



**INSTITUTE FOR ANIMAL HEALTH**

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## FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00023

Sender Details:



Date Received: 22<sup>nd</sup> June 2012

Country of Origin: Thailand

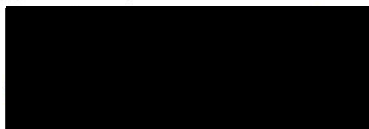
Date Reported: 20<sup>th</sup> July 2012

Dear Panithan Thongtha

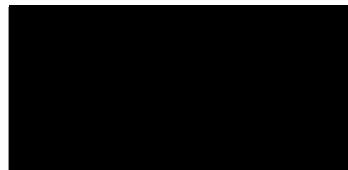
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date:

20/7/12

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: [gareth.shimmon@iah.ac.uk](mailto:gareth.shimmon@iah.ac.uk). IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

## Genotyping Report

Report Date for this Batch: 18 July 2012

FMDV type O

Country: Thailand

Period: 2011-2012

No. of samples: 4

BATCH: WRLFMD/2012/00023



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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: 18/07/2012
WRLFMD Ref No: TAI/21/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00023	Checked by: D.P. King
Sender Ref: O 95/11 R2B4	
Location: Ratchaburi, Thailand	Topotype: SEA
Date collected: 12/11/2011	Genotype/strain: Mya-98
Date received by WRLFMD: 22/06/2012	Sequence filename: TAI11-21.SEQ
Date received for sequencing: 04/07/2012	Date sequence last updated: 10/07/2012
Species: Cattle	No. of Nt determined: 639
Material used: R2B5 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 14 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/TAI/2/2011	TAI11-02	639	634	0	99.22	0.78	SEA	Mya-98
2	O/TAI/5/2011	TAI11-05	639	633	0	99.06	0.94	SEA	Mya-98
3	O/TAI/4/2011	TAI11-04	639	632	0	98.90	1.10	SEA	Mya-98
4	O/TAI/25/2011	TAI11-25	639	624	0	97.65	2.35	SEA	Mya-98
5	O/MYA/2/2008 (HQ116226)	MYA08-02	639	620	0	97.03	2.97	SEA	Mya-98
6	O/LAO/2/2008 (HQ116180)	LAO08-02	639	618	0	96.71	3.29	SEA	Mya-98
7	O/LAO/3/2008 (HQ116181)	LAO08-03	639	618	0	96.71	3.29	SEA	Mya-98
8	O/TAI/2/2008 (HQ116250)	TAI08-02	639	618	0	96.71	3.29	SEA	Mya-98
9	O/TAI/3/2008 (HQ116251)	TAI08-03	639	618	0	96.71	3.29	SEA	Mya-98
10	O/TAI/3/2009 (HQ116258)	TAI09-03	639	618	0	96.71	3.29	SEA	Mya-98
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
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	583	0	91.24	8.76	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	559	0	87.48	12.52	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	543	0	84.98	15.02	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	540	0	84.51	15.49	ME-SA	unnamed
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	536	0	83.88	16.12	ME-SA	Pak-98
