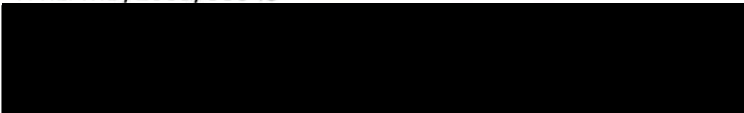




INSTITUTE FOR ANIMAL HEALTH  
Director: Professor Martin W. Shirley, PhD  
PIRBRIGHT LABORATORY  
Ash Road,  
Pirbright,  
Surrey,  
GU24 0NF  
Intn Tel: 00 44 1483 232441  
Tel: 01483 232441 Fax: 01483 232621

## FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2009/00043  
Sender Details: 

Date Received: 3<sup>rd</sup> September 2009  
Country of Origin: Ethiopia  
Date Reported: 21<sup>st</sup> September 2009

Dear 

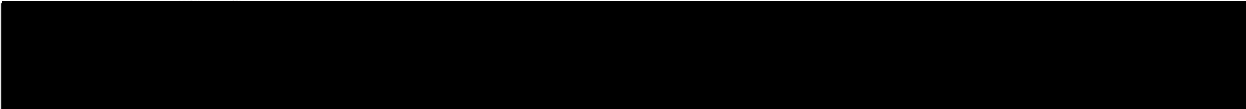
Re.: Serotype SAT2

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: 22/9/2009



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](mailto:elizabeth.byrom@bbsrc.ac.uk))

# Molecular Epidemiology Report Form

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

Page 1 of 1

<p>Serotype: SAT2                  WRL Ref No: ETH/42/2009                  Sender Ref: ETH/9/09/ Ga OP                  Date collected: 16/06/2009                  Date received by WRLFMD: 03/09/2009                  Date received for sequencing: 10/09/2009                  Species: Not known                  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: 18/09/2009                  Reported by: N.J. Knowles                  Checked by: D.P. King                    Topotype: XIII                  Genotype/strain: none designated                  Sequence filename: ETH09-42.SEQ                  Date sequence last updated: 18/09/2009                  Total no. of comparisons: 466                  Min. no. of nt for comparison: 300                  Total turn-around time: 15 days                  Sequencing time: 8 days</p>																																																																																								
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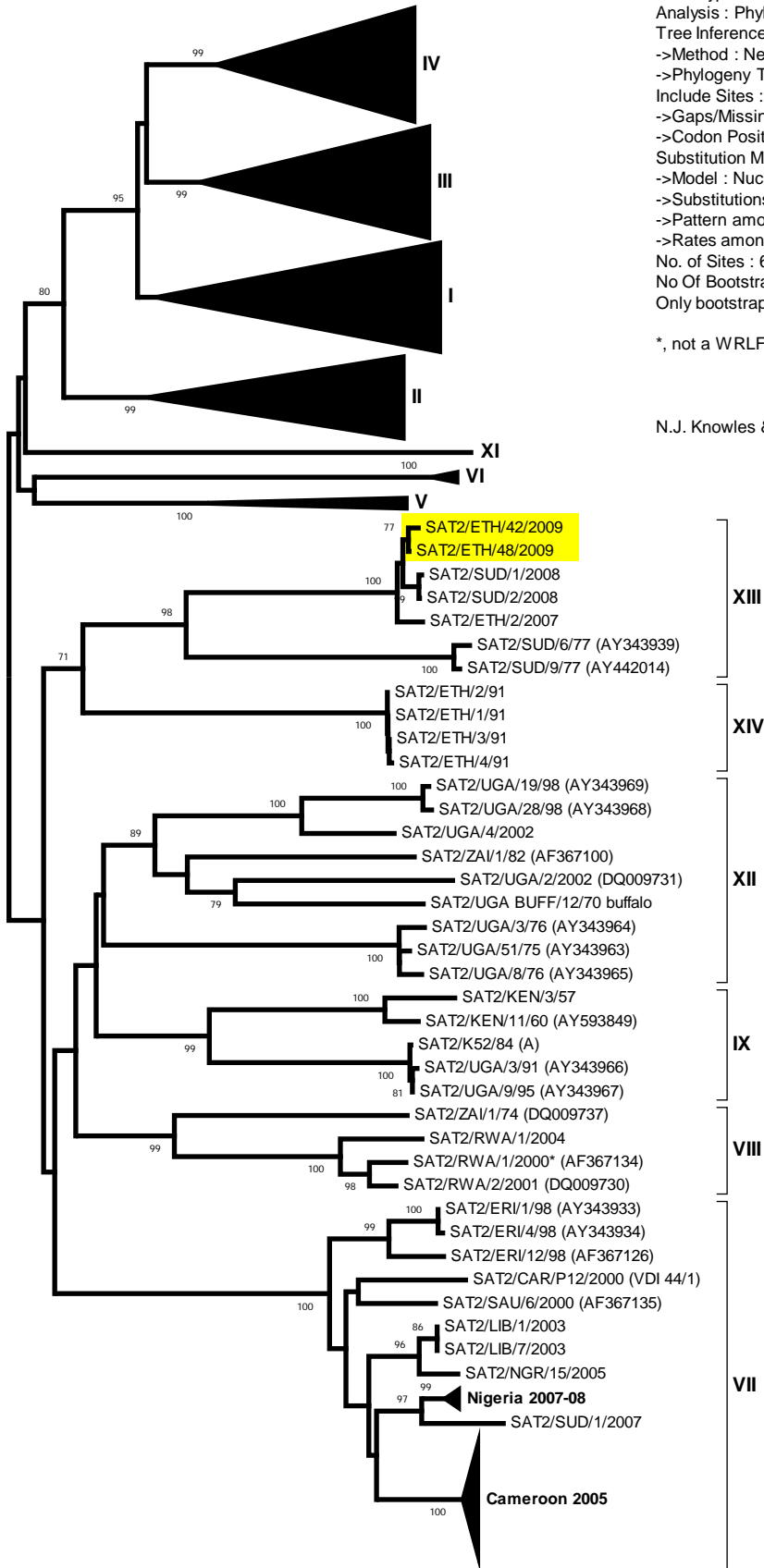
Page 1 of 1

Serotype: SAT2 WRL Ref No: ETH/48/2009 Sender Ref: Eth/6/09/ Ga Date collected: 12/08/2009 Date received by WRLFMD: 03/09/2009 Date received for sequencing: 10/09/2009 Species: Not known 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: 18/09/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: XIII Genotype/strain: none designated Sequence filename: ETH09-48.SEQ Date sequence last updated: 18/09/2009 Total no. of comparisons: 466 Min. no. of nt for comparison: 300 Total turn-around time: 15 days Sequencing time: 8 days																																																																																								
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8	SAT2/K183/74 (Kenya)	KEN74183	648	458	0	70.68	29.32																																																																																		
9	SAT2/GHA/2/90 (AF479415)	GHA90A02	648	456	0	70.37	29.63																																																																																		
10	SAT2/ANG/4/74 [AF479417]	ANG74-04	648	451	0	69.6	30.4																																																																																		
nt, nucleotides *, not a WRLFMD reference number																																																																																									

# Report on FMDV SAT 2 in Ethiopia in 2009

Batch: WRLFMD/2009/00043

Software: MEGA 4.0  
 No. of Taxa : 281  
 Data File : n:\evd\meg\db\fmdv\sat2\ETH2009a.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, 18 September 2009