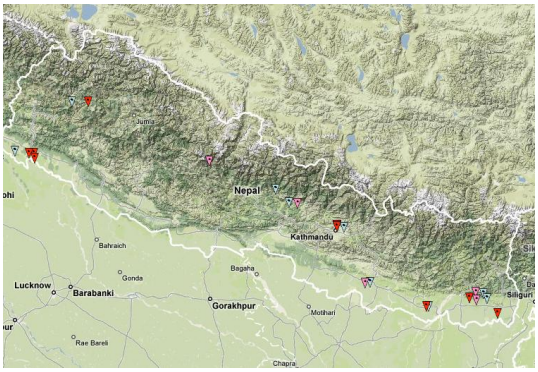


Myanmar: Two type O viruses were received from the Thailand RRL during the last reporting period (O/MYA/2/2006 and O/MYA/2/2008). Phylogenetic analysis showed they both belonged to the SEA topotype, Mya-98 lineage.

Batch: WRLFMD/2009/00027;
received: 01/05/2009

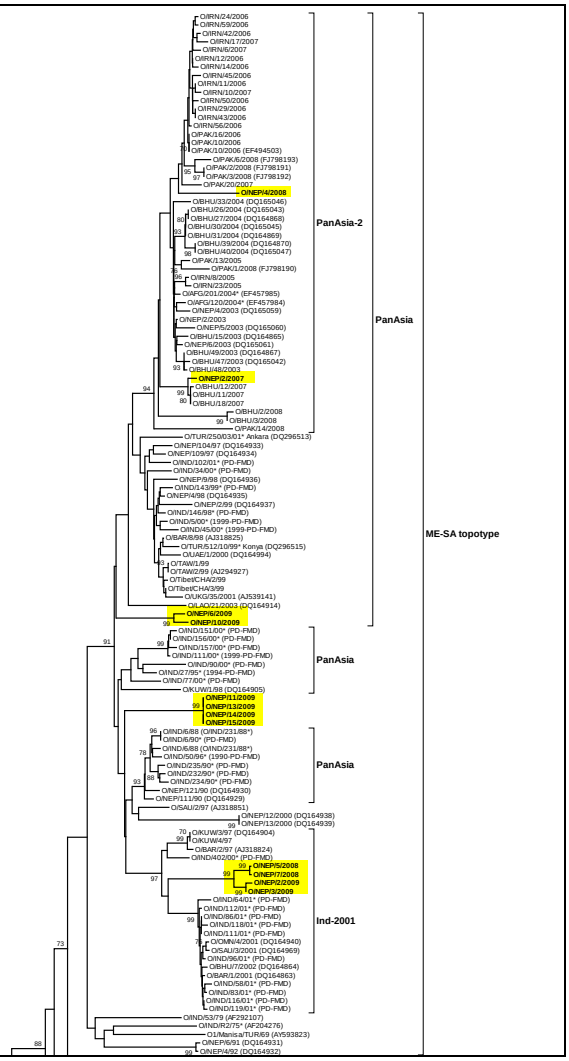


Nepal: During the previous reporting period, 12 FMD type O viruses were isolated from samples collected in 2009; phylogenetic analysis showed that all belonged to the ME-SA topotype. Two of the virus isolates belonged to the PanAsia-2 lineage (O/NEP/2/2007 & O/NEP/4/2008) and four to the Ind-2001 lineage (O/NEP/5/2008, O/NEP/7/2008, O/NEP/2/2009 & O/NEP/3/2009), while six others fell into two distinct lineages which were not easy to classify (NEP/6/2009 & NEP/10/2009 and NEP/11/2009, NEP/13/2009, NEP/14/2009 & NEP/15/2009).

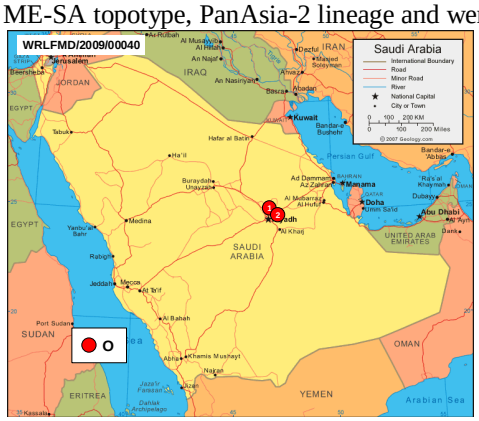


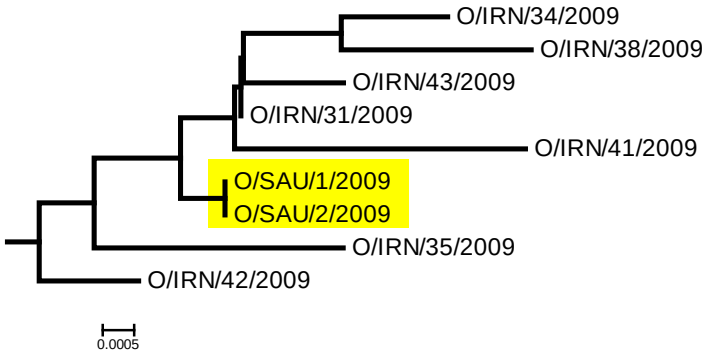
Red – type O; light blue – FMDV-GD; pink – NVD.

Batch: WRLFMD/2009/00033; received: 22/06/2009



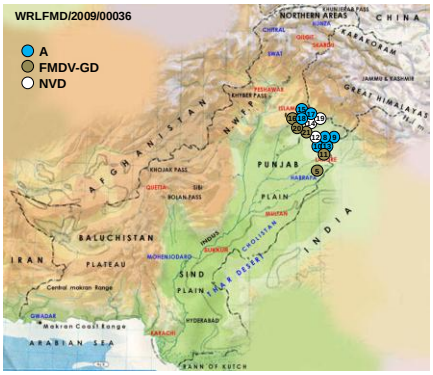
Saudi Arabia: Two FMD type O viruses isolated from cattle epithelium collected on 10/08/2009 belonged to the ME-SA topotype, PanAsia-2 lineage and were most closely related to viruses from Iran.