6	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	536	0	83.88	16.12	ME-SA	unnamed
7	O/IRN/31/2009	IRN09-31	639	533	0	83.41	16.59	ME-SA	PanAsia-2 <sup>FAR-09</sup>
8	O/OMN/7/2001 (DQ164941)	OMN01-07	639	532	0	83.26	16.74	ME-SA	Ind-2001b
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	532	0	83.26	16.74	ME-SA	PanAsia-2 <sup>TER-08</sup>
10	O/IND/53/79 (AF292107)	IND79A53	639	531	0	83.10	16.90	ME-SA	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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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: 18/07/2012
WRLFMD Ref No: TAI/22/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00023	Checked by: D.P. King
Sender Ref: O 97/11 R1B2	
Location: Nakhonsrithum, Thailand	Topotype: ME-SA
Date collected: 12/11/2011	Genotype/strain: PanAsia
Date received by WRLFMD: 22/06/2012	Sequence filename: TAI11-22.SEQ
Date received for sequencing: 04/07/2012	Date sequence last updated: 10/07/2012
Species: Cattle	No. of Nt determined: 639
Material used: R1B2 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 14 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/TAI/11/2012	TAI12-11	639	636	0	99.53	0.47	ME-SA	PanAsia
2	O/VIT/16/2011	VIT11-16	639	625	0	97.81	2.19	ME-SA	PanAsia
3	O/VIT/5/2011	VIT11-05	639	625	0	97.81	2.19	ME-SA	PanAsia
4	O/VIT/6/2011	VIT11-06	639	625	0	97.81	2.19	ME-SA	PanAsia
5	O/VIT/7/2010	VIT10-07	639	625	0	97.81	2.19	ME-SA	PanAsia
6	O/VIT/8/2010	VIT10-08	639	625	0	97.81	2.19	ME-SA	PanAsia
7	O/CAM/2/2010	CAM10-02	639	624	0	97.65	2.35	ME-SA	PanAsia
8	O/CAM/4/2010	CAM10-04	639	624	0	97.65	2.35	ME-SA	PanAsia
9	O/CAM/5/2010	CAM10-05	639	624	0	97.65	2.35	ME-SA	PanAsia
10	O/CAM/8/2010	CAM10-08	639	624	0	97.65	2.35	ME-SA	PanAsia
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/UKG/35/2001 (AJ539141)	UKG01-35	639	591	0	92.49	7.51	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
3	O/IRN/8/2005	IRN05-08	639	576	0	90.14	9.86	ME-SA	PanAsia-2
4	O/OMN/7/2001 (DQ164941)	OMN01-07	639	575	0	89.98	10.02	ME-SA	Ind-2001b
5	O/IRN/31/2009	IRN09-31	639	574	0	89.83	10.17	ME-SA	PanAsia-2 <sup>FAR-09</sup>
6	O/BHU/3/2009	BHU09-03	639	573	0	89.67	10.33	ME-SA	Ind-2001d
7	O/UAE/4/2008	UAE08-04	636	569	0	89.47	10.53	ME-SA	Ind-2001c
8	O/IRN/18/2010	IRN10-18	639	571	0	89.36	10.64	ME-SA	PanAsia-2 <sup>BAL-09</sup>
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	571	0	89.36	10.64	ME-SA	PanAsia-2 <sup>TER-08</sup>
10	O/IRN/88/2009	IRN09-88	639	569	0	89.05	10.95	ME-SA	PanAsia-2 <sup>ANT-10</sup>

