



INSTITUTE FOR ANIMAL HEALTH
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GU24 0NF
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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00050

Sender Details:

Date Received:

Country of Origin:

Date Reported:

Malaysia

4th January 2009

Dear

Re.: Type A Results

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:

4th Jan 2010

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)

Molecular Epidemiology Report Form

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

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Serotype: A WRL Ref No: MAY/2/2009 Sender Ref: MVKKB 1087/09 Date collected: 17/03/2009 Date received by WRLFMD: 26/10/2009 Date received for sequencing: 02/11/2009 Species: Cattle Material used: OS in Trizol 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: 23/12/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: none designated Sequence filename: MAY09-02.SEQ Date sequence last updated: 21/12/2009 Total no. of comparisons: 1201 Min. no. of nt for comparison: 300 Total turn-around time: 58 days Sequencing time: 51 days																																																																																								
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Report on FMDV A in Malaysia in 2009

Batch: WRLFMD/2009/00050

Software: MEGA 4.0
 No. of Taxa : 133
 Data File : n:\evd\meg\db\fmv\la\MAY2009a.meg
 Data Title : A Malaysia 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 : 642
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

Samples with the code "VN" are from Vietnam.

F. Hamid, N.J. Knowles & J. Wadsworth, 23 December 2009



ASIA

AFRICA
EURO-SA

0.02