

FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: SAT2 WRLFMD Ref No: MAL05/2023 Batch No: WRLMEG/2023/00026 Sender Ref: MAL05/23 Location: not known, Malawi Date collected: 2023 Date received by WRLFMD: 11/08/2023 Date received for sequencing: Species: Bovine Material used: Epithelial tissue RNA extract Region sequenced: VP1 RT-PCR primers: SAT2-P1-1223F/SAT-2B208R	Report date: 15/08/2023 Reported by: N.J. Knowles Checked by: D.P. King Topotype: II Genotype/strain: Sequence filename: MAL23-AA.seq Date sequence last updated: 13/08/2023 No. of Nt determined: 549 No. of ambiguities: 0 Gene length: 648 Total no. of comparisons: 1149 Min. no. of nt for comparison: 525 Total turn-around 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/ZIM/P25/91 UR-3 buffalo (MT385647)	ZIM91B23	549	482	0	87.80	12.20	II	unnamed
2	SAT2/ZIM/P25/91 (UR-17)(DQ009727)(buffalo)	ZIM91-AB	543	476	0	87.66	12.34	II	unnamed
3	SAT2/ZIM/P25/91 UR-17 buffalo (MT385648)	ZIM91B34	549	480	0	87.43	12.57	II	unnamed
4	SAT2/ZIM/P25/91 UR-34 buffalo (MT385649)	ZIM91B48	549	480	0	87.43	12.57	II	unnamed
5	SAT2/ZIM/P27/90 (DSA-14)(DQ009728)(buffalo)	ZIM90-AA	543	474	0	87.29	12.71	II	unnamed
6	SAT2/ZIM/P27/90 DSA-12 buffalo (MT385637)	ZIM90B20	549	477	0	86.89	13.11	II	unnamed
7	SAT2/ZIM/P27/90 DSA-14 buffalo (MT385638)	ZIM90B21	549	477	0	86.89	13.11	II	unnamed
8	SAT2/ZIM/P27/90 DSA-20 buffalo (MT385639)	ZIM90B25	549	477	0	86.89	13.11	II	unnamed
9	SAT2/ZIM/P27/90 DSA-29 buffalo (MT385640)	ZIM90B29	549	474	0	86.34	13.66	II	unnamed
10	SAT2/ZIM/1/00* (AF367136)(buffalo)	ZIM00-AA	549	461	0	83.97	16.03	II	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/ZIM/5/81 (EF134951)	ZIM81-AA	549	461	0	83.97	16.03	II	unnamed
2	SAT2/ZIM/7/83 (AF540910)	ZIM83A07	549	446	0	81.24	18.76	II	unnamed
3	SAT2/ZIM/14/2002 (KF219689)	ZIM02-14	549	424	0	77.23	22.77	I	unnamed
4	SAT2/RHO/1/48 (AY593847)	ZAM48B01	549	423	0	77.05	22.95	III	unnamed
5	SAT2/SA/106/59 (AY593848)	RSA59--A	549	423	0	77.05	22.95	I	unnamed
6	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	549	421	0	76.68	23.32	IV	unnamed
7	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	549	421	0	76.68	23.32	IV	unnamed
8	SAT2/KEN/11/2009 (JX570628)	KEN09-11	549	421	0	76.68	23.32	IV	Ken-09
9	SAT2/NIG/2/75 (AF367139)	NIG75-02	549	415	0	75.59	24.41	V	unnamed
10	SAT2/ANG/4/74 (AF479417)	ANG74-04	549	413	0	75.23	24.77	XI	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Report on FMDV SAT 2 in Malawi in 2023

Batch: WRLMEG/2023/00026

◆ indicates viruses in this batch

Software: MEGA 7.0.21

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.

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15/08/2023

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