

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

Genotyping Report

Report Date for this Batch: 29 April 2024

FMDV type SAT 1

Country: Uganda

Period: 2023

No. of sequences: 2



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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	Report date: 29/04/2024
WRLFMD Ref No: UGA/14/2023	Reported by: N.J. Knowles
Batch No: WRLFMD/2024/000004	Checked by: D.P. King
Sender Ref: 388	
Location: Wakiso district, Central region, Uganda	Topotype: VII
Date collected: 03/11/2023	Genotype/strain:
Date received by WRLFMD: 19/03/2024	Sequence filename: UGA23-14.seq
Date received for sequencing: 16/04/2024	Date sequence last updated: 19/04/2024
Species: Bovine	No. of Nt determined: 663
Material used: WRL-LFBK1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 663
RT-PCR primers: SAT1-1C559F/SAT-2B208R	Total no. of comparisons: 734
SAT1U-OS/SAT-2B208R	Min. no. of nt for comparison: 600
FMD-3161F/FMD-4303R	
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT1/UGA/15/2023	UGA23-15	663	663	0	100.00	0.00	VII	unnamed
2	SAT1/UGA/47/71 (MH053324)	UGA71-47	663	573	0	86.43	13.57	VII	unnamed
3	SAT1/UGA/6/78	UGA78-06	663	552	0	83.26	16.74	VII	unnamed
4	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	544	0	82.05	17.95	VII	unnamed
5	SAT1/SUD/8/74 (AY441998)	SUD74S08	663	518	0	78.13	21.87	VI	unnamed
6	SAT1/SUD/9/74 (AY441999)	SUD74S09	663	518	0	78.13	21.87	VI	unnamed
7	SAT1/SUD/13/74 (AY442000)	SUD74S13	663	515	0	77.68	22.32	VI	unnamed
8	SAT1/SUD/4/76	SUD76-04	663	515	0	77.68	22.32	VI	unnamed
9	SAT1/SUD/3/76 (DQ009725)	SUD76M03	657	510	0	77.63	22.37	VI	unnamed
10	SAT1/SUD/4/76 (AY441997)	SUD76S04	663	514	0	77.53	22.47	VI	unnamed
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(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
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4	SAT1/ISR/4/62 (AY593844)	ISR62-04	663	508	0	76.62	23.38	VI	unnamed
5	SAT1/TCH/1/72 (MG972459)	TCH72A01	660	492	0	74.55	25.45	XI	unnamed
6	SAT1/ETH/3/2007 (FJ798154)	ETH07-03	663	486	0	73.30	26.70	IX	unnamed
7	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	481	0	72.88	27.12	V	unnamed
8	SAT1/NIG/1/2015a* (KX822796)	NIG15-AA	660	472	0	71.52	28.48	X	unnamed
9	SAT1/TAN/T155/71 (KF561706)	TAN71155	663	473	0	71.34	28.66	I	unnamed
10	SAT1/MOZ/P13/2010 BUF B16 (KF219691)	MOZ10-AE	663	472	0	71.19	28.81	XIII	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Report on FMDV SAT 1 in Uganda in 2023

Batch: WRLFMD/2024/000004

◆ indicates viruses in this batch

Software: MEGA 7.0.26

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 ----- Gamma Distributed (G)

Gamma Parameter ----- 1

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

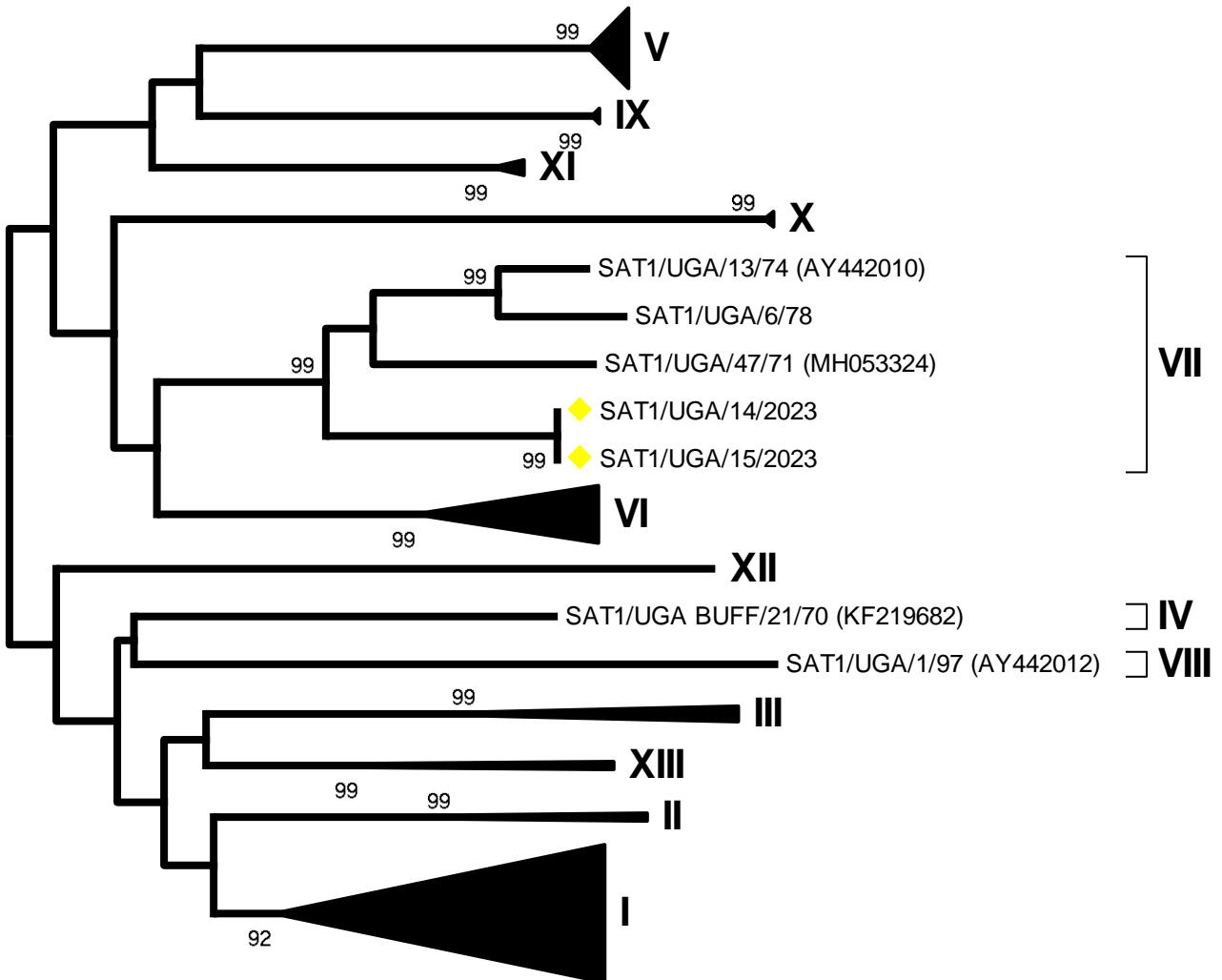
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

N.J. Knowles, J. Wadsworth & Hayley M. Hicks,
29 April 2024

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0.05