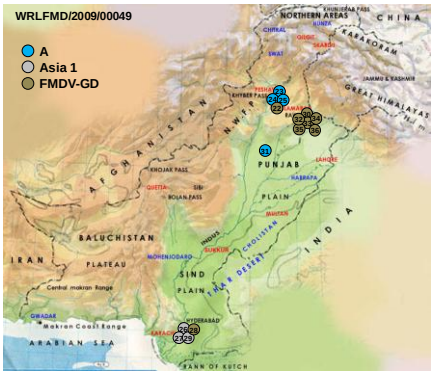


Batch: WRLFMD/2009/00040; received: 19/08/2009

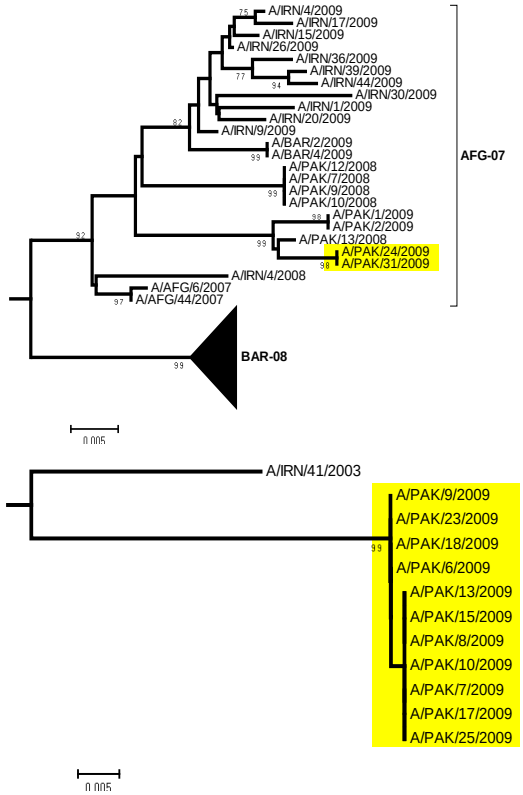
Pakistan: Nine type A viruses (A/PAK/6-10/2009, A/PAK/13/2009, A/PAK/15/2009 & A/PAK/17-18/2009) were isolated during the previous reporting period and all belonged to a new sub-lineage of the A-Iran-05 strain. A subsequent batch of samples was received on 28/09/2009 and four type A and three type Asia 1 viruses were identified (although two of the Asia 1 virus failed to grow in cell culture). Phylogenetic analyses revealed that two of the type A viruses (A/PAK/24/2009 & A/PAK/31/2009) belonged to the A-Iran-05^{AFG-07} sub-lineage while the other two (A/PAK/23/2009 & A/PAK/25/2009) belonged to a newly identified, but as yet unnamed, A-Iran-05 sub-lineage. The Asia 1 viruses (Asia1/PAK/26/2009, Asia1/PAK/27/2009 & Asia1/PAK/29/2009) were closely related to a virus (Asia1/PAK/8/2008) collected from the same region (Sindh) in 2008.

