



# Institute for Animal Health

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Page 1 of 3

To:

Email:

To:

Email:

From:

Date: 20<sup>th</sup> April 2009

Subject: Sequencing Report

No. Of Pages: 3

# Email

This message is intended for the use of the person named above and may contain confidential information. Any other distribution, copying or disclosure is strictly prohibited. If you have received this telefax in error, please notify us immediately by telephone or E-mail and then return the original transmission to us by mail.

Thank you.

Dear [REDACTED]

## Virus isolate: ASIA 1 PAK/8/2008

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 27<sup>th</sup> of March 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/Picornaviridae/Aphthovirus/index.html](http://www.iah.bbsrc.ac.uk/primary_index/current_research/virus/Picornaviridae/Aphthovirus/index.html)

Yours sincerely [REDACTED]

Head, World Reference Laboratory for FMD

The Institute is sponsored by the Biotechnology and Biological Sciences Research Council. An Associated Institute of the University of Reading.

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# Molecular Epidemiology Report Form

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

Serotype: ASIA1 WRL Ref No: PAK/8/2008 Sender Ref: PKS2 Date collected: 24/12/2008 Date received by WRLFMD: 27/03/2009 Date received for sequencing: 07/04/2009 Species: Buffalo Material used: 10% epith susp Region sequenced: VP1 RT-PCR primers: As1-1C530F/EUR-2B52R; As1-1C613F/EUR-2B52R No. of Nt determined: 633 No. of ambiguities: 0 Gene length: 633	Report date: 17/04/2009 Reported by: N.J. Knowles Checked by: J.M. Hammond  Topotype: none defined Genotype/strain: none designated Sequence filename: PAK08-08.SEQ Date sequence last updated: 15/04/2009 Total no. of comparisons: 331 Min. no. of nt for comparison: 300 Total turn-around time: 21 days Sequencing time: 10 days																																																																																								
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<b>Ten Most Closely Related Viruses</b>																																																																																									
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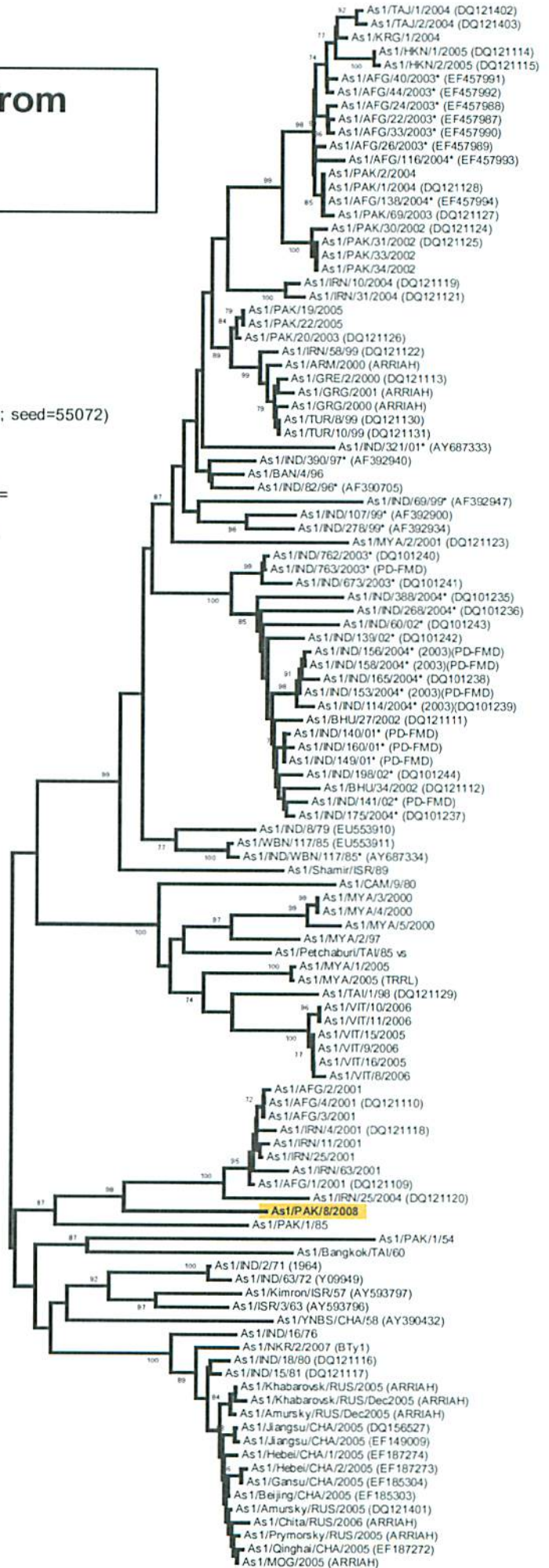
# Report on FMDV Asia 1 from Pakistan in 2008

Batch: WRLFMD/2009/00014

Software: MEGA 4.0  
 No. of Taxa : 115  
 Data File : n:\levd\meg\dlb\lmdv\asia1\PAK2008a.meg  
 Data Title : Asia1 Pakistan 2008  
 Data Type : Nucleotide (Coding)  
 Analysis : Phylogeny reconstruction  
 Tree Inference : =====  
 ->Method : Neighbor-Joining  
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=55072)  
 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 : 636  
 No Of Bootstrap Reps = 1000  
 Only bootstrap values of 70% and above are shown

\* , not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 17 April 2009



0.02