nt, nucleotides

\*, not a WRLFMD reference number

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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: 18/07/2012
WRLFMD Ref No: TAI/25/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00023	Checked by: D.P. King
Sender Ref: O 101-2/11 R1B3	
Location: Supanburi, Thailand	Topotype: SEA
Date collected: 14/12/2011	Genotype/strain: Mya-98
Date received by WRLFMD: 22/06/2012	Sequence filename: TAI11-25.SEQ
Date received for sequencing: 04/07/2012	Date sequence last updated: 10/07/2012
Species: Cattle	No. of Nt determined: 639
Material used: R1B3 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 14 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/TAI/2/2011	TAI11-02	639	627	0	98.12	1.88	SEA	Mya-98
2	O/TAI/5/2011	TAI11-05	639	626	0	97.97	2.03	SEA	Mya-98
3	O/TAI/4/2011	TAI11-04	639	625	0	97.81	2.19	SEA	Mya-98
4	O/TAI/21/2011	TAI11-21	639	624	0	97.65	2.35	SEA	Mya-98
5	O/LAO/1/2007 (HQ116175)	LAO07-01	639	620	0	97.03	2.97	SEA	Mya-98
6	O/MYA/2/2008 (HQ116226)	MYA08-02	639	619	0	96.87	3.13	SEA	Mya-98
7	O/MAY/4/2007 (HQ116208)	MAY07-04	639	618	0	96.71	3.29	SEA	Mya-98
8	O/MAY/7/2007 (HQ116211)	MAY07-07	639	618	0	96.71	3.29	SEA	Mya-98
9	O/TAI/12/2007 (HQ116247)	TAI07-12	639	618	0	96.71	3.29	SEA	Mya-98
10	O/TAI/6/2007 (HQ116242)	TAI07-06	639	618	0	96.71	3.29	SEA	Mya-98
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
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	584	0	91.39	8.61	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	558	0	87.32	12.68	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	542	0	84.82	15.18	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	540	0	84.51	15.49	ME-SA	unnamed
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	537	0	84.04	15.96	ME-SA	Pak-98
6	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	536	0	83.88	16.12	ME-SA	unnamed
7	O/IRN/31/2009	IRN09-31	639	534	0	83.57	16.43	ME-SA	PanAsia-2 <sup>FAR-09</sup>
8	O/PAK/16/2010	PAK10-16	639	533	0	83.41	16.59	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/ETH/1/2007 (FJ798137)	ETH07-01	639	531	0	83.10	16.90	EA-3	unnamed
10	O/IND/53/79 (AF292107)	IND79A53	639	531	0	83.10	16.90	ME-SA	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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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: 18/07/2012
WRLFMD Ref No: TAI/11/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00023	Checked by: D.P. King
Sender Ref: O 104/11 R2B4	
Location: Songkhla, Thailand	Topotype: ME-SA
Date collected: 18/01/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 22/06/2012	Sequence filename: TAI12-11.SEQ
Date received for sequencing: 04/07/2012	Date sequence last updated: 15/07/2012
Species: Cattle	No. of Nt determined: 639
Material used: R2B4 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3264
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 14 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/TAI/22/2011	TAI11-22	639	636	0	99.53	0.47	ME-SA	PanAsia
2	O/VIT/16/2011	VIT11-16	639	626	0	97.97	2.03	ME-SA	PanAsia
3	O/VIT/5/2011	VIT11-05	639	626	0	97.97	2.03	ME-SA	PanAsia
4	O/VIT/6/2011	VIT11-06	639	626	0	97.97	2.03	ME-SA	PanAsia
5	O/VIT/7/2010	VIT10-07	639	626	0	97.97	2.03	ME-SA	PanAsia
6	O/VIT/8/2010	VIT10-08	639	626	0	97.97	2.03	ME-SA	PanAsia
7	O/CAM/2/2010	CAM10-02	639	625	0	97.81	2.19	ME-SA	PanAsia
8	O/CAM/4/2010	CAM10-04	639	625	0	97.81	2.19	ME-SA	PanAsia
9	O/CAM/5/2010	CAM10-05	639	625	0	97.81	2.19	ME-SA	PanAsia
10	O/CAM/8/2010	CAM10-08	639	625	0	97.81	2.19	ME-SA	PanAsia
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/UKG/35/2001 (AJ539141)	UKG01-35	639	592	0	92.64	7.36	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	582	0	91.08	8.92	ME-SA	Ind-2001a
3	O/IRN/8/2005	IRN05-08	639	577	0	90.30	9.70	ME-SA	PanAsia-2
4	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/BHU/3/2009	BHU09-03	639	574	0	89.83	10.17	ME-SA	Ind-2001d
6	O/OMN/7/2001 (DQ164941)	OMN01-07	639	574	0	89.83	10.17	ME-SA	Ind-2001b
7	O/UAE/4/2008	UAE08-04	636	570	0	89.62	10.38	ME-SA	Ind-2001c
8	O/IRN/18/2010	IRN10-18	639	572	0	89.51	10.49	ME-SA	PanAsia-2 <sup>BAL-09</sup>
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	572	0	89.51	10.49	ME-SA	PanAsia-2 <sup>TER-08</sup>
10	O/IRN/88/2009	IRN09-88	639	570	0	89.20	10.80	ME-SA	PanAsia-2 <sup>ANT-10</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV O in Thailand in 2011-2012