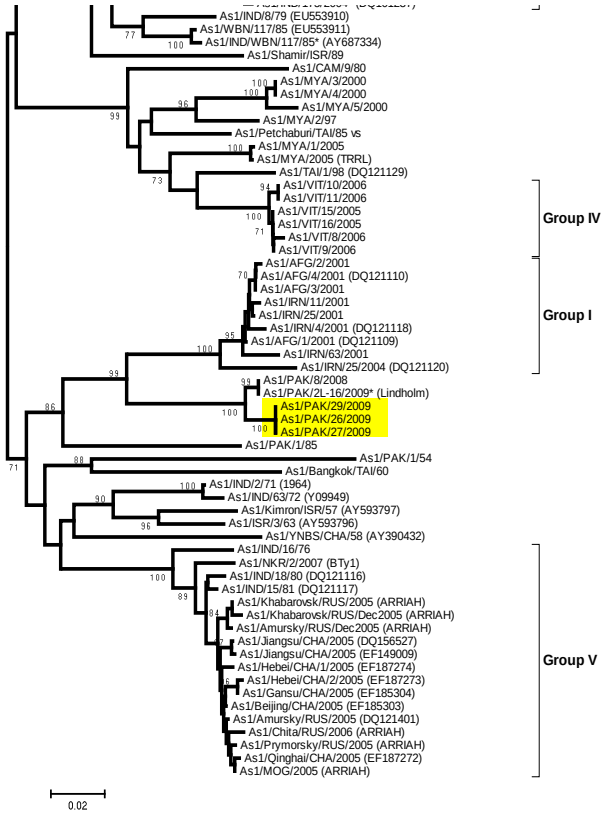


Batch: WRLFMD/2009/00036; received: 15/06/2009

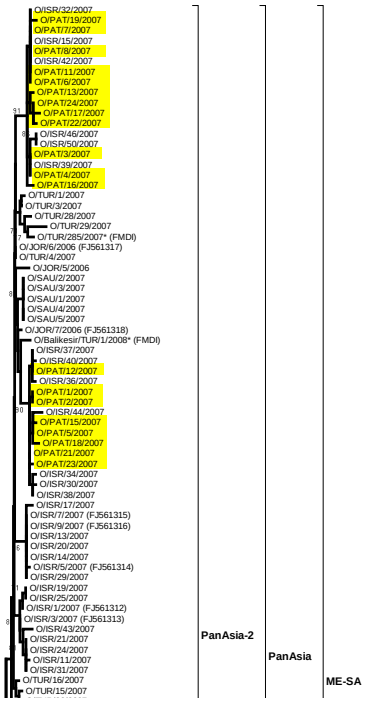


Batch: WRLFMD/2009/00049; received: 28/09/2009



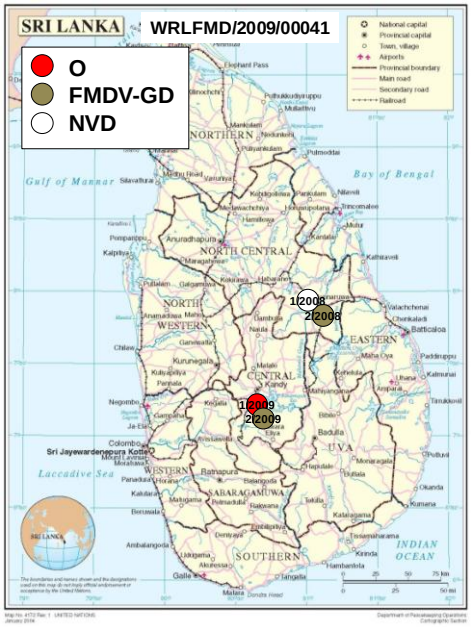


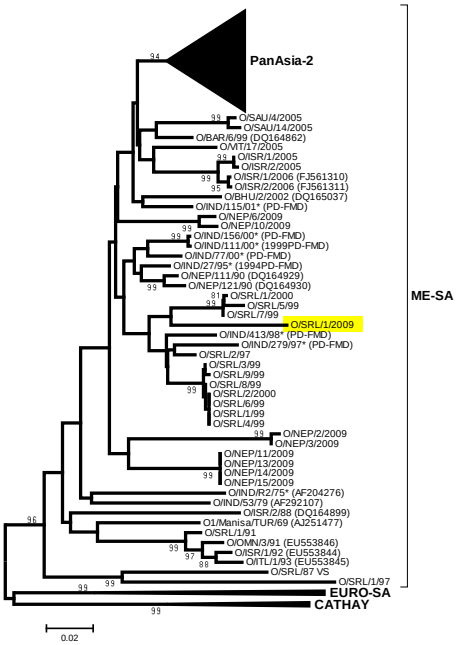
Palestinian Autonomous Territories: 20 FMD type O viruses, collected in 2007, were identified during the previous reporting period. Phylogenetic analysis showed that they were all closely related and belonged to the ME-SA topotype, PanAsia-2 lineage.



Batch: WRLFMD/2009/00032; received: 02/06/2009

Sri Lanka: A single type O virus was isolated from a batch of four samples (two collected in 2008 and two in 2009). This virus belonged to the ME-SA topotype and was most closely related to viruses isolated in Sri Lanka in 1997-2000 and to Indian viruses from 1997-1998.



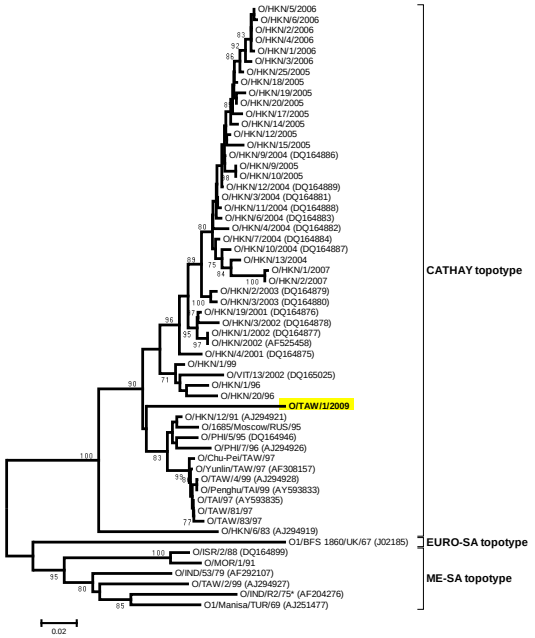


Batch: WRLFMD/2009/00041; received: 24/08/2009

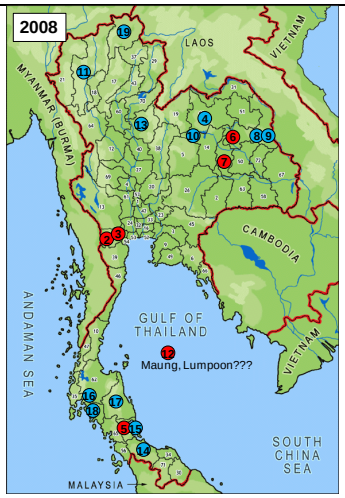
Taiwan, POC: A type O virus was isolated during the last reporting period and phylogenetic analysis showed it to belong to the CATHAY topotype. Subsequently FMDV O was reported on the 25/06/2009 (sub-clinical infection in pigs in Wandan Township, P'ing-Tung), 13/07/2009 (clinical disease in pigs in Jhubei City, Hsin-Chu) and 25/08/2009, sub-clinical infection in pigs in Sinwu Township, T'ao-Yuan). No new samples have been received by the WRLFMD.

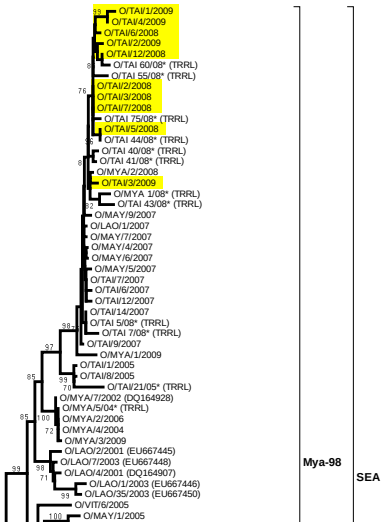
WRLFMD/2009/00035; Received 22/06/2009

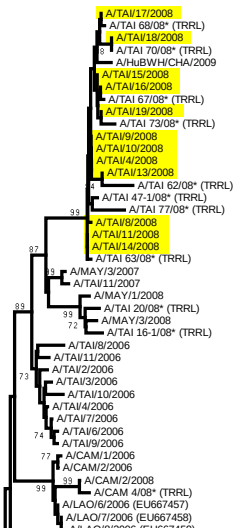
Outbreaks reported to the OIE, 25 June to 25 August 2009



Thailand: 22 FMD viruses were received from the Thailand RRL. Ten were type O (six from 2008 and four from 2009) and 12 were type A (all from 2008). The type O viruses (SEA topotype, Mya-98 lineage) were all closely related to each other and to previous virus isolates from the region. Likewise, the type A viruses (ASIA topotype) were all closely related to each other and to a recent outbreak in the People's Republic of China.

