



INSTITUTE FOR ANIMAL HEALTH  
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## FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00052

Sender Details:

Date Received: 19<sup>th</sup> November 2009

Country of Origin: Myanmar

Date Reported: 14<sup>th</sup> December 2009

Dear Dr. Khin Maung Latt,

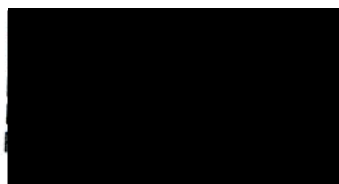
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

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

Results Approved By:



Official Stamp:



Date:

14/12/09

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: [elizabeth.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.ac.uk))

# Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: O WRL Ref No: MYA/5/2009 Sender Ref: 2253 Date collected: 10/06/2009 Date received by WRLFMD: 19/11/2009 Date received for sequencing: 30/11/2009 Species: Cattle Material used: BTy2 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 11/12/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: SEA Genotype/strain: Mya-98 Sequence filename: MYA09-05.SEQ Date sequence last updated: 11/12/2009 Total no. of comparisons: 2139 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 11 days						
Comments:							
<b>Ten Most Closely Related Viruses</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/MYA/6/2009	MYA09-06	639	639	0	100	0
2	O/MYA/1/04* [TRRL]	MYA04-AA	639	609	0	95.31	4.69
3	O/MYA/2/04* [TRRL]	MYA04-AB	639	609	0	95.31	4.69
4	O/VIT/6/05* [TRRL]	VIT05-AF	639	606	0	94.84	5.16
5	O/TAI/36/04* [TRRL]	TAI04-AB	639	605	0	94.68	5.32
6	O/HLJOC12/03 [DQ119643]	CHA03-AA	633	599	0	94.63	5.37
7	O/MOG/2004 (ARRIAH)	MOG04--A	637	602	2	94.51	5.49
8	O/VIT/9/05* [TRRL]	VIT05-AI	639	602	0	94.21	5.79
9	O/MYA/4/98	MYA98-04	351	330	8	94.02	5.98
10	O/MYA/1/98 (AJ303521)	MYA98-01	630	592	9	93.97	6.03
<b>Relationships to Reference Virus Strains</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	O/TAI/189/87* [TRRL]	TAI87-AC	639	575	0	89.98	10.02
2	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02
3	O/TAW/2/99 (AJ294927)	TAW99-02	639	542	0	84.82	15.18
4	O/IND/53/79 [AF292107]	IND79A53	639	531	0	83.1	16.9
5	O1/Manisa/TUR/69 (AJ251477)	TUR69--E	639	531	0	83.1	16.9
6	O/ISR/2/88 (DQ164899)	ISR88-02	639	525	0	82.16	17.84
7	O/MOR/1/91	MOR91-01	639	523	0	81.85	18.15
8	O1/BFS 1860/UK/67 (J02185)	UKG67--A	639	503	0	78.72	21.28
9	O/PHI/5/95 (DQ164946)	PHI95-05	639	498	0	77.93	22.07
10	O/HKN/6/83 (AJ294919)	HKN83-06	637	496	2	77.86	22.14
nt, nucleotides *, not a WRLFMD reference number							

# Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: O WRL Ref No: MYA/6/2009 Sender Ref: 2255 Date collected: 17/06/2009 Date received by WRLFMD: 19/11/2009 Date received for sequencing: 30/11/2009 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R; O-1C272F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 11/12/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: SEA Genotype/strain: Mya-98 Sequence filename: MYA09-06.SEQ Date sequence last updated: 11/12/2009 Total no. of comparisons: 2139 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 11 days																																																																																								
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# Report on FMDV O in Myanmar in 2009

Batch: WRLFMD/2009/00052

Software: MEGA 4.0

No. of Taxa : 194

Data File : n:\evd\meg\db\fmdv\o\MYA2009b.meg

Data Title : O Myanmar 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

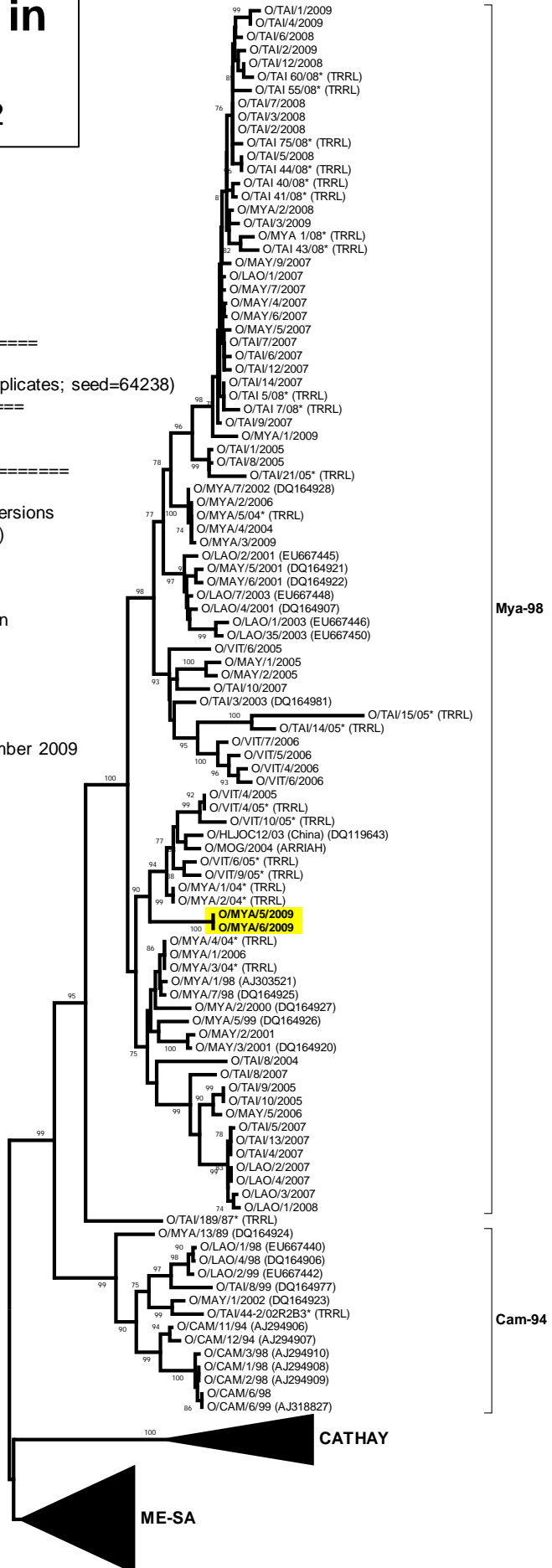
No. of Sites : 639

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

F. Hamid, N.J. Knowles & J. Wadsworth, 11 December 2009



Mya-98

SEA

Cam-94

CATHAY

ME-SA

0.02