Batch: WRLFMD/2012/00023

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

Analysis ----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included -----

1st+2nd+3rd+Non-Coding

No. of Sites : 645

No Of Bootstrap Reps = 1000

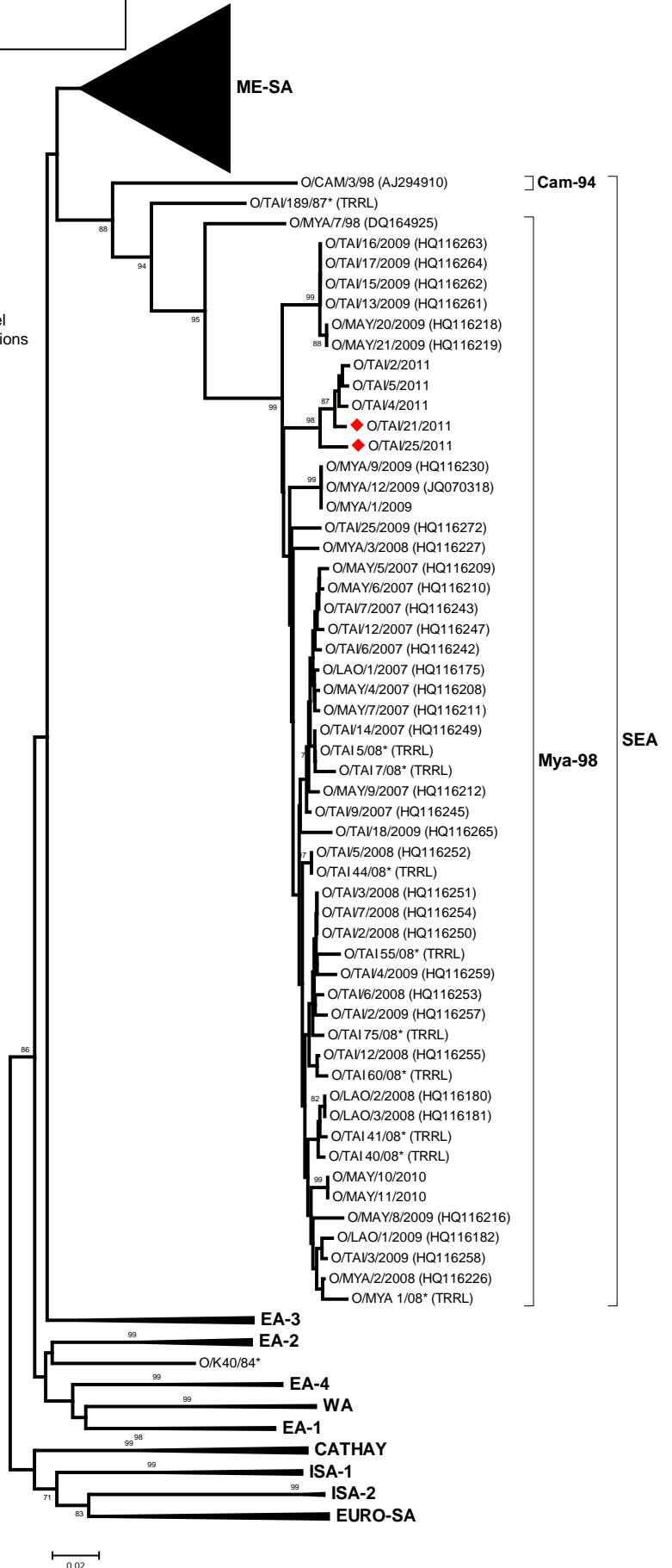
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 18 July 2012

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# Report on FMDV O in Thailand in 2011-2012

Batch: WRLFMD/2012/00023

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

Analysis ----- Phylogeny Reconstruction

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Rates among Sites ----- Uniform rates

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Data Subset to Use

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Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 645

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 18 July 2012

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