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FAX

To: [redacted]
Fax Number:
To:
Email:
From:
Date: 11th May 2009
Subject: Sequencing Report
No. Of Pages: 3

Dear [redacted]

Virus isolates: A BAR/6/2009

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 1st of May 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

[redacted]

[redacted]
Head: World Reference Laboratory for FMD

[redacted]

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

Molecular Epidemiology Report Form

Serotype: A
WRL Ref No: BAR/6/2009
Sender Ref: 0446
Date collected: 23/04/2009
Date received by WRLFMD: 01/05/2009
Date received for sequencing: 07/05/2009
Species: Cattle
Material used: BTy2
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: 09/05/2009
Reported by: N.J. Knowles
Checked by: D.P. King

Topotype: ASIA
Genotype/strain: Iran-05^{BAR-08}
Sequence filename: BAR09-06.SEQ
Date sequence last updated: 08/05/2009
Total no. of comparisons: 1122
Min. no. of nt for comparison: 300
Total turn-around time: 8 days
Sequencing time: 2 days

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/IRN/2/2009	IRN09-02	639	637	0	99.69	0.31
2	A/IRN/21/2009	IRN09-21	639	637	0	99.69	0.31
3	A/IRN/22/2009	IRN09-22	639	637	0	99.69	0.31
4	A/IRN/29/2009	IRN09-29	639	637	0	99.69	0.31
5	A/IRQ/10/2009	IRQ09-10	639	637	0	99.69	0.31
6	A/IRQ/11/2009	IRQ09-11	639	637	0	99.69	0.31
7	A/IRQ/12/2009	IRQ09-12	639	637	0	99.69	0.31
8	A/IRQ/15/2009	IRQ09-15	639	637	0	99.69	0.31
9	A/IRQ/17/2009	IRQ09-17	639	637	0	99.69	0.31
10	A/IRQ/19/2009	IRQ09-19	639	637	0	99.69	0.31

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/IRN/1/2005 (EF208769)	IRN05-01	639	610	0	95.46	4.54
2	A/SAU/41/91	SAU91-41	636	539	0	84.75	15.25
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	537	0	84.43	15.57
4	A/IRN/2/87 (EF208770)	IRN87-02	636	533	0	83.81	16.19
5	A/SAU/23/86 (EU414536)	SAU86-23	639	534	0	83.57	16.43
6	A/IRN/1/96 (EF208771)	IRN96-01	638	532	1	83.39	16.61
7	A/IRN/22/99 (EF208772)	IRN99-22	636	530	0	83.33	16.67
8	A/TAI/2/97 (EF208778)	TAI97-02	636	528	0	83.02	16.98
9	A22/IRQ/24/64 (AJ251474)	IRQ64-24	639	525	0	82.16	17.84
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	639	514	0	80.44	19.56

nt, nucleotides
*, not a WRLFMD reference number

Report on FMDV A from Bahrain in 2009

Batch: WRLFMD/2009/00021

Software: MEGA 4.0
No. of Taxa : 252
Data File : n:\evd\meg\db\fmdv\a\BAR2009b.meg
Data Title : Bahrain 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 and J. Wadsworth, 9 May 2009