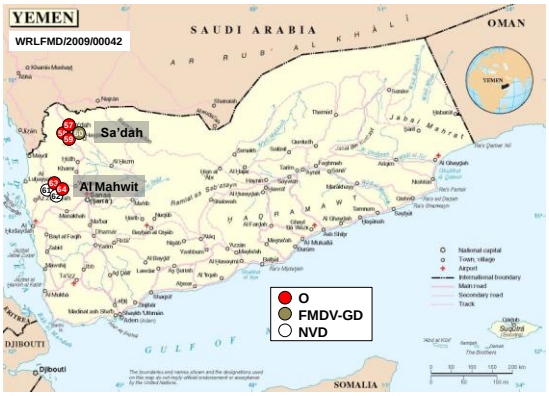


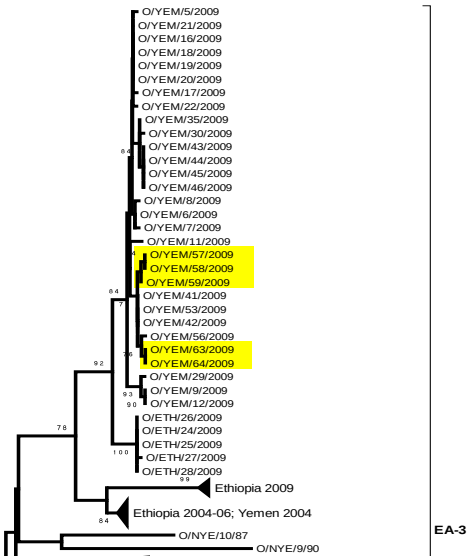




Batch: WRLFMD/2009/00025; received: 01/05/2009

Yemen Arab Republic: Five type O viruses collected in 2009 were closely related to each other and to viruses isolated earlier in the year from Yemen and Ethiopia (EA-3 topotype).

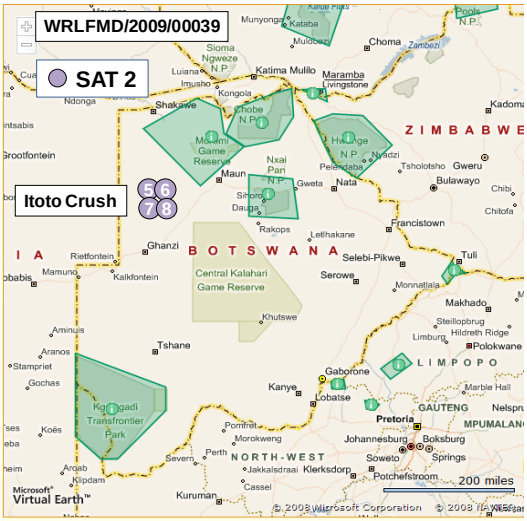


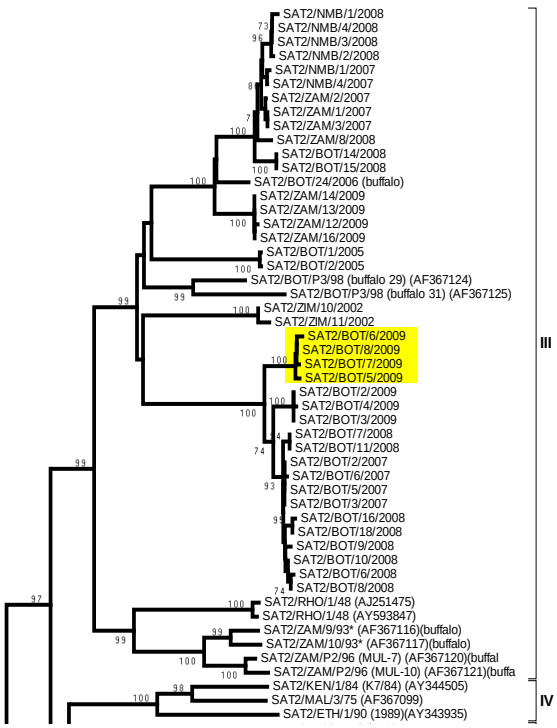


Batch: WRLFMD/2009/00042; received: 03/09/2009

Detailed Analysis: AFRICA

Botswana: Four viruses were isolated from samples from Itoto Crush in north-western Botswana. All were closely related to each other and to previously isolated viruses from the region collected in 2007-2009 and belonged to topotype III.

