

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

Genotyping Report

Report Date for this Batch: 20 October 2015

FMDV type SAT 1
Country: Namibia
Period: 2015
No. of samples: 1

BATCH: WRLFMD/2015/00020



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

Page 1 of 1

Serotype: SAT1 WRLFMD Ref No: NMB/1/2015 Batch No: WRLFMD/2015/00020 Sender Ref: NAM 03/15 Location: not known, Namibia Date collected: 20/05/2015 Date received by WRLFMD: 13/08/2015 Date received for sequencing: 13/10/2015 Species: Bovine Material used: BTy1 11/09/2015 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 19/10/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: III (WZ) Genotype/strain: unnamed Sequence filename: NMB15-01.SEQ Date sequence last updated: 19/10/2015 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 502 Min. no. of nt for comparison: 600 Total turn-around time: 67 days Sequencing time: 6 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/BOT/1/77 (KF219686)	BOT77-01	663	662	0	99.85	0.15	III (WZ)	unnamed
2	SAT1/BOT/17/77 kudu (KF219687)	BOT77-17	663	660	0	99.55	0.45	III (WZ)	unnamed
3	SAT1/BOT/24/77 (KF219688)	BOT77-24	663	660	0	99.55	0.45	III (WZ)	unnamed
4	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	601	0	90.65	9.35	III (WZ)	unnamed
5	SAT1/SWA/40/61 (AY593843)	SWA61A40	663	598	0	90.2	9.8	III (WZ)	unnamed
6	SAT1/SWA/80/62	SWA62-80	663	597	0	90.05	9.95	III (WZ)	unnamed
7	SAT1/BOT/2/2014	BOT14-02	663	584	0	88.08	11.92	III (WZ)	unnamed
8	SAT1/BOT/3/2014	BOT14-03	663	584	0	88.08	11.92	III (WZ)	unnamed
9	SAT1/BOT/4/2014	BOT14-04	663	584	0	88.08	11.92	III (WZ)	unnamed
10	SAT1/BOT/6/2014 (BVI)	BOT14-AB	653	575	0	88.06	11.94	III (WZ)	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/BOT/1/77 (KF219686)	BOT77-01	663	662	0	99.85	0.15	III (WZ)	unnamed
2	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	601	0	90.65	9.35	III (WZ)	unnamed
3	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	558	0	84.16	15.84	III (WZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	497	0	74.96	25.04	II (SEZ)	unnamed
5	SAT1/RV/11/37 (AY593839)	RHO37-11	663	492	0	74.21	25.79	II (SEZ)	unnamed
6	SAT1/T155/71 (KF561706)	TAN71155	663	491	0	74.06	25.94	I (NWZ)	unnamed
7	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	489	0	73.76	26.24	IV (EA-1)	unnamed
8	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	478	0	72.42	27.58	V	unnamed
9	SAT1/ZIM/23/2003 (KF219690)	ZIM03-23	663	476	0	71.79	28.21	I (NWZ)	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	473	0	71.34	28.66	VII (EA-2)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV SAT 1 in Namibia in 2015

Batch: WRLFMD/2015/00020

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

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

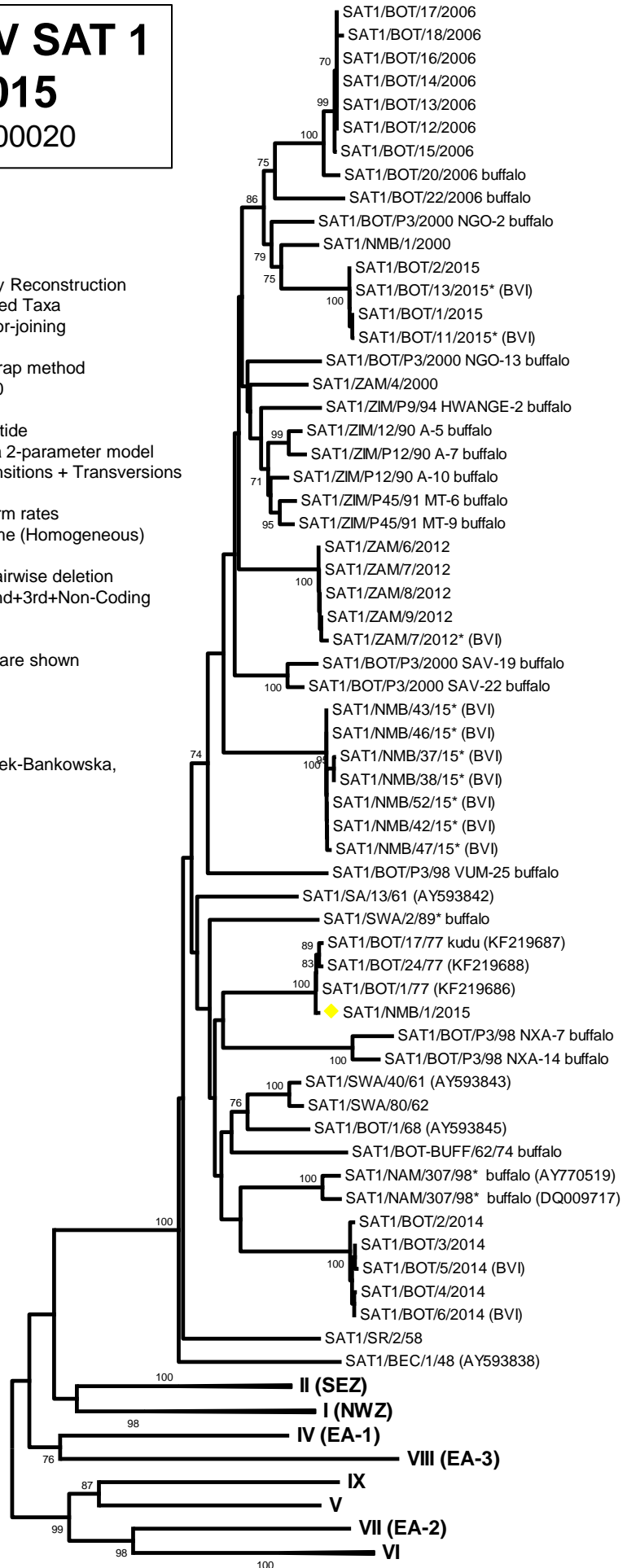
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
20 October 2015

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III (WZ)