



**WRLFMD**

**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/2009/00022

Sender Details:



Date Received: 30<sup>th</sup> April 2009

Country of Origin: Kenya

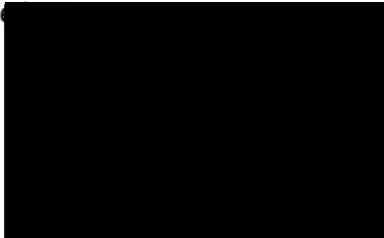
Date Reported: 17<sup>th</sup> August 2009

Dear Dr. Eunice,

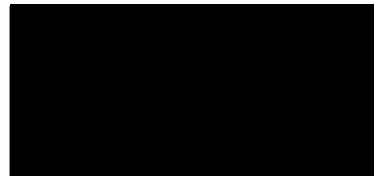
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

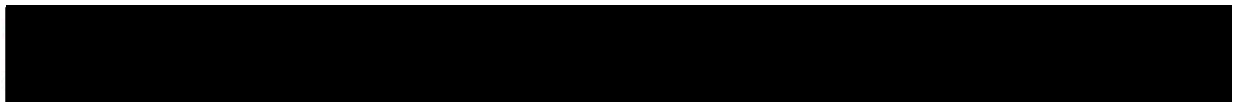
Results Approved



Official Stamp:



Date: 17/08/09



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





# Molecular Epidemiology Report Form

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

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Serotype: SAT1 WRL Ref No: KEN/25/2008 Sender Ref: K67/08 Date collected: 01/08/2008 Date received by WRLFMD: 30/04/2009 Date received for sequencing: 01/06/2009 Species: CATTLE Material used: BTyI Region sequenced: VPI RT-PCR primers: SAT1-1C559F/SAT-2B208R; SATIU-OS/SAT-2B208R No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663	Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: II (NWZ) Genotype/strain: none designated Sequence filename: KEN08-25.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 335 Min. no. of nt for comparison: 300 Total turn-around time: 106 days Sequencing time: 74 days
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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	SAT1/KEN/22/2008	KEN08-22	663	660	0	99.55	0.45
2	SAT1/KEN/23/2008	KEN08-23	663	660	0	99.55	0.45
3	SAT1/KEN/32/2008	KEN08-32	663	660	0	99.55	0.45
4	SAT1/KEN/34/2008	KEN08-34	663	660	0	99.55	0.45
5	SAT1/KEN/35/2008	KEN08-35	663	660	0	99.55	0.45
6	SAT1/KEN/26/2008	KEN08-26	663	659	0	99.4	0.6
7	SAT1/KEN/8/2009	KEN09-08	663	658	0	99.25	0.75
8	SAT1/KEN/16/2009	KEN09-16	663	657	0	99.1	0.9
9	SAT1/TAN/25/99	TAN99-25	315	300	16	95.24	4.76
10	SAT1/TAN/51/99 (AY442004)	TAN99S51	663	631	0	95.17	4.83

### Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT1/T155/71	TAN71155	663	600	0	90.5	9.5
2	SAT1/SAR/9/81	SAR81-09	629	488	11	77.58	22.42
3	SAT1/RV/11/37 (AY593839)	RHO37-11	663	513	0	77.38	22.62
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	510	0	76.92	23.08
5	SAT1/SA/13/61 (AY593842)	SAR61-13	663	497	0	74.96	25.04
6	SAT1/BOT/1/68 (Z98203)	BOT68-B1	663	496	0	74.81	25.19
7	SAT1/SWA/40/61	SWA61-40	663	495	0	74.66	25.34
8	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	487	0	73.45	26.55
9	SAT1/SR/2/58	ZIM58-02	663	486	0	73.3	26.7
10	SAT1/ISR/4/62 (AY593844)	ISR62-04	663	467	0	70.44	29.56

nt, nucleotides

\*, not a WRLFMD reference number















# Molecular Epidemiology Report Form

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

Page 1 of 1

Serotype: SAT1 WRL Ref No: KEN/9/2009 Sender Ref: K28/09 Date collected: 01/02/2009 Date received by WRLFMD: 30/04/2009 Date received for sequencing: 01/06/2009 Species: CATTLE Material used: BTy1 Region sequenced: VPI RT-PCR primers: SAT1-1C559F/SAT-2B208R; SAT1U-OS/SAT-2B208R No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663	Report date: 14/08/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: II (NWZ) Genotype/strain: none designated Sequence filename: KEN09-09.SEQ Date sequence last updated: 07/08/2009 Total no. of comparisons: 335 Min. no. of nt for comparison: 300 Total turn-around time: 106 days Sequencing time: 74 days
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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	SAT1/KEN/14/2009	KEN09-14	663	663	0	100	0
2	SAT1/KEN/15/2009	KEN09-15	663	662	0	99.85	0.15
3	SAT1/TAN/51/99 (AY442004)	TAN99S51	663	622	0	93.82	6.18
4	SAT1/TAN/19/96 (AY442013)	TAN96S19	663	620	0	93.51	6.49
5	SAT1/KEN/35/2008	KEN08-35	663	613	0	92.46	7.54
6	SAT1/TAN/25/99	TAN99-25	315	291	16	92.38	7.62
7	SAT1/KEN/25/2008	KEN08-25	663	612	0	92.31	7.69
8	SAT1/KEN/22/2008	KEN08-22	663	611	0	92.16	7.84
9	SAT1/KEN/23/2008	KEN08-23	663	611	0	92.16	7.84
10	SAT1/KEN/32/2008	KEN08-32	663	611	0	92.16	7.84

### Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	SAT1/T155/71	TAN71155	663	594	0	89.59	10.41
2	SAT1/SAR/9/81	SAR81-09	629	494	11	78.54	21.46
3	SAT1/RV/11/37 (AY593839)	RHO37-11	663	520	0	78.43	21.57
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	513	0	77.38	22.62
5	SAT1/SA/13/61 (AY593842)	SAR61-13	663	498	0	75.11	24.89
6	SAT1/SWA/40/61	SWA61-40	663	495	0	74.66	25.34
7	SAT1/SR/2/58	ZIM58-02	663	493	0	74.36	25.64
8	SAT1/BOT/1/68 (Z98203)	BOT68-B1	663	491	0	74.06	25.94
9	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	485	0	73.15	26.85
10	SAT1/ISR/4/62 (AY593844)	ISR62-04	663	463	0	69.83	30.17

nt, nucleotides  
 \*, not a WRLFMD reference number









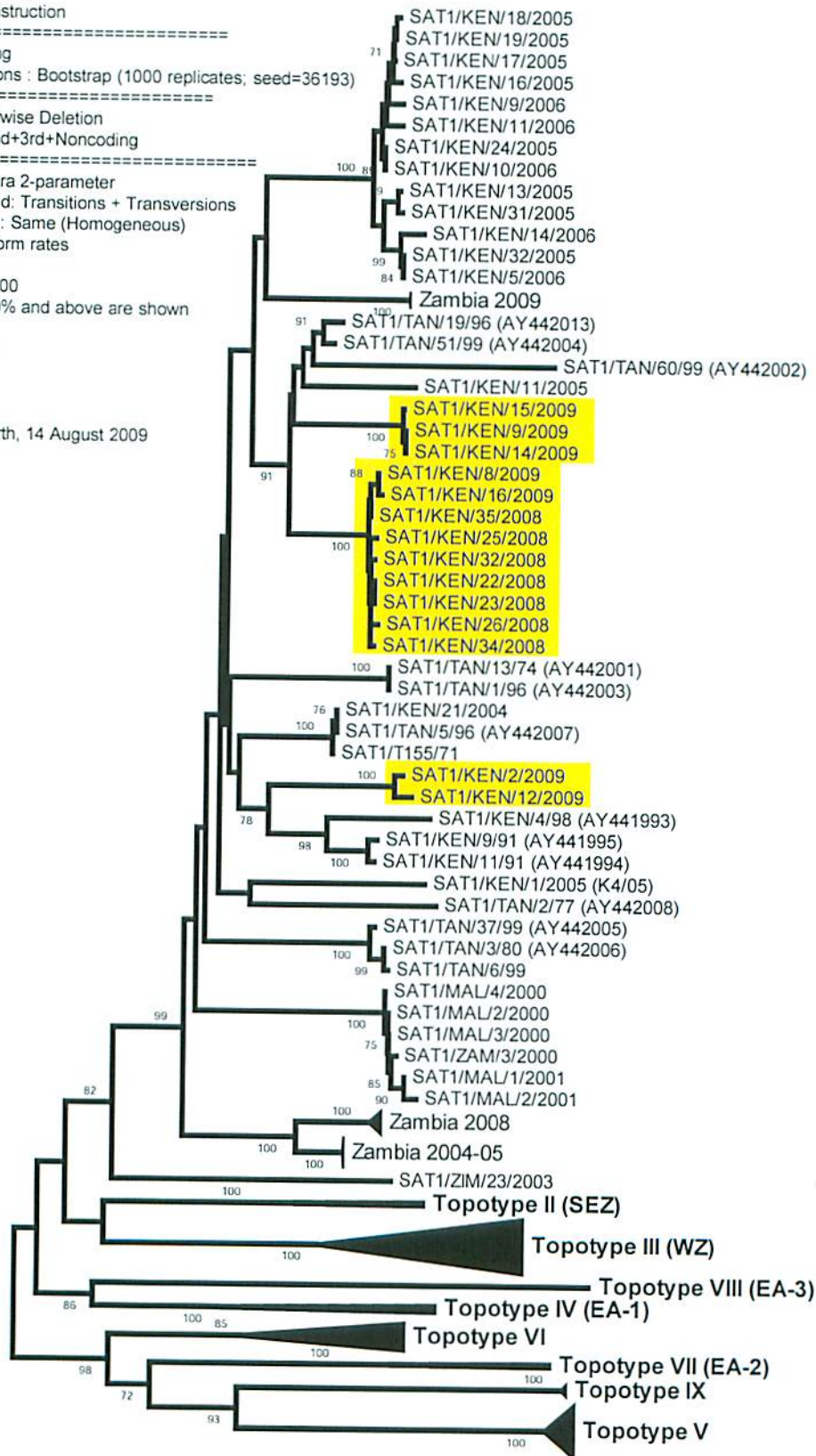
# Report on FMDV SAT 1 in Kenya in 2008-2009

Batch: WRLFMD/2009/00022

Software: MEGA 4.0  
 No. of Taxa : 137  
 Data File : n:\evd\meg\db\fmv\sat1\KEN2009a.meg  
 Data Title : SAT 1 Kenya 2008-2009  
 Data Type : Nucleotide (Coding)  
 Analysis : Phylogeny reconstruction  
 Tree Inference : =====  
 ->Method : Neighbor-Joining  
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=36193)  
 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 : 663  
 No Of Bootstrap Reps = 1000  
 Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 14 August 2009



Topotype II (NWZ)

0.05