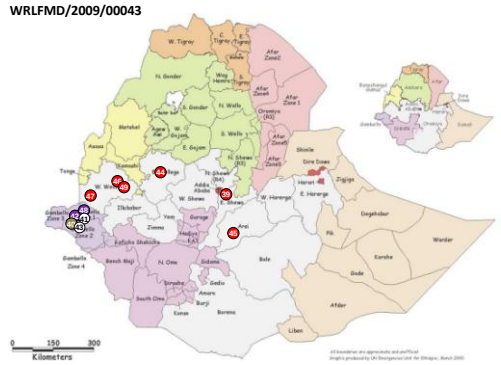




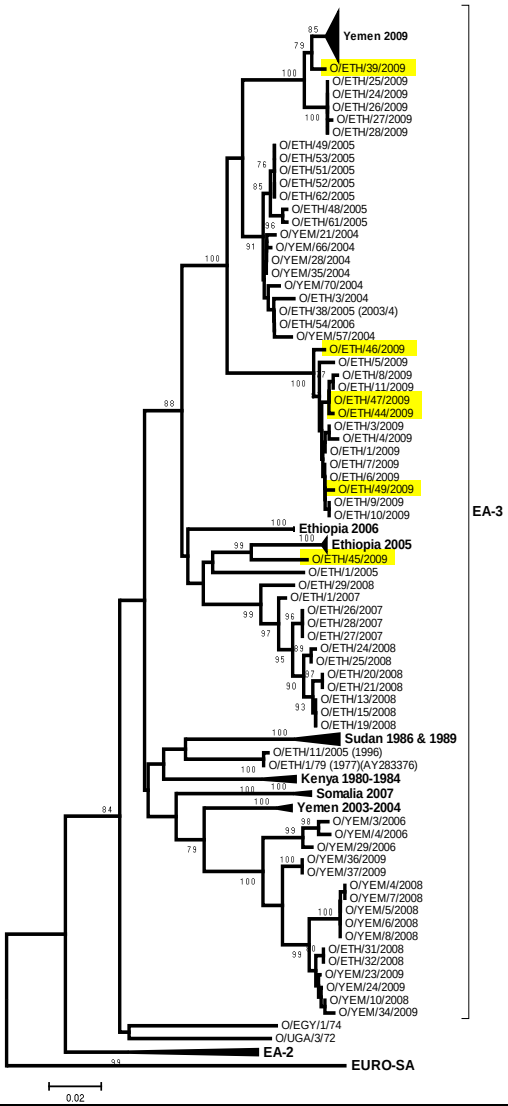
Batch: WRLFMD/2009/00039; received 31/07/2009

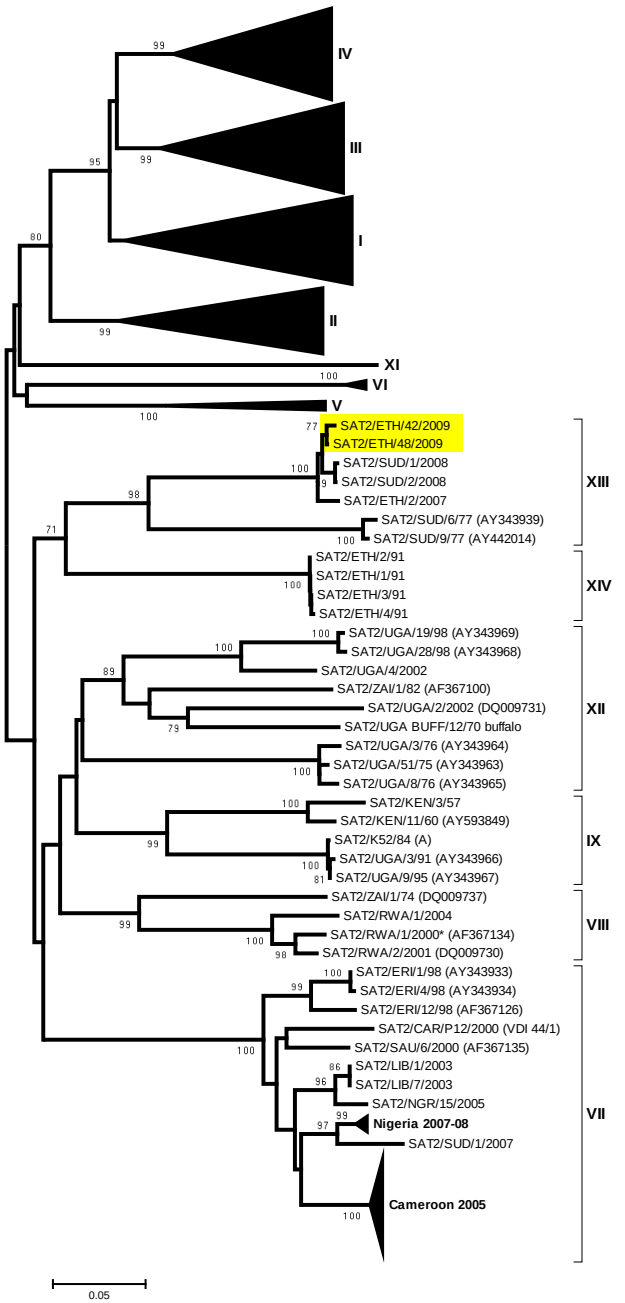
Egypt: On 17/08/2009 five outbreaks of FMDV were reported to the OIE. They occurred in cattle and buffalo during May and June 2009. Five samples from sheep were received from one of these outbreaks (at Dyarb negm, Ash Sharqiyah) during the previous reporting period (EGY/29/2009, EGY/30/2009, EGY/31/2009 & EGY/32/2009) (see previous report).

Ethiopia: Six type O and two type SAT 2 viruses were isolated during September 2009. The type O viruses belonged to three distinct sub-lineages of the EA-3 topotype. The groupings corresponded to districts within the Oromia region: i) O/ETH/39/2009 from East Shoa; ii) O/ETH/45/2009 from Arsi; iii) O/ETH/44/2009 (East Welega) and O/ETH/46/2009, O/ETH/47/2009 and O/ETH/49/2009 (West Welega). The two SAT 2 viruses belonged to topotype XIII and were closely related to each other. They were also closely related to a 2007 virus from the same part of Ethiopia and to viruses from neighbouring Sudan in 2008.

