

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Date: 3 March 2010

FMDV type O

Country: Laos

Period: 2008-2009

No. of isolates: 3

BATCH: WRLFMD/2010/00005



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FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: O	Report date: 02/03/2010
WRLFMD Ref No: LAO/2/2008	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00005	Checked by: D.P. King
Sender Ref: LAO 6/08 R2	
Location: Sikhottabong, Vientian Capital, Laos	Topotype: SEA
Date collected: 02/04/2008	Genotype/strain: Mya-98
Date received by WRLFMD: 05/02/2010	Sequence filename: LAO08-02.SEQ
Date received for sequencing: 24/02/2010	Date sequence last updated: 02/03/2010
Species: Pig	No. of Nt determined: 639
Material used: LK2 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 300
	Total turn-around time: 25 days
	Sequencing time: 6 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/LAO/3/2008	LAO08-03	639	639	0	100.00	0.00	SEA	Mya-98
2	O/TAI 41/08* (TRRL)	TAI08-AD	639	636	0	99.53	0.47	SEA	Mya-98
3	O/MYA/2/2008	MYA08-02	639	635	0	99.37	0.63	SEA	Mya-98
4	O/TAI/2/2008	TAI08-02	639	635	0	99.37	0.63	SEA	Mya-98
5	O/TAI/3/2008	TAI08-03	639	635	0	99.37	0.63	SEA	Mya-98
6	O/TAI/7/2008	TAI08-07	639	635	0	99.37	0.63	SEA	Mya-98
7	O/TAI 40/08* (TRRL)	TAI08-AC	639	635	0	99.37	0.63	SEA	Mya-98
8	O/LAO/1/2007	LAO07-01	639	634	0	99.22	0.78	SEA	Mya-98
9	O/MAY/4/2007	MAY07-04	639	634	0	99.22	0.78	SEA	Mya-98
10	O/MAY/7/2007	MAY07-07	639	634	0	99.22	0.78	SEA	Mya-98
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/MYA/7/98 (DQ164925)	MYA98-07	639	594	0	92.96	7.04	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	570	0	89.20	10.80	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	544	0	85.13	14.87	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	541	0	84.66	15.34	SEA	Cam-94
5	O/IND/53/79 (AF292107)	IND79A53	639	540	0	84.51	15.49	ME-SA	unnamed
6	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	540	0	84.51	15.49	ME-SA	unnamed
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	536	0	83.88	16.12	ME-SA	PanAsia
8	O/IRN/8/2005	IRN05-08	639	535	0	83.72	16.28	ME-SA	PanAsia-2
9	O/K83/79* (AJ303511)	KEN79B83	638	532	1	83.39	16.61	EA-1	unnamed
10	O/ETH/1/2007 (FJ798137)	ETH07-01	639	532	0	83.26	16.74	EA-3	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O	Report date: 02/03/2010
WRLFMD Ref No: LAO/3/2008	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00005	Checked by: D.P. King
Sender Ref: LAO 7/08 R2	
Location: Sikhottabong, Vientian Capital, Laos	Topotype: SEA
Date collected: 02/04/2008	Genotype/strain: Mya-98
Date received by WRLFMD: 05/02/2010	Sequence filename: LAO08-03.SEQ
Date received for sequencing: 24/02/2010	Date sequence last updated: 02/03/2010
Species: Pig	No. of Nt determined: 639
Material used: LK2 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 300
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3	O/MYA/2/2008	MYA08-02	639	635	0	99.37	0.63	SEA	Mya-98
4	O/TAI/2/2008	TAI08-02	639	635	0	99.37	0.63	SEA	Mya-98
5	O/TAI/3/2008	TAI08-03	639	635	0	99.37	0.63	SEA	Mya-98
6	O/TAI/7/2008	TAI08-07	639	635	0	99.37	0.63	SEA	Mya-98
7	O/TAI 40/08* (TRRL)	TAI08-AC	639	635	0	99.37	0.63	SEA	Mya-98
8	O/LAO/1/2007	LAO07-01	639	634	0	99.22	0.78	SEA	Mya-98
9	O/MAY/4/2007	MAY07-04	639	634	0	99.22	0.78	SEA	Mya-98
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5	O/IND/53/79 (AF292107)	IND79A53	639	540	0	84.51	15.49	ME-SA	unnamed
6	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	540	0	84.51	15.49	ME-SA	unnamed
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	536	0	83.88	16.12	ME-SA	PanAsia
8	O/IRN/8/2005	IRN05-08	639	535	0	83.72	16.28	ME-SA	PanAsia-2
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Serotype: O	Report date: 02/03/2010
WRLFMD Ref No: LAO/1/2009	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00005	Checked by: D.P. King
Sender Ref: LAO 5/09 R2	
Location: Phonethung, Champasak, Laos	Topotype: SEA
Date collected: 22/01/2009	Genotype/strain: Mya-98
Date received by WRLFMD: 05/02/2010	Sequence filename: LAO09-01.SEQ
Date received for sequencing: 24/02/2010	Date sequence last updated: 02/03/2010
Species: Buffalo	No. of Nt determined: 639
Material used: LK2 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 300
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2	O/MYA/2/2008	MYA08-02	639	633	0	99.06	0.94	SEA	Mya-98
3	O/LAO/2/2008	LAO08-02	639	631	0	98.75	1.25	SEA	Mya-98
4	O/LAO/3/2008	LAO08-03	639	631	0	98.75	1.25	SEA	Mya-98
5	O/MAY/9/2007	MAY07-09	639	631	0	98.75	1.25	SEA	Mya-98
6	O/TAI/14/2007	TAI07-14	639	631	0	98.75	1.25	SEA	Mya-98
7	O/TAI/2/2008	TAI08-02	639	631	0	98.75	1.25	SEA	Mya-98
8	O/TAI/3/2008	TAI08-03	639	631	0	98.75	1.25	SEA	Mya-98
9	O/TAI/7/2008	TAI08-07	639	631	0	98.75	1.25	SEA	Mya-98
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2	O/TAI/189/87* (TRRL)	TAI87-AC	639	566	0	88.58	11.42	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	542	0	84.82	15.18	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	539	0	84.35	15.65	SEA	Cam-94
5	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	539	0	84.35	15.65	ME-SA	unnamed
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8	O/IRN/8/2005	IRN05-08	639	534	0	83.57	16.43	ME-SA	PanAsia-2
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10	O/K83/79* (AJ303511)	KEN79B83	638	529	1	82.92	17.08	EA-1	unnamed

