



# Institute for Animal Health

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To:

Email:

To:

Fax Number:

From:

Date: 15<sup>th</sup> of April 2009

Subject: Sequencing Report

No. Of Pages: 4

FAX

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Thank you.

Dear [REDACTED]

## Virus isolates: A ETH/12/2009 and A ETH/13/2009

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 26<sup>th</sup> of February 2009 and the details are as attached. Please note all of our phylogenetic trees can be accessed via the internet at:

[http://www.iah.bbsrc.ac.uk/primary\\_index/current\\_research/virus/Picomaviridae/Aphthovirus/index.html](http://www.iah.bbsrc.ac.uk/primary_index/current_research/virus/Picomaviridae/Aphthovirus/index.html)

Yours sincerely

[REDACTED]  
Head: World Reference Laboratory for FMD

Cc: [REDACTED]

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# Molecular Epidemiology Report Form

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

Page 1 of 1

Serotype: A WRL Ref No: ETH/12/2009 Sender Ref: Eth/39/09/ORO Date collected: 14/02/2009 Date received by WRLFMD: 26/02/2009 Date received for sequencing: 07/04/2009 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 09/04/2009 Reported by: N.J. Knowles Checked by: J.M. Hammond  Topotype: AFRICA Genotype/strain: none designated Sequence filename: ETH09-12.SEQ Date sequence last updated: 09/04/2009 Total no. of comparisons: 1078 Min. no. of nt for comparison: 300 Total turn-around time: 42 days Sequencing time: 2 days																																																																																								
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8	A/SAU/23/86 (EU414536)	SAU86-23	639	502	0	78.56	21.44																																																																																		
9	A/IRN/1/2005 (EF208769)	IRN05-01	639	499	0	78.09	21.91																																																																																		
10	A/IRN/22/99 (EF208772)	IRN99-22	636	494	0	77.67	22.33																																																																																		
nt, nucleotides *, not a WRLFMD reference number																																																																																									

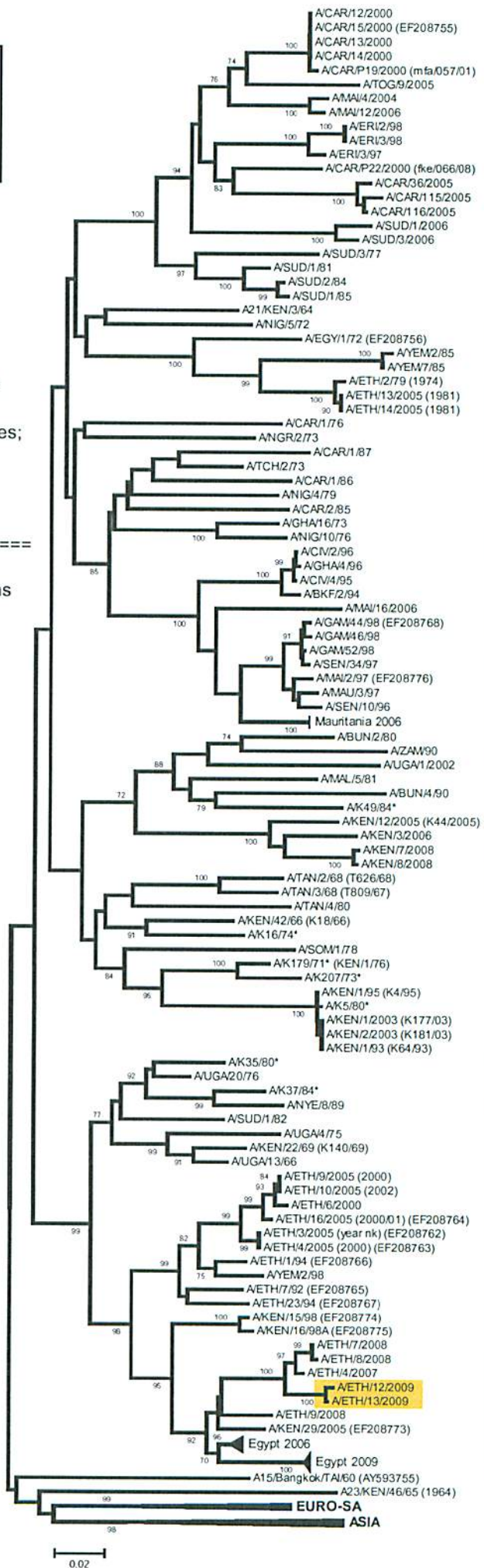
# Report on FMDV A from Ethiopia in 2009

Batch: WRLFMD/2009/00008

Software: MEGA 4.0  
 No. of Taxa : 133  
 Data File : n:\levd\meg\ldb\fm\mdv\A\ETH2009a.meg  
 Data Title : A Ethiopia 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.

N.J. Knowles & J. Wadsworth, 13 April 2009



AFRICA