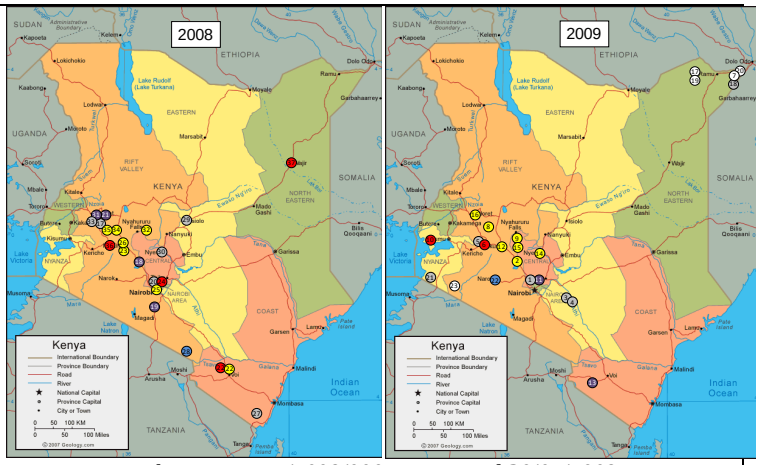


Batch: WRLFMD/2009/00043; received 03/09/2009

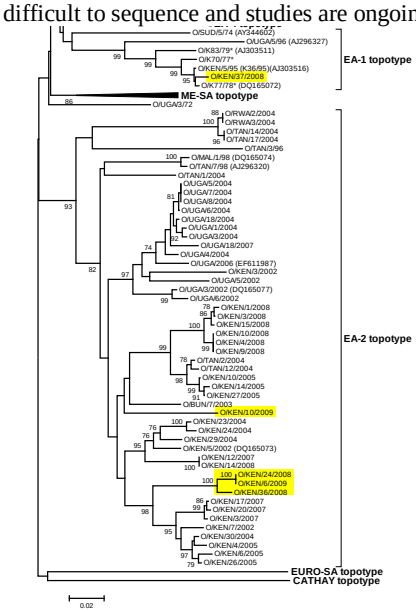


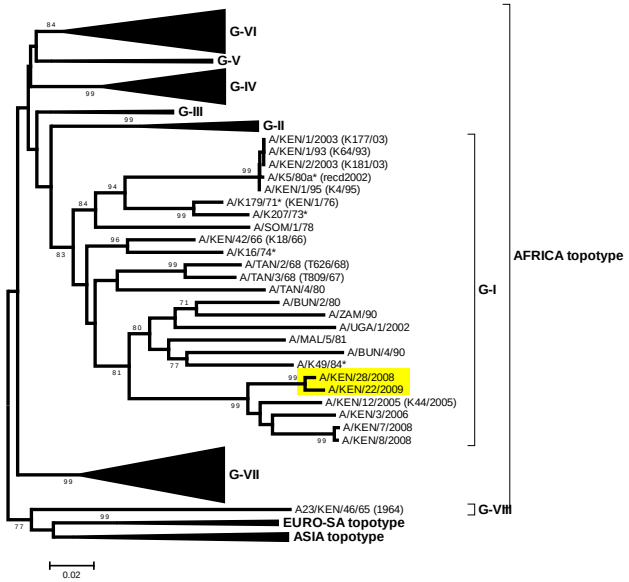


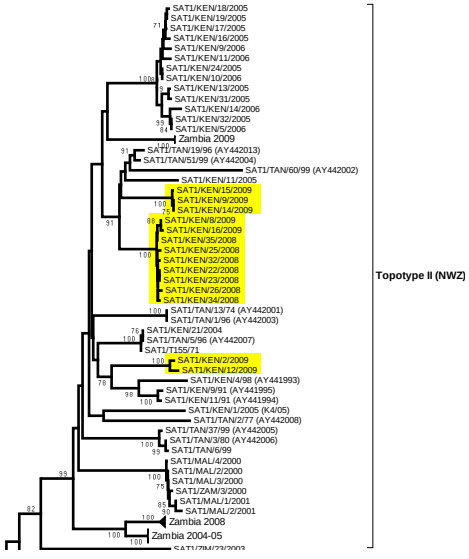
Kenya: During the previous reporting period, 27 FMD viruses were isolated from samples collected in 2008 and 2009. Of the 2008 viruses, one was type A, three were type O, six were type SAT 1, four were type SAT 2 and one was a mixture of O and SAT 1. Of the 2009 viruses, one was type A, two were type O, seven were type SAT 1 and two were type SAT 2. One of the type O viruses (O/KEN/37/2008) was closely related to the vaccine strain K77/78 (EA-1 topotype), while all the others belonged to two distinct sub-lineages of the EA-2 topotype. Both type A viruses belonged to genotype I of the AFRICA topotype and were most closely related to Kenyan viruses from 2005-2008. The 14 SAT 1 viruses all belonged to topotype II (aka NWZ) and fell into three different sub-lineages. The six SAT 2 viruses all belonged to topotype IV, but fell into two sub-lineages. A single sample which contained both O and SAT 1 virus has proven difficult to sequence and studies are ongoing.



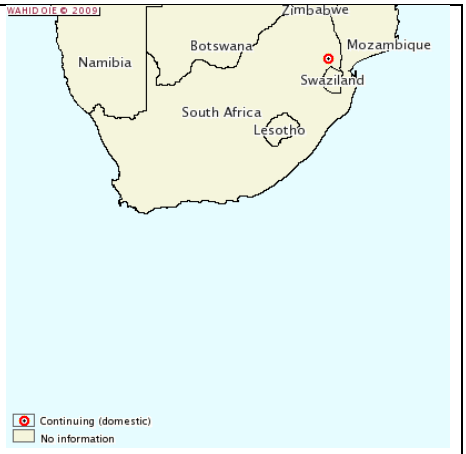
Batch: WRLFMD/2009/00022; received 30/04/2009







South Africa: On 06/09/2009 FMDV SAT 1 was reported in cattle at the Makoko dip tank, Mbombela, Mpumalanga. The outbreak occurred in the FMD Buffer Zone and will not have an effect on the FMD free status of South Africa. The affected cattle (481 in a herd of 3215) were identified at a dip tank in a rural settlement adjacent to the FMD Infected Zone (Kruger National Park) on the border between the FMD Buffer Zone and the FMD Infected Zone. 64 animals with clinical signs of disease were observed at the Makoko dip tank (estimated population at risk at the Makoko dip tank: 727 cattle). None of the cattle at the 3 adjacent dip tanks (2,488 cattle) were originally involved in the outbreak. However, subsequently, 273 (out of 5152) cattle were found to be infected at Phameni dip tank, Mbombela, Mpumalanga (adjacent to the Makoko dip tank). The origin is thought to be contact with nearby African buffalo. Phylogenetic analysis is awaited from the OVI.



Detailed Analysis: SOUTH AMERICA

Colombia: 29/07/2009: FMDV O was reported in pigs at the local slaughterhouse of Ipiales, El Charco, Ipiales, Nariño. The slaughterhouse is 5.23km from the border with Ecuador.