nt, nucleotides

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Report on FMDV O in Laos in 2008-2009

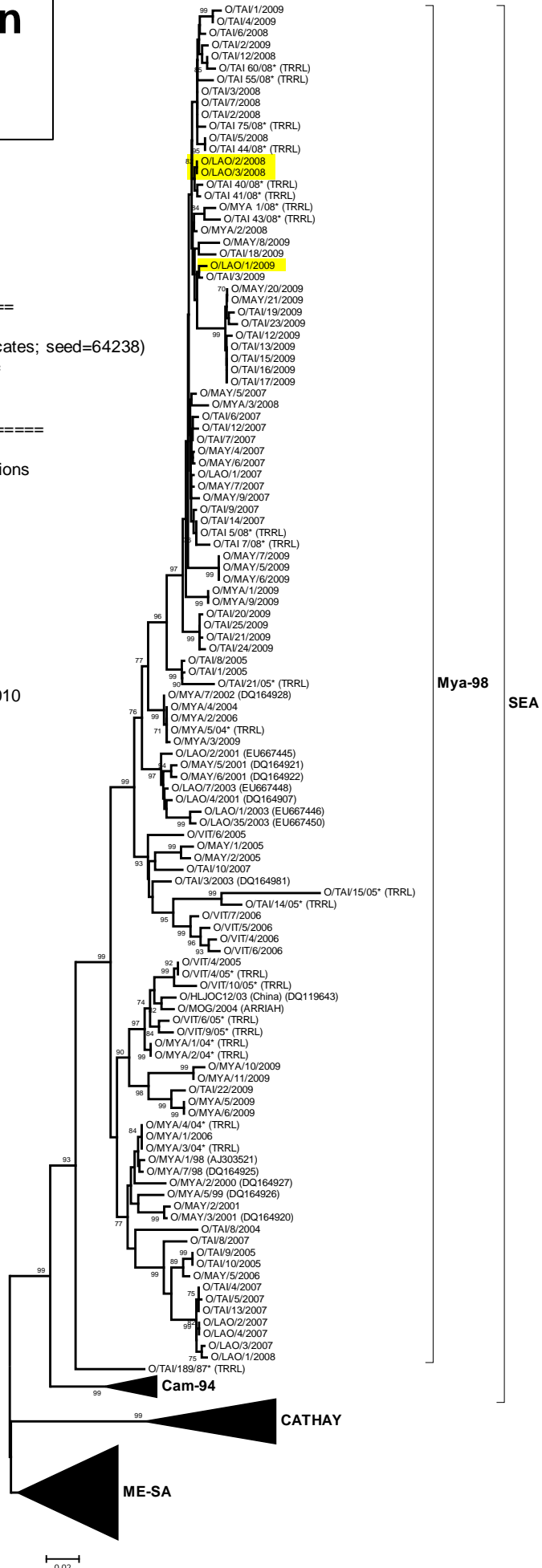
Batch: WRLFMD/2010/00005

Software: MEGA 4.0
 No. of Taxa : 222
 Data File : n:\evd\meg\db\fmv\lo\SEA2010a.meg
 Data Title : Southeast Asia 2008-2009
 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 above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & F. Hamid, 03 March 2010

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