



INSTITUTE FOR ANIMAL HEALTH

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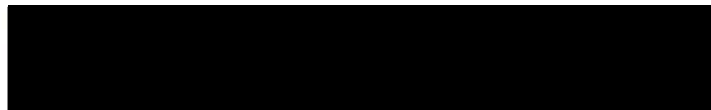
Intn Tel: 00 44 1483 232441

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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00024

Sender Details:



Date Received: 29th June 2012

Country of Origin: Kenya

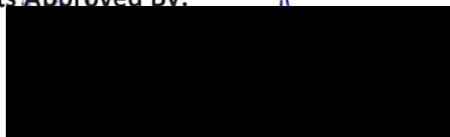
Date Reported: 18th July 2012

Dear Dr EC Chepkwony

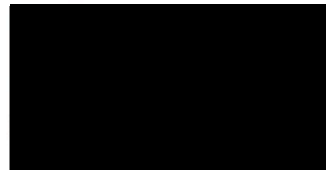
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

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

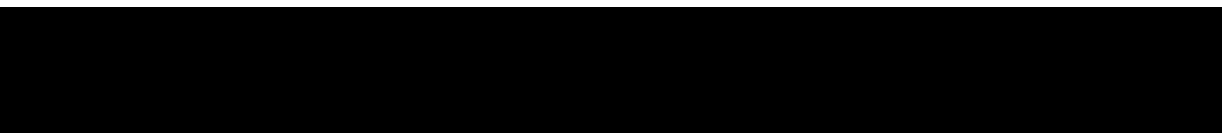
Results Approved By:



Official Stamp:



Date: 20/7/12



A UKAS accredited testing laboratory No. 4025.

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: gareth.shimmon@iah.ac.uk. IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date for this Batch: 18 July 2012

FMDV type SAT 1

Country: Kenya

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2012/00024



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FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: SAT1 WRLFMD Ref No: KEN/2/2011 Batch No: WRLFMD/2012/00024 Sender Ref: K22/11 Location: Mabusi, Bungoma North, Western Province, Kenya Date collected: 17/01/2011 Date received by WRLFMD: 29/06/2012 Date received for sequencing: 11/07/2012 Species: Cattle Material used: RS1 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 18/07/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: I (NWZ) Genotype/strain: unnamed Sequence filename: KEN11-02.SEQ Date sequence last updated: 13/07/2012 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 394 Min. no. of nt for comparison: 600 Total turn-around time: 19 days Sequencing time: 7 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT1/KEN/118/2010	KEN10118	663	662	0	99.85	0.15	I (NWZ)	unnamed
2	SAT1/KEN/119/2010	KEN10119	663	662	0	99.85	0.15	I (NWZ)	unnamed
3	SAT1/KEN/97/2010	KEN10-97	663	662	0	99.85	0.15	I (NWZ)	unnamed
4	SAT1/KEN/136/2010	KEN10136	663	661	0	99.70	0.30	I (NWZ)	Unnamed
5	SAT1/KEN/138/2010	KEN10138	663	661	0	99.70	0.30	I (NWZ)	Unnamed
6	SAT1/KEN/98/2010	KEN10-98	663	661	0	99.70	0.30	I (NWZ)	unnamed
7	SAT1/KEN/120/2010	KEN10120	663	660	0	99.55	0.45	I (NWZ)	unnamed
8	SAT1/KEN/96/2010	KEN10-96	663	660	0	99.55	0.45	I (NWZ)	unnamed
9	SAT1/KEN/1/2010	KEN10-01	663	658	0	99.25	0.75	I (NWZ)	Unnamed
10	SAT1/KEN/101/2010	KEN10101	663	658	0	99.25	0.75	I (NWZ)	unnamed
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT1/T155/71	TAN71155	663	599	0	90.35	9.65	I (NWZ)	unnamed
2	SAT1/ZIM/23/2003	ZIM03-23	663	531	0	80.09	19.91	I (NWZ)	unnamed
3	SAT1/RV/11/37 (AY593839)	RHO37-11	663	514	0	77.53	22.47	II (SEZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	513	0	77.38	22.62	II (SEZ)	unnamed
5	SAT1/UGA BUFF/21/70 buffalo	UGA70-21	663	500	0	75.41	24.59	IV (EA-1)	unnamed
6	SAT1/BOT/1/77	BOT77-01	663	496	0	74.81	25.19	III (WZ)	unnamed
7	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	491	0	74.06	25.94	III (WZ)	unnamed
8	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	488	0	73.60	26.40	III (WZ)	unnamed
9	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	471	0	71.04	28.96	VII (EA-2)	unnamed
10	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	470	0	70.89	29.11	VIII (EA-3)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV SAT 1 in Kenya in 2011

Batch: WRLFMD/2012/00024

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 663

No Of Bootstrap Reps = 1000

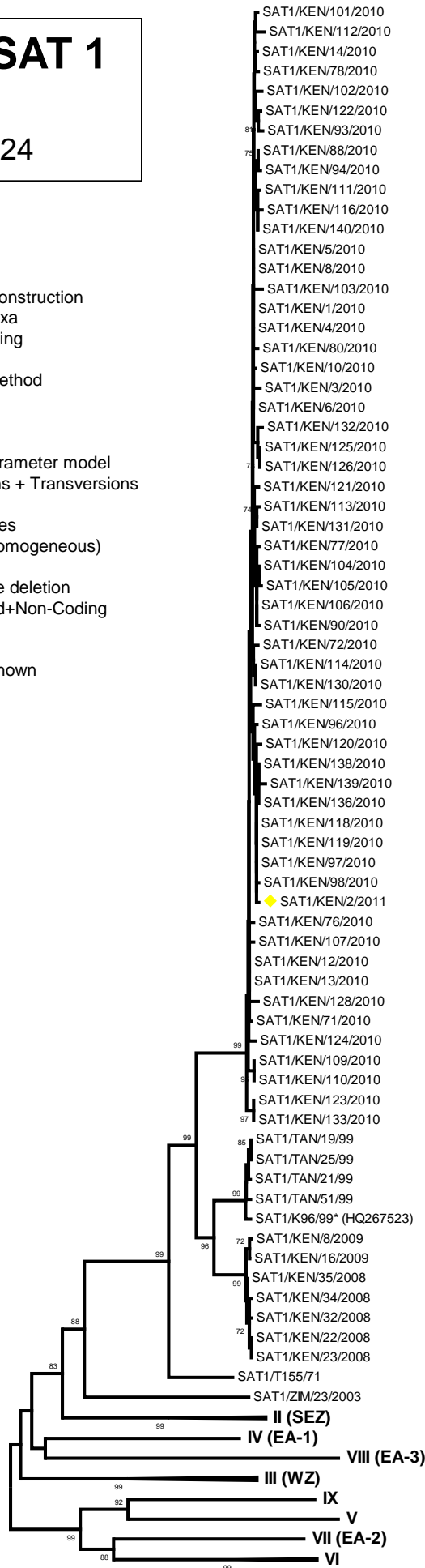
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 18 July 2012

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I (NWZ)