Vaccine matching

Eighteen FMDV type O isolates (see table C for details) from Pakistan, Turkey, Ethiopia, Myanmar, Yemen, Israel, Hong Kong, Taiwan, Kenya and Saudi Arabia collected in 2007, 2008 and 2009 were analysed antigenically by two dimensional virus neutralisation test (2dmVNT) and/or LPBE. The results showed that the majority of isolates were matched with O IND R2/75 vaccine strain by VNT. Fifteen out of seventeen tested viruses were close to O1 Manisa either by VNT or LPBE. Only six out of 17 tested virus showed an antigenic match with O BFS. O 3039 and O 4625 vaccines also gave relatively good coverage to 5 out of six and 9 out of 11 tested viruses, respectively (Table C).

Seven FMDV type A viruses (see table C for details) from Lebanon, Pakistan and Israel collected in 2008 and 2009, were analysed for antigenic relationship with various vaccine strains by 2dmVNT and/or LPBE. All isolates tested showed close match to the A TUR 06 and A SAU 41/91 (except A PAK 4/2009) vaccine strains and almost all failed to match with A_{22} IRQ. The exceptions were A PAK 13/2008 and A PAK 2/2009 which showed a relative match with A_{22} by VNT. Vaccines A Eritrea 98, A IRN 87 and A IRN 99 did not provide antigenic coverage to the tested isolates (Table C).

Five FMDV SAT 2 viruses (see table C for details) from Zambia, Kenya and Botswana collected in 2009, were analysed for antigenic relationship with various vaccine strains by 2dmVNT and/or LPBE. SAT 2 KEN 11/2009 and SAT 2 BOT 4/2009 showed an antigenic match with SAT 2 Eritrea vaccine virus. Neither SAT 2 ZIM nor SAT 2 K65/82 vaccine showed coverage to the tested field isolates by either VNT or LPBE (Table C).

Annex 1.
TABLE A: Clinical sample diagnostics made by the WRL between July and September 2009

Country	WRL for FMD Sample Identification	Animal	Date of Collection	Results		
				VI/ELISA	RT-PCR	Final report
BOTSWANA	BOT 5/2009	NK	04.07.09	SAT 2	Positive	SAT 2
4	BOT 6/2009	NK	07.07.09	SAT 2	Positive	SAT 2
	BOT 7/2009	NK	NK	SAT 2	Positive	SAT 2
	BOT 8/2009	NK	NK	SAT 2	Positive	SAT 2
ETHIOPIA	ETH 39/2009	NK	26.03.09	O	Positive	O
11	ETH 40/2009	NK	16.06.09	NVD	Positive	FMDV GD
	ETH 41/2009	NK	16.06.09	NVD	Negative	NVD
	ETH 42/2009	NK	16.06.09	SAT 2	Positive	SAT 2
	ETH 43/2009	NK	16.06.09	NVD	Negative	NVD
	ETH 44/2009	NK	19.06.09	O	Positive	O
	ETH 45/2009	NK	20.06.09	O	Positive	O
	ETH 46/2009	NK	23.06.09	O	Positive	O
	ETH 47/2009	NK	25.06.09	O	Positive	O
	ETH 48/2009	NK	12.08.09	SAT 2	Positive	SAT 2
	ETH 49/2009	Cattle	NK	O	Positive	O
ISRAEL	ISR 19/2009	Goat	NK	NVD	Negative	NVD
3	ISR 20/2009	Goat	NK	A	Positive	A
	ISR 21/2009	Sheep	12.07.09	A	Positive	A
MALAWI	MAL 1/2008	NK	00.00.08	SAT 1		SAT 1
1						
MOZAMBIQUE	MOZ 2/2002	NK	00.00.02	SAT 1		SAT 1
1						
PAKISTAN	PAK 22/2009	Cattle	30.06.09	NVD	Positive	FMDV GD
15	PAK 23/2009	Buffalo	30.06..09	A	Positive	A
	PAK 24/2009	Buffalo	30.06.09	A	Positive	A
	PAK 25/2009	Buffalo	30.06.09	A	Positive	A
	PAK 26/2009	Buffalo	07.07.09	Asia 1	Positive	Asia 1
	PAK 27/2009	Buffalo	07.07.09	Asia 1	Positive	Asia 1
	PAK 28/2009	Buffalo	07.07.09	NVD	Positive	FMDV GD
	PAK 29/2009	Buffalo	07.07.09	Asia 1	Positive	Asia 1
	PAK 30/2009	Buffalo	12.07.09	NVD	Positive	FMDV GD
	PAK 31/2009	Buffalo	15.07.09	A	Positive	A
	PAK 32/2009	Buffalo	18.07.09	NVD	Positive	FMDV GD
	PAK 33/2009	Cattle	27.07.09	NVD	Positive	FMDV GD
	PAK 34/2009	Buffalo	27.07.09	NVD	Positive	FMDV GD
	PAK 35/2009	Buffalo	06.08.09	NVD	Positive	FMDV GD
	PAK 36/2009	Buffalo	06.08.09	NVD	Positive	FMDV GD
SAUDI ARABIA	SAU 1/2009	Cattle	10.08.09	O	Positive	O
2	SAU 2/2009	Cattle	10.08.09	O	Positive	O

SOUTH AFRICA	2	SAR 1/2006	NK	00.00.06	SAT 3		SAT 3
		SAR 2/2006	NK	00.00.06	SAT 3		SAT 3
SRI LANKA	4	SRL 1/2008	Cattle	08.02.08	NVD	Negative	NVD
		SRL 2/2008	Cattle	08.02.08	NVD	Positive	FMDV GD
		SRL 1/2009	Buffalo	18.02.09	O	Positive	O
		SRL 2/2009	Buffalo	18.02.09	NVD	Positive	FMDV GD
SWAZILAND	2	SWZ 1/2000	NK	00.00.00	SAT 1		SAT 1
		SWZ 2/2000	NK	00.00.00	SAT 1		SAT 1
UGANDA	1	UGA 10/97	Buffalo	00.00.97	SAT 3		SAT 3
YEMEN	8	YEM 57/2009	Cattle	15.03.09	O	Positive	O
		YEM 58/2009	Cattle	15.03.09	O	Positive	O
		YEM 59/2009	Cattle	18.03.09	O	Positive	O
		YEM 60/2009	Sheep	04.04.09	NVD	Positive	FMDV GD
		YEM 61/2009	Goat	08.04.09	NVD	Negative	NVD
		YEM 62/2009	Goat	08.04.09	NVD	Negative	NVD
		YEM 63/2009	Cattle	06.07.09	O	Positive	O
		YEM 64/2009	Cattle	06.07.09	O	Positive	O

