



INSTITUTE FOR ANIMAL HEALTH
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Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00027

Sender Details:



Date Received: 1st of May 2009

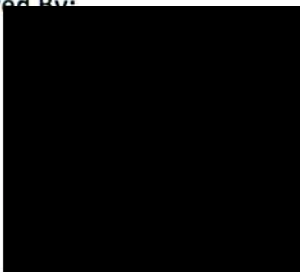
Country of Origin: Myanmar

Date Reported: 14th of September 2009

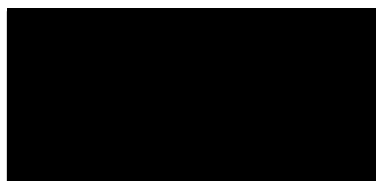
Dear

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: 14/09/09



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.byrom@bbsrc.ac.uk)

Molecular Epidemiology Report Form

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Serotype: O WRL Ref No: MYA/2/2006 Sender Ref: 24 MYA 4/06 R1B1 Date collected: 25/10/2006 Date received by WRLFMD: 01/05/2009 Date received for sequencing: 01/06/2009 Species: Cattle Material used: R1B1 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: 07/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: SEA Genotype/strain: Mya-98 Sequence filename: MYA06-02.SEQ Date sequence last updated: 13/08/2009 Total no. of comparisons: 2096 Min. no. of nt for comparison: 300 Total turn-around time: 129 days Sequencing time: 98 days																																																																																								
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10	O/HKN/6/83 (AJ294919)	HKN83-06	637	493	2	77.39	22.61																																																																																		
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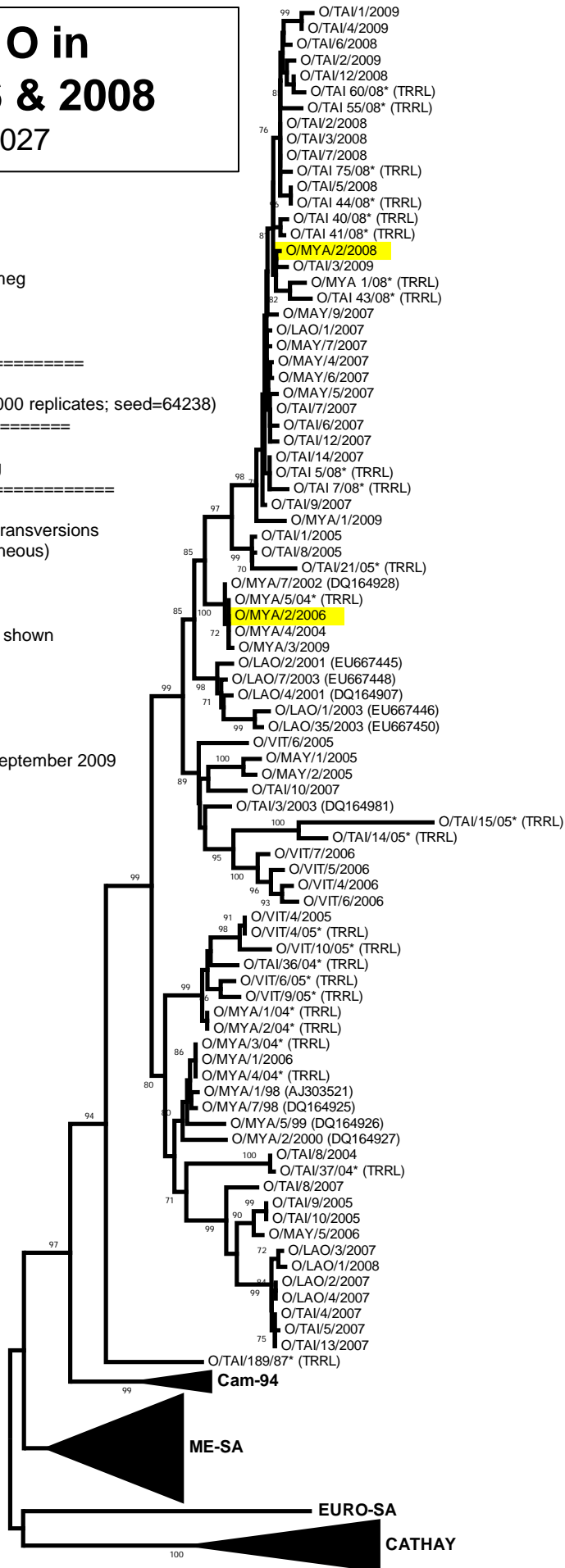
Report on FMDV O in Myanmar in 2006 & 2008

Batch: WRLFMD/2009/00027

Software: MEGA 4.0
 No. of Taxa : 172
 Data File : n:\evd\meg\db\fmdv\o\TAI2009a.meg
 Data Title : Thailand 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.

F. Hamid, N.J. Knowles & J. Wadsworth, 7 September 2009



0.02