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Page 1 of 3

To:

Email:

To:

Email:

From:

Date: 20th April 2009

Subject: Sequencing Report

No. Of Pages: 3

Email

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Thank you.



Dear 

Virus isolate: O PAK/14/2008

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 27th 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

Yours sincerely



Head: World Reference Laboratory for FMD

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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: O WRL RefNo: PAK/14/2008 Sender Ref: PK S8 Date collected: 26/12/2008 Date received by WRLFMD: 27/03/2009 Date received for sequencing: 07/04/2009 Species: Buffalo Material used: BTy2 Region sequenced: VPI 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: 17/04/2009 Reported by: N.J. Knowles Checked by: J.M. Hammond Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: PAK08-14.SEQ Date sequence last updated: 15/04/2009 Total no. of comparisons: 1926 Min. no. of nt for comparison: 300 Total turn-around time: 21 days Sequencing time: 10 days																																																																																								
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Ten Most Closely Related Viruses																																																																																									
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8	O/PAK/63/2006 (FJ798170)	PAK06-63	639	623	0	97.5	2.5																																																																																		
9	O/PAK/73/2006 (FJ798177)	PAK06-73	639	623	0	97.5	2.5																																																																																		
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Report on FMDV O from Pakistan in 2008

Batch: WRLFMD/2009/00014

Software: MEGA 4.0

No. of Taxa : 236

Data File : n:\evd\meg\db\fmdv\o\PAK2008c.meg

Data Title : O Pakistan 2008

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=28923)

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.

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

