

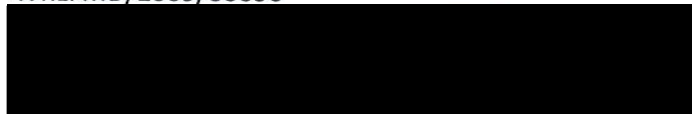


INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00056

Sender Details:



Date Received: 19th January 2009
Country of Origin: Ethiopia
Date Reported: 19th January 2010

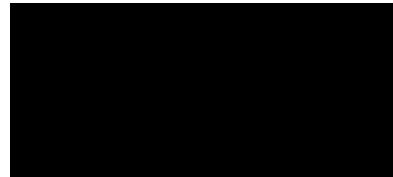
Dear Dr. Rufael,

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:

20/1/10



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.wilson@bbsrc.ac.uk)

Molecular Epidemiology Report Form

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

Page 1 of 1

Serotype: SAT2 WRL Ref No: ETH/51/2009 Sender Ref: Eth/71/09 NS Date collected: 05/11/2009 Date received by WRLFMD: 19/12/2009 Date received for sequencing: 12/01/2010 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648	Report date: 19/01/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: XIII Genotype/strain: none designated Sequence filename: ETH09-51.SEQ Date sequence last updated: 18/01/2010 Total no. of comparisons: 483 Min. no. of nt for comparison: 300 Total turn-around time: 31 days Sequencing time: 7 days																																																																																								
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Molecular Epidemiology Report Form

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

Page 1 of 1

Serotype: SAT2	Report date: 19/01/2010						
WRL Ref No: ETH/52/2009	Reported by: N.J. Knowles						
Sender Ref: Eth/72/09 NS	Checked by: D.P. King						
Date collected: 17/11/2009							
Date received by WRLFMD: 19/12/2009	Topotype: XIII						
Date received for sequencing: 12/01/2010	Genotype/strain: none designated						
Species: Cattle	Sequence filename: ETH09-52.SEQ						
Material used: BTy1	Date sequence last updated: 18/01/2010						
Region sequenced: VP1	Total no. of comparisons: 483						
RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 300						
No. of Nt determined: 648	Total turn-around time: 31 days						
No. of ambiguities: 0	Sequencing time: 7 days						
Gene length: 648							
Comments:							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/ETH/53/2009	ETH09-53	648	648	0	100	0
2	SAT2/ETH/48/2009	ETH09-48	648	646	0	99.69	0.31
3	SAT2/ETH/42/2009	ETH09-42	648	645	0	99.54	0.46
4	SAT2/ETH/51/2009	ETH09-51	648	645	0	99.54	0.46
5	SAT2/ETH/56/2009	ETH09-56	648	643	0	99.23	0.77
6	SAT2/SUD/2/2008	SUD08-02	648	641	0	98.92	1.08
7	SAT2/SUD/1/2008	SUD08-01	648	640	0	98.77	1.23
8	SAT2/ETH/2/2007 (FJ798161)	ETH07-02	648	633	0	97.69	2.31
9	SAT2/SUD/9/77 (AY442014)	SUD77-AB	648	531	0	81.94	18.06
10	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	528	0	81.48	18.52
Relationships to Reference Virus Strains							
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3	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	495	0	76.39	23.61
4	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	488	0	76.01	23.99
5	SAT2/RWA/1/2000* [AF367134]	RWA00-01	648	491	0	75.77	24.23
6	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	477	0	73.61	26.39
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9	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	473	0	72.99	27.01
10	SAT2/ZAI/1/82 [AF367100]	ZAI82-01	647	470	1	72.64	27.36
nt, nucleotides							
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Molecular Epidemiology Report Form

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

Page 1 of 1

<p>Serotype: SAT2 WRL Ref No: ETH/56/2009 Sender Ref: Eth/76/09/LZ Date collected: 02/12/2009 Date received by WRLFMD: 19/12/2009 Date received for sequencing: 12/01/2010 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT-2B208R; SAT2-P1-1223F/SAT-2B208R No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648</p>	<p>Report date: 19/01/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: XIII Genotype/strain: none designated Sequence filename: ETH09-56.SEQ Date sequence last updated: 18/01/2010 Total no. of comparisons: 483 Min. no. of nt for comparison: 300 Total turn-around time: 31 days Sequencing time: 7 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/ETH/51/2009	ETH09-51	648	644	0	99.38	0.62
2	SAT2/ETH/48/2009	ETH09-48	648	643	0	99.23	0.77
3	SAT2/ETH/52/2009	ETH09-52	648	643	0	99.23	0.77
4	SAT2/ETH/53/2009	ETH09-53	648	643	0	99.23	0.77
5	SAT2/ETH/42/2009	ETH09-42	648	642	0	99.07	0.93
6	SAT2/SUD/2/2008	SUD08-02	648	638	0	98.46	1.54
7	SAT2/SUD/1/2008	SUD08-01	648	637	0	98.3	1.7
8	SAT2/ETH/2/2007 (FJ798161)	ETH07-02	648	630	0	97.22	2.78
9	SAT2/SUD/9/77 (AY442014)	SUD77-AB	648	528	0	81.48	18.52
10	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	525	0	81.02	18.98

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT2/ETH/2/2007 (FJ798161)	ETH07-02	648	630	0	97.22	2.78
2	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	525	0	81.02	18.98
3	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	498	0	76.85	23.15
4	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	490	0	76.32	23.68
5	SAT2/RWA/1/2000* [AF367134]	RWA00-01	648	493	0	76.08	23.92
6	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	478	0	73.77	26.23
7	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	476	0	73.46	26.54
8	SAT2/SAU/6/2000 [AF367135]	SAU00A06	647	475	1	73.42	26.58
9	SAT2/NIG/2/75 [AF367139]	NIG75-02	648	471	0	72.69	27.31
10	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	471	0	72.69	27.31

nt, nucleotides

*, not a WRLFMD reference number

Report on FMDV SAT 2 in Ethiopia in 2009

Batch: WRLFMD/2009/00056

Software: MEGA 4.0

No. of Taxa : 286

Data File : n:\evd\meg\db\fmvd\sat2\ETH2009b.meg

Data Title : SAT2 Ethiopia 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,
19 January 2010

