

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

Genotyping Report

Report Date for this Batch: 29 October 2014

FMDV type SAT 2

Country: Mozambique

Period: 2014

No. of samples: 4

BATCH: WRLFMD/2014/00032



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: SAT2	Report date: 29/10/2014
WRLFMD Ref No: MOZ/1/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00032	Checked by: K. Bachanek-Bankowska
Sender Ref: MOZ03/14	
Location: Maputo, Mozambique	Topotype: I
Date collected: 24/07/2014	Genotype/strain: unnamed
Date received by WRLFMD: 13/10/2014	Sequence filename: MOZ14-01.SEQ
Date received for sequencing: 27/10/2014	Date sequence last updated: 28/10/2014
Species: Bovine	No. of Nt determined: 648
Material used: BTy1 17/10/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 677
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 16 days
	Sequencing time: 2 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/MOZ/2/2014	MOZ14-02	648	645	0	99.54	0.46	I	unnamed
2	SAT2/MOZ/4/2014* (BVI)	MOZ14-AB	637	634	2	99.53	0.47	I	unnamed
3	SAT2/MOZ/5/2014* (BVI)	MOZ14-AC	620	617	1	99.52	0.48	I	unnamed
4	SAT2/MOZ/3/2014	MOZ14-03	648	644	0	99.38	0.62	I	unnamed
5	SAT2/MOZ/4/2014	MOZ14-04	648	644	0	99.38	0.62	I	unnamed
6	SAT2/KNP/31/95* (AF367119)(buffalo)	KNP95-AB	646	579	2	89.63	10.37	I	unnamed
7	SAT2/KNP/18/95* (AF367118)(buffalo)	KNP95-AA	647	577	1	89.18	10.82	I	unnamed
8	SAT2/KNP/16/88* (AF367104)(impala)	KNP88-AB	648	577	0	89.04	10.96	I	unnamed
9	SAT2/KNP/19/88* (AF367106)(impala)	KNP88-AE	648	577	0	89.04	10.96	I	unnamed
10	SAT2/KNP/20/88* (AF367107)(impala)	KNP88-AF	648	577	0	89.04	10.96	I	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/SA/106/59 (AY593848)	RSA59--A	648	536	0	82.72	17.28	I	unnamed
2	SAT2/ZIM/14/2002 (KF219689)	ZIM02-14	648	530	0	81.79	18.21	I	unnamed
3	SAT2/MAL/1/2003	MAL03-01	648	524	0	80.86	19.14	I	unnamed
4	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	511	0	78.86	21.14	IV	unnamed
5	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	511	0	78.86	21.14	III	unnamed
6	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	510	1	78.83	21.17	III	unnamed
7	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	506	0	78.09	21.91	IV	unnamed
8	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	490	0	75.62	24.38	II	unnamed
9	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	483	0	74.54	25.46	II	unnamed
10	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	476	0	73.46	26.54	V	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Serotype: SAT2	Report date: 29/10/2014
WRLFMD Ref No: MOZ/4/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00032	Checked by: K. Bachanek-Bankowska
Sender Ref: MOZ06/14	
Location: Maputo, Mozambique	Topotype: I
Date collected: 24/07/2014	Genotype/strain: unnamed
Date received by WRLFMD: 13/10/2014	Sequence filename: MOZ14-04.SEQ
Date received for sequencing: 27/10/2014	Date sequence last updated: 28/10/2014
Species: Bovine	No. of Nt determined: 648
Material used: BTy1 17/10/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 677
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1	SAT2/MOZ/3/2014	MOZ14-03	648	646	0	99.69	0.31	I	unnamed
2	SAT2/MOZ/2/2014	MOZ14-02	648	645	0	99.54	0.46	I	unnamed
3	SAT2/MOZ/4/2014* (BVI)	MOZ14-AB	637	634	2	99.53	0.47	I	unnamed
4	SAT2/MOZ/5/2014* (BVI)	MOZ14-AC	620	617	1	99.52	0.48	I	unnamed
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8	SAT2/KNP/16/88* (AF367104)(impala)	KNP88-AB	648	575	0	88.73	11.27	I	unnamed
9	SAT2/KNP/19/88* (AF367106)(impala)	KNP88-AE	648	575	0	88.73	11.27	I	unnamed
10	SAT2/KNP/20/88* (AF367107)(impala)	KNP88-AF	648	575	0	88.73	11.27	I	unnamed
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5	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	511	0	78.86	21.14	III	unnamed
6	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	509	1	78.67	21.33	III	unnamed
7	SAT2/KEN/1/84 (K7/84) (AY3444505)	KEN84-AB	648	506	0	78.09	21.91	IV	unnamed
8	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	490	0	75.62	24.38	II	unnamed
9	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	483	0	74.54	25.46	II	unnamed
10	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	476	0	73.46	26.54	V	unnamed