Total 54

	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 viral genome
NVD	no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected
NK	not known

TABLE B: Summary of samples collected and received to IAH-Pirbright (July-September 2009)

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
BOTSWANA	4	-	-	-	-	4	-	-	-	-	4	-
ETHIOPIA	11	6	-	-	-	2	-	-	-	3	9	2
ISRAEL	3	-	2	-	-	-	-	-	-	1	2	1
MALAWI	1	-	-	-	-	1	-	-	-	-	1	-
MOZAMBIQUE	1	-	-	-	1	-	-	-	-	-	1	-
PAKISTAN	15	-	4	-	-	-	-	3	-	8	15	-
SAUDI ARABIA	2	2	-	-	-	-	-	-	-	-	2	-
SOUTH AFRICA	2	-	-	-	-	-	2	-	-	-	2	-
SRI LANKA	4	1	-	-	-	-	-	-	-	3	3	1
SWAZILAND	2	-	-	-	2	-	-	-	-	-	2	-
UGANDA	1	-	-	-	-	-	1	-	-	-	1	-
YEMEN	8	5	-	-	-	-	-	-	-	3	6	2
TOTAL	**54**	**14**	**6**	**-**	**3**	**7**	**3**	**3**	**-**	**18**	**48**	**6**

*	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
**	samples from Malawi, Mozambique, South Africa, Swaziland and Uganda submitted for characterisation

TABLE C: Antigenic characterisation of FMD field isolates by matching with vaccine strains by VNT and/or LPBE – r1 value data from 1st July to 30th September 2009

Type O:

Field Isolate	r1 values by 2dmVNT			r1 values by LPBE						
	O Manisa	O BFS	O Ind R2/75	O 4174	O BFS	O Hkn 6/83	O K77/78	O 4625	O Manisa	O 3039
O Pak 14/2008	0.69	0.21	0.79	0.15	0.13	0.50	0.15	0.44	0.50	
O Tur 3/2009	>0.86	0.25	>1.0	0.05	0.03				0.15	
O Tur 35/2009	0.24	0.28	0.43	0.28						
O Eth 24/2009	0.32	0.43	>1.0	0.11	0.13	0.25	0.13		0.75	
O Eth 28/2009	0.32	0.74	>1.0	0.16	0.13	0.5			0.46	
O Mya 3/2009	0.20	0.19	0.27							
O Yem 5/2009	0.08	0.15	>0.63	0.17	0.08			0.71	0.44	0.50
O Yem 42/2009	0.04	0.05	0.65	0.18	0.18			0.88	0.44	0.57
O Yem 56/2009	0.21	0.36	>1.0	0.25	0.17			0.71	0.71	0.84
O Isr 43/2007	0.36	0.17	>0.74	0.18	0.10			0.50	0.63	0.84
O Isr 50/2007	0.21	0.20	>1.0	0.25	0.18			0.32	0.44	0.33
O Isr 1/2008					0.05					0.11
O Hkn 1/2009	0.24	0.08	0.46	0.15	0.00		0.05	0.11	0.63	
O Hkn 2/2009	0.29	0.07	0.32	0.15	0.00		0.09	0.11	0.44	
O Taw 1/2009	>0.76	0.25	0.66	0.13					0.59	
O Ken 10/2009	0.92	0.82	0.63	0.59	0.59	0.84	0.54	0.38	>1	
O Sau 1/2009	0.74	0.72	0.46	0.15	0.20	0.75	>0.63	0.38	1.00	
O Sau 2/2009	0.72	0.66	0.35	0.13	0.22	0.75		0.20	0.63	

Type A:

Field Isolate	r1 values by 2dmVNT							r1 values by LPBE					
	A Eri 98	A Ind 17/82	A Irn87	A22 Irq	A May97	A Tur06	A Sau 41/91	A22 Irq 24	A Eri 98	A Irn 99	A May 97	A Irn 87	A Sau 95
A Leb 1/2009	0.05	0.29	0.08	0.25	0.03	0.58	0.37	0.21			0.36	0.11	
A Leb 5/2009	0.04	0.20	0.05	0.12	0.01	0.47	0.35	0.17	0.16		0.30	0.08	
A Isr 2/2009	0.08	0.28	0.12	0.28	0.05	0.86	0.51	0.36	0.05		0.42	0.14	
A Isr 18/2009	0.08	0.31	0.11	0.23	0.07	>1.0	0.60	0.32			0.50	0.14	
A Pak 13/2008		0.08		0.45		>1.0	0.42	0.29			0.34		0.09
A Pak 2/2009		0.08		0.63		>1.0	>1.0	0.27			0.23		0.09
A Pak 4/2009		0.35		0.09		0.46	0.08	0.05		0.16	0.56		

Type SAT 2:

Field Isolate	r1 values by 2dmVNT		r1 values by LPBE
	Sat2 Eritrea	Sat2 Zim	Sat2 K65/82
Sat2 Zam 14/2009	0.22	0.04	0.05
Sat2 Zam 16/2009	0.17	0.08	0.06
Sat2 Ken 11/2009	0.35	0.28	0.11
Sat2 Bot 2/2009	0.23	0.09	0.06
Sat2 Bot 4/2009	0.32	0.07	0.07

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 LPB 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. Recent FMD Publications cited by PubMed

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Annex 3. RECOMMENDATIONS FROM WRLFMD ON FMD VIRUS STRAINS TO BE INCLUDED IN FMDV ANTIGEN BANKS – September 2009

High Priority

O Manisa (*covers panasian topotype)*
O BFS or Campos
A24 Cruzeiro
Asia 1 Shamir
*A Iran-05
A22 Iraq
SAT 2 Saudi Arabia *(or equivalent)*

(not in order of importance)

Medium Priority

A Eritrea
A Iran '96
SAT 2 Zimbabwe
A Iran 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)

*= recently available