



WRLFMD

INSTITUTE FOR ANIMAL HEALTH

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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00038

Sender Details:

Date Received: 27th July 2009

Country of Origin: Israel

Date Reported: 17th August 2009

Dea

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

Official Stamp:

Date:

17/08/09

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

<p>Serotype: A WRL Ref No: ISR/21/2009 Sender Ref: KVI Nr 44174 Date collected: 12/07/2009 Date received by WRLFMD: 27/07/2009 Date received for sequencing: 30/07/2009 Species: SHEEP 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</p>	<p>Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Iran-05^{BAR-08} Sequence filename: ISR09-21.SEQ Date sequence last updated: 13/08/2009 Total no. of comparisons: 1183 Min. no. of nt for comparison: 300 Total turn-around time: 18 days Sequencing time: 15 days</p>																																																																																								
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<p>Ten Most Closely Related Viruses</p>																																																																																									
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<p>nt, nucleotides *, not a WRLFMD reference number</p>																																																																																									

Report on FMDV A in Israel in 2009

Batch: WRLFMD/2009/00038

Software: MEGA 4.0
 No. of Taxa : 141
 Data File : n:\levd\meg\db\fmvdv\ISR2009b.meg
 Data Title : A Israel 2009
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=60765)
 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 & J. Wadsworth, 14 August 2009

