



INSTITUTE FOR ANIMAL HEALTH
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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00026

Sender Details:

Date Received: 1st May 2009
Country of Origin: Cambodia
Date Reported: 14th September 2009

Dear [REDACTED]

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 [REDACTED] 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

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

Page 1 of 1

Serotype: A WRL Ref No: CAM/2/2008 Sender Ref: 22 CAM 4/08 R1B1 Date collected: 26/06/2008 Date received by WRLFMD: 01/05/2009 Date received for sequencing: 01/06/2009 Species: Cattle Material used: LK1 BHK1 BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 636 No. of ambiguities: 0 Gene length: 636	Report date: 07/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: none designated Sequence filename: CAM08-02.SEQ Date sequence last updated: 12/08/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 129 days Sequencing time: 98 days																																																																																								
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Ten Most Closely Related Viruses																																																																																									
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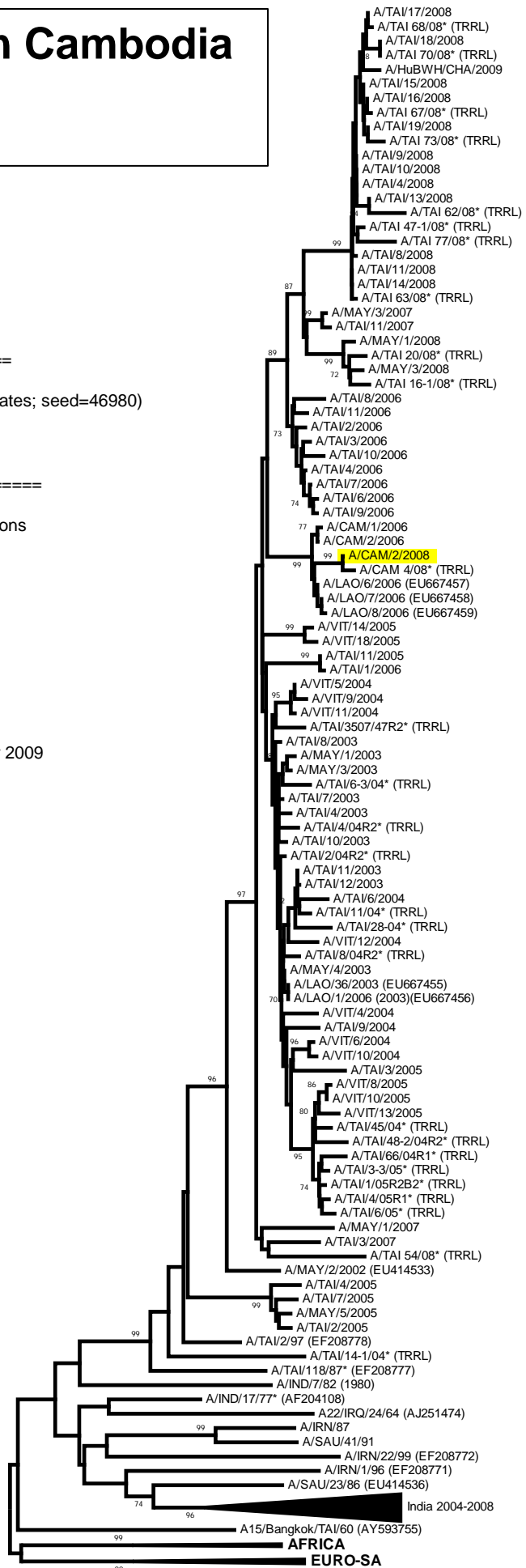
Report on FMDV A in Cambodia in 2008

Batch: WRLFMD/2009/00026

Software: MEGA 4.0
 No. of Taxa : 136
 Data File : n:\evd\meg\db\fmdv\atAI2008b.meg
 Data Title : A Thailand & Cambodia 2008
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=46980)
 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 : 642
 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