

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

Genotyping Report

Report Date for this Batch: 20 October 2015

FMDV type SAT 2

Country: Mozambique

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2015/00023



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

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Serotype: SAT2 WRLFMD Ref No: MOZ/1/2015 Batch No: WRLFMD/2015/00023 Sender Ref: MOZ 01/15 Location: not known, Mozambique Date collected: 01/05/2015 Date received by WRLFMD: 13/08/2015 Date received for sequencing: 13/10/2015 Species: Bovine Material used: BTy1 10/09/2015 Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT-2B208R SAT2-P1-1223F/SAT-2B208R	Report date: 19/10/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: I Genotype/strain: unnamed Sequence filename: MOZ15-01.SEQ Date sequence last updated: 19/10/2015 No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648 Total no. of comparisons: 705 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	SAT2/MOZ/1/2014	MOZ14-01	648	643	0	99.23	0.77	I	unnamed
2	SAT2/MOZ/1/2015* (BVI)	MOZ15-AA	648	642	0	99.07	0.93	I	unnamed
3	SAT2/MOZ/4/2014* (BVI)	MOZ14-AB	637	630	2	98.90	1.10	I	unnamed
4	SAT2/MOZ/5/2014* (BVI)	MOZ14-AC	620	613	1	98.87	1.13	I	unnamed
5	SAT2/MOZ/2/2014	MOZ14-02	648	640	0	98.77	1.23	I	unnamed
6	SAT2/MOZ/3/2014	MOZ14-03	648	639	0	98.61	1.39	I	unnamed
7	SAT2/MOZ/4/2014	MOZ14-04	648	639	0	98.61	1.39	I	unnamed
8	SAT2/KNP/31/95* (AF367119)(buffalo)	KNP95-AB	646	578	2	89.47	10.53	I	unnamed
9	SAT2/KNP/18/95* (AF367118)(buffalo)	KNP95-AA	647	576	1	89.03	10.97	I	unnamed
10	SAT2/KNP/16/88* (AF367104)(impala)	KNP88-AB	648	576	0	88.89	11.11	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	533	0	82.25	17.75	I	unnamed
3	SAT2/MAL/1/2003	MAL03-01	648	522	0	80.56	19.44	I	unnamed
4	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	510	1	78.83	21.17	III	unnamed
5	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	509	0	78.55	21.45	III	unnamed
6	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	508	0	78.40	21.60	IV	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	484	0	74.69	25.31	II	unnamed
10	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	477	0	73.61	26.39	V	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV SAT 2 in Mozambique in 2015

Batch: WRLFMD/2015/00023

◆ 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,
20 October 2015

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