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To: [REDACTED]
Fax Number: [REDACTED]
From: [REDACTED]
Date: 17th April 2009
Subject: Sequencing Report
No. Of Pages: 5

FAX

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Thank you.

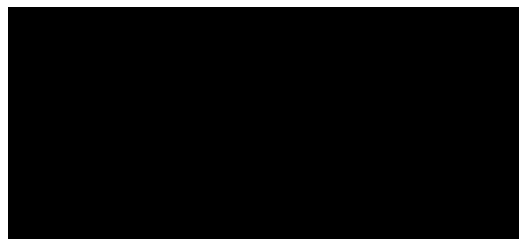
Dear [REDACTED]

Virus isolates: SAT2 ZAM/12/2009, SAT2 ZAM/13/2009, SAT2 ZAM/14/2009 and SAT2 ZAM/16/2009

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 30th 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



[REDACTED]
Head: World Reference Laboratory for FMD

Cc: [REDACTED]

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Molecular Epidemiology Report Form

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

<p>Serotype: SAT2 WRL RefNo: ZAM/12/2009 Sender Ref: ZAM 14/09 Date collected: 01/01/2009 Date received by WRLFMD: 30/03/2009 Date received for sequencing: 09/04/2009 Species: Cattle Material used: BTyI Region sequenced: VPI RT-PCR primers: SAT2-1C445F/SAT2B-208R; SAT2-P1-1223F/SAT2B-208R No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648</p>	<p>Report date: 17/04/2009 Reported by: N.J. Knowles Checked by: J.M. Hammond Topotype: III Genotype/strain: none designated Sequence filename: ZAM09-12.SEQ Date sequence last updated: 15/04/2009 Total no. of comparisons: 451 Min. no. of nt for comparison: 300 Total turn-around time: 18 days Sequencing time: 8 days</p>																																																																																								
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Comments:							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/ZAM/14/2009	ZAM09-14	648	648	0	100	0
2	SAT2/ZAM/16/2009	ZAM09-16	648	648	0	100	0
3	SAT2/ZAM/12/2009	ZAM09-12	648	647	0	99.85	0.15
4	SAT2/BOT/24/2006 (buffalo)	BOT06-24	648	621	0	95.83	4.17
5	SAT2/NMB/2/2008	NMB08-02	648	617	0	95.22	4.78
6	SAT2/NMB/4/2007	NMB07-04	648	617	0	95.22	4.78
7	SAT2/ZAM/1/2007	ZAM07-01	648	617	0	95.22	4.78
8	SAT2/ZAM/3/2007	ZAM07-03	648	617	0	95.22	4.78
9	SAT2/NMB/1/2007	NMB07-01	648	616	0	95.06	4.94
10	SAT2/NMB/3/2008	NMB08-03	648	616	0	95.06	4.94
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/RHO/1/48 [AJ251475]	ZAM48A01	648	544	0	83.95	16.05
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3	SAT2/SA/106/59 (AY593848)	RSA59--A	648	516	0	79.63	20.37
4	SAT2/K183/74 (Kenya)	KEN74183	648	515	0	79.48	20.52
5	SAT2/ZIM/7/83 [AF136607]	ZIM83A07	648	498	0	76.85	23.15
6	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	489	0	75.46	24.54
7	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	478	0	73.77	26.23
8	SAT2/KEN/3/57	KEN57-03	648	474	0	73.15	26.85
9	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	465	1	71.87	28.13
10	SAT2/GAM/8/79 [AF479410]	GAM79-08	648	465	0	71.76	28.24
nt, nucleotides							
*, not a WRLFMD reference number							

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Serotype: SAT2 WRL Ref No: ZAM/14/2009 Sender Ref: ZAM 16/09 Date collected: 01/01/2009 Date received by WRLFMD: 30/03/2009 Date received for sequencing: 09/04/2009 Species: Cattle Material used: BTyl Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT2B-208R; SAT2-P1-1223F/SAT2B-208R No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648	Report date: 17/04/2009 Reported by: N.J. Knowles Checked by: J.M. Hammond Topotype: III Genotype/strain: none designated Sequence filename: ZAM09-14.SEQ Date sequence last updated: 15/04/2009 Total no. of comparisons: 451 Min. no. of nt for comparison: 300 Total turn-around time: 18 days Sequencing time: 8 days						
Comments:							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/ZAM/13/2009	ZAM09-13	648	648	0	100	0
2	SAT2/ZAM/16/2009	ZAM09-16	648	648	0	100	0
3	SAT2/ZAM/12/2009	ZAM09-12	648	647	0	99.85	0.15
4	SAT2/BOT/24/2006 (buffalo)	BOT06-24	648	621	0	95.83	4.17
5	SAT2/NMB/2/2008	NMB08-02	648	617	0	95.22	4.78
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8	SAT2/ZAM/3/2007	ZAM07-03	648	617	0	95.22	4.78
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nt, nucleotides *, not a WRLFMD reference number							

Report on FMDV SAT 2 from Zambia in 2009

Batch no. WRLFMD/2009/00016

Software: MEGA 4.0
 No. of Taxa : 98
 Data File : n:\levd\meg\db\fmvdv\sat2\ZAM2009a.meg
 Data Title : SAT2 Zambia 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 : 651
 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