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Report on FMDV SAT 2 in Mozambique in 2014

Batch: WRLFMD/2014/00032

◆ 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 : 651

No Of Bootstrap Reps = 1000

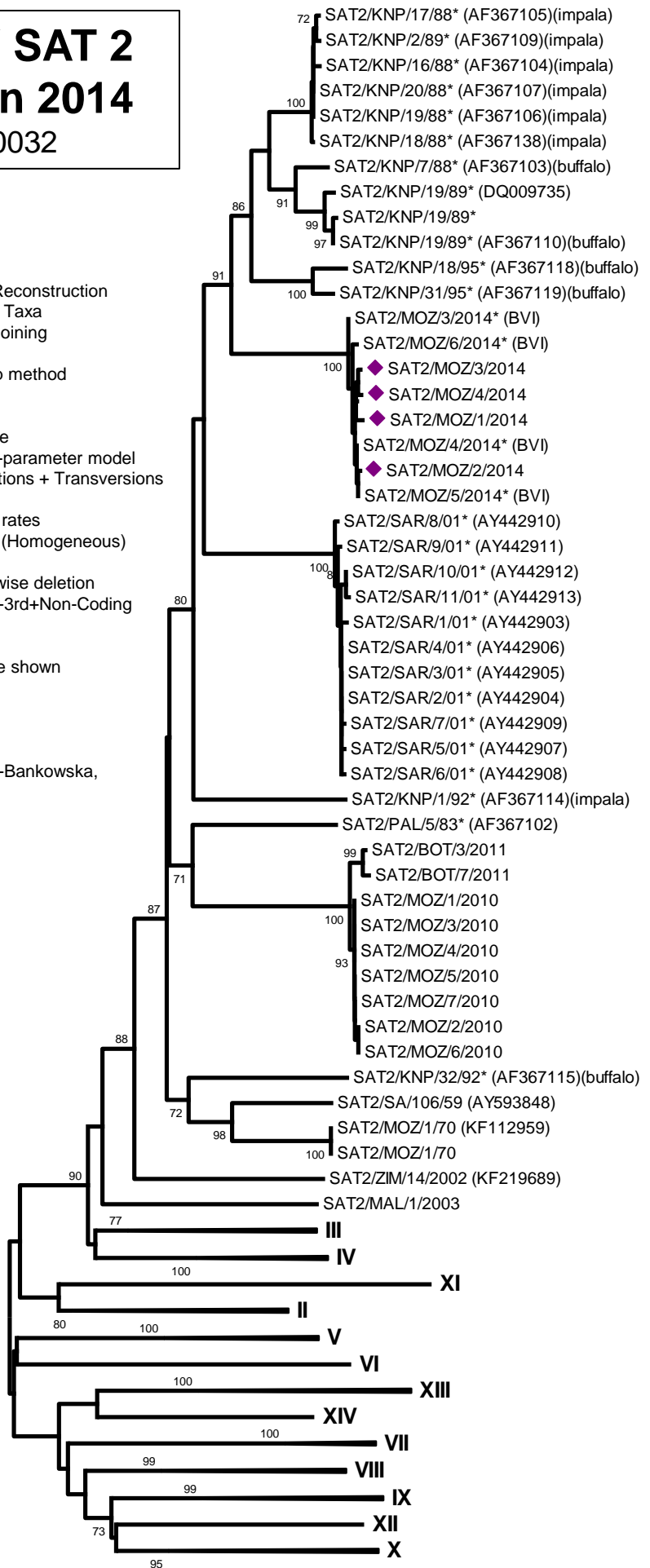
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
29 October 2014

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