

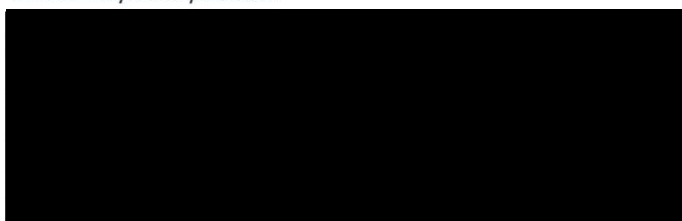


INSTITUTE FOR ANIMAL HEALTH
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441, Fax: 01483 232621

FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00036

Sender Details:



Date Received: 28th September 2012

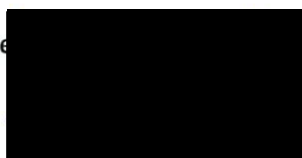
Country of Origin: ZAMBIA

Date Reported: 22nd January 2013

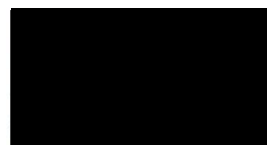
Dear Dr Thobokwe,

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:

22/1/13



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: trish.ryder@p.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: 15 January 2013

FMDV type SAT 2

Country: Zambia

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2012/00036



The contents of this report are copyright and should not be reproduced without permission

© The Pirbright Institute

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT2	Report date: 11/01/2013
WRLFMD Ref No: ZAM/1/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00036	Checked by: D.P. King
Sender Ref: ZAM 01/12	
Location: Mbala, Mbala, Mbala, Zambia	Topotype: IV
Date collected: 01/02/2012	Genotype/strain: unnamed
Date received by WRLFMD: 28/09/2012	Sequence filename: ZAM12-01.SEQ
Date received for sequencing: 07/01/2013	Date sequence last updated: 11/01/2013
Species: Bovine	No. of Nt determined: 648
Material used: BTy1 06/12/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 622
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 105 days
	Sequencing time: 4 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/ZAM/2/2012	ZAM12-02	648	647	0	99.85	0.15	IV	unnamed
2	SAT2/KEN/12/2011	KEN11-12	648	643	0	99.23	0.77	IV	unnamed
3	SAT2/KEN/19/2011	KEN11-19	648	643	0	99.23	0.77	IV	unnamed
4	SAT2/KEN/18/2011	KEN11-18	648	642	0	99.07	0.93	IV	unnamed
5	SAT2/KEN/21/2011	KEN11-21	648	642	0	99.07	0.93	IV	unnamed
6	SAT2/TAN/3/2011	TAN11-03	648	642	0	99.07	0.93	IV	unnamed
7	SAT2/TAN/4/2011	TAN11-04	648	642	0	99.07	0.93	IV	unnamed
8	SAT2/TAN/6/2011	TAN11-06	648	642	0	99.07	0.93	IV	unnamed
9	SAT2/KEN/20/2011	KEN11-20	648	641	0	98.92	1.08	IV	unnamed
10	SAT2/TAN/1/2012	TAN12-01	648	641	0	98.92	1.08	IV	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	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	559	0	86.27	13.73	IV	unnamed
2	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	548	0	84.57	15.43	IV	unnamed
3	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	518	0	79.94	20.06	III	unnamed
4	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	516	1	79.75	20.25	III	unnamed
5	SAT2/MAL/1/2003	MAL03-01	648	510	0	78.70	21.30	I	unnamed
6	SAT2/SA/106/59 (AY593848)	RSA59--A	648	505	0	77.93	22.07	I	unnamed
7	SAT2/ZIM/14/2002	ZIM02-14	648	504	0	77.78	22.22	I	unnamed
8	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	486	0	75.00	25.00	II	unnamed
9	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	483	0	74.54	25.46	II	unnamed
10	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	473	0	73.68	26.32	VIII	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© The Pirbright Institute (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT2	Report date: 11/01/2013
WRLFMD Ref No: ZAM/2/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00036	Checked by: D.P. King
Sender Ref: ZAM 02/12	
Location: Mbala, Mbala, Mbala, Zambia	Topotype: IV
Date collected: 01/02/2012	Genotype/strain: unnamed
Date received by WRLFMD: 28/09/2012	Sequence filename: ZAM12-02.SEQ
Date received for sequencing: 07/01/2013	Date sequence last updated: 11/01/2013
Species: Bovine	No. of Nt determined: 648
Material used: BTy1 06/12/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 622
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 105 days
	Sequencing time: 4 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/ZAM/1/2012	ZAM12-01	648	647	0	99.85	0.15	IV	unnamed
2	SAT2/KEN/12/2011	KEN11-12	648	642	0	99.07	0.93	IV	unnamed
3	SAT2/KEN/19/2011	KEN11-19	648	642	0	99.07	0.93	IV	unnamed
4	SAT2/TAN/1/2012	TAN12-01	648	642	0	99.07	0.93	IV	unnamed
5	SAT2/TAN/3/2012	TAN12-03	648	642	0	99.07	0.93	IV	unnamed
6	SAT2/TAN/37/2012	TAN12-37	648	642	0	99.07	0.93	IV	unnamed
7	SAT2/KEN/18/2011	KEN11-18	648	641	0	98.92	1.08	IV	unnamed
8	SAT2/KEN/21/2011	KEN11-21	648	641	0	98.92	1.08	IV	unnamed
9	SAT2/TAN/10/2012	TAN12-10	648	641	0	98.92	1.08	IV	unnamed
10	SAT2/TAN/3/2011	TAN11-03	648	641	0	98.92	1.08	IV	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	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	560	0	86.42	13.58	IV	unnamed
2	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	549	0	84.72	15.28	IV	unnamed
3	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	519	0	80.09	19.91	III	unnamed
4	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	517	1	79.91	20.09	III	unnamed
5	SAT2/MAL/1/2003	MAL03-01	648	511	0	78.86	21.14	I	unnamed
6	SAT2/SA/106/59 (AY593848)	RSA59--A	648	506	0	78.09	21.91	I	unnamed
7	SAT2/ZIM/14/2002	ZIM02-14	648	505	0	77.93	22.07	I	unnamed
8	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	485	0	74.85	25.15	II	unnamed
9	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	482	0	74.38	25.62	II	unnamed
10	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	473	0	73.68	26.32	VIII	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© The Pirbright Institute (not to be reproduced without permission)

