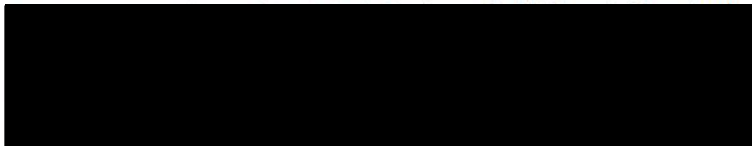




INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00040
Sender Details:

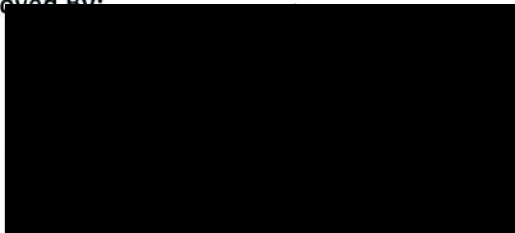


Date Received: 19th August 2009
Country of Origin: Saudi Arabia
Date Reported: 14th September 2009

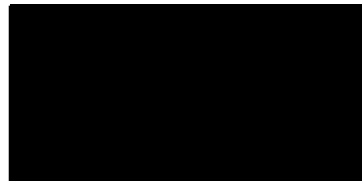
Dear Dr. Scott Waight and Dr. Mark Redwood,

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/>

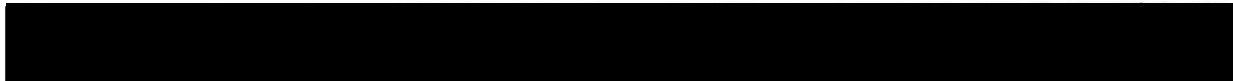
Results Approved By:



Official Stamp:



Date: 14/09/09



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

Serotype: O WRL Ref No: SAU/1/2009 Sender Ref: AL NAKHEEL Date collected: 10/08/2009 Date received by WRLFMD: 19/08/2009 Date received for sequencing: 24/08/2009 Species: Cattle Material used: BTy1 Region sequenced: VP1 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: 11/09/2009 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: SAU09-01.SEQ Date sequence last updated: 11/09/2009 Total no. of comparisons: 2099 Min. no. of nt for comparison: 300 Total turn-around time: 23 days Sequencing time: 18 days																																																																																								
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Molecular Epidemiology Report Form

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

Page 1 of 1

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Report on FMDV O in Saudi Arabia in 2009

Batch: WRLFMD/2009/00040

Software: MEGA 4.0

No. of Taxa : 265

Data File : n:\evd\meg\db\fmv\o\SAU2009a.meg

Data Title : O SAU & SRL 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

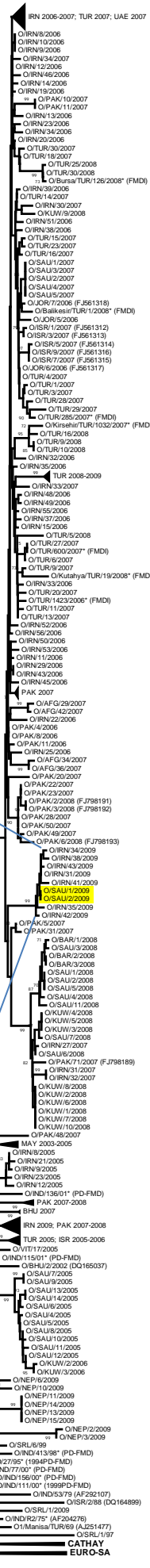
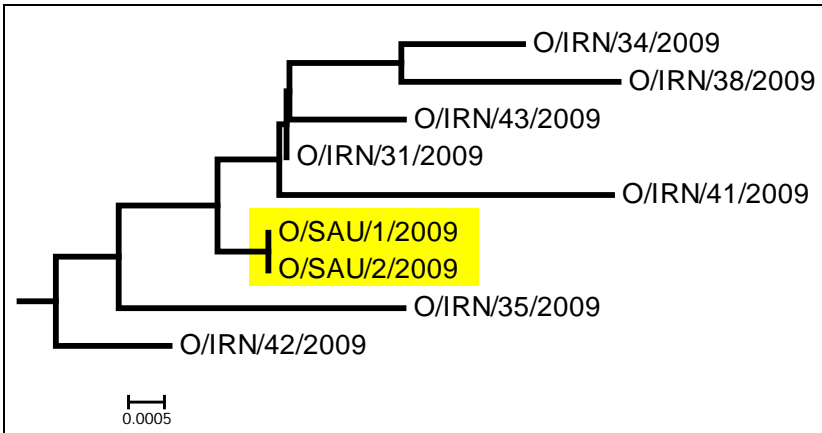
No. of Sites : 639

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 11 September 2009



PanAsia-2

PanAsia

ME-SA