

FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: SAT2 WRLFMD Ref No: BOT02/2022 Batch No: WRLMEG/2022/00029 Sender Ref: SAT2/BOT02/2022 Location: Butale crush, Masungu, North-East district, Botswana Date collected: 24/08/2022 Date received by WRLFMD: 27/08/2022 Species: Cattle Material used: Epithelial tissue RNA extract Region sequenced: VP1 RT-PCR primers: SAT-1D209F/SAT-2B208R	Report date: 31/08/2022 Reported by: N.J. Knowles Checked by: - Topotype: II Genotype/strain: Sequence filename: BOT22-AA.seq Date sequence last updated: 31/08/2022 No. of Nt determined: 418 No. of ambiguities: 0 Gene length: 648 Total no. of comparisons: 1172 Min. no. of nt for comparison: 400
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/1/2015a* (BVI)	ZIM15-AB	413	385	8	93.22	6.78	II	unnamed
2	SAT2/ZIM/25/2015	ZIM15-25	418	389	0	93.06	6.94	II	unnamed
3	SAT2/ZIM/1/2015	ZIM15-01	418	388	0	92.82	7.18	II	unnamed
4	SAT2/ZIM/1/2015* (BVI)	ZIM15-AA	418	388	0	92.82	7.18	II	unnamed
5	SAT2/ZIM/11/2015	ZIM15-11	418	388	0	92.82	7.18	II	unnamed
6	SAT2/ZIM/2/2017* (BVI)	ZIM17-AB	418	388	0	92.82	7.18	II	unnamed
7	SAT2/ZIM/23/2015	ZIM15-23	418	388	0	92.82	7.18	II	unnamed
8	SAT2/ZIM/1/2014	ZIM14-01	418	387	0	92.58	7.42	II	unnamed
9	SAT2/ZIM02/2018* (BVI)	ZIM18-AA	418	386	0	92.34	7.66	II	unnamed
10	SAT2/ZIM/9/2015	ZIM15-09	418	385	0	92.11	7.89	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/7/83 (AF540910)	ZIM83A07	418	374	0	89.47	10.53	II	unnamed
2	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	418	342	0	81.82	18.18	II	unnamed
3	SAT2/KEN/11/2009 (JX570628)	KEN09-11	418	324	0	77.51	22.49	IV	Ken-09
4	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	418	321	0	76.79	23.21	IV	unnamed
5	SAT2/RHO/1/48 (AY593847)	ZAM48B01	418	321	0	76.79	23.21	III	unnamed
6	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	418	312	0	74.64	25.36	IV	unnamed
7	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	412	305	0	74.03	25.97	VIII	unnamed
8	SAT2/NIG/2/75 (AF367139)	NIG75-02	418	309	0	73.92	26.08	V	unnamed
9	SAT2/ANG/4/74 (AF479417)	ANG74-04	418	308	0	73.68	26.32	XI	unnamed
10	SAT2/SA/106/59 (AY593848)	RSA59-A	418	308	0	73.68	26.32	I	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Analysis (MEGA 7)

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