Report on FMDV SAT 2 in Zambia in 2012

Batch: WRLFMD/2012/00036

◆ indicates viruses in this batch

Software: MEGA 5.1

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 : 651

No Of Bootstrap Reps = 1000

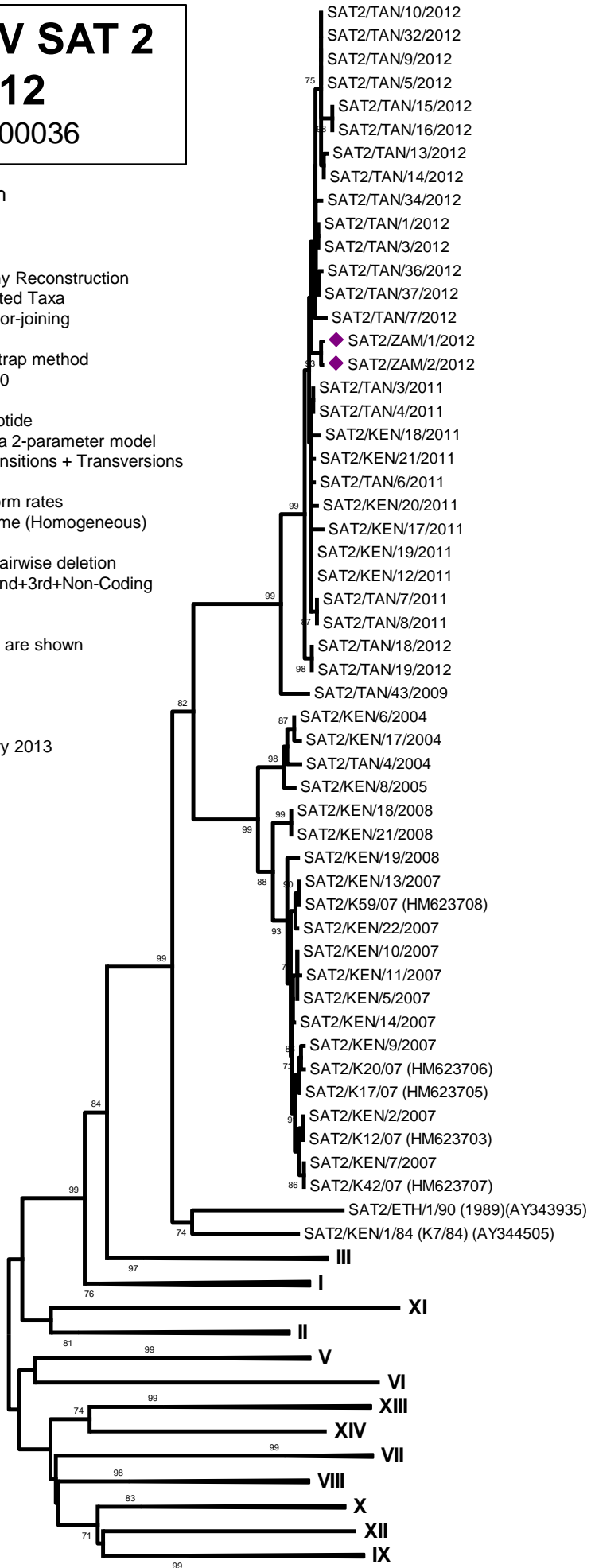
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 15 January 2013

© The Pirbright Institute

(not to be reproduced without permission)



IV