

# 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: Zimbabwe

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2015/00022



The contents of this report are copyright and should not be reproduced without permission

© The Pirbright Institute

# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT2	Report date: 19/10/2015
WRLFMD Ref No: ZIM/1/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00022	Checked by: K. Bachanek-Bankowska
Sender Ref: ZIM 01/15	
Location: not known, Zimbabwe	Topotype: II
Date collected: 15/04/2015	Genotype/strain: unnamed
Date received by WRLFMD: 13/08/2015	Sequence filename: ZIM15-01.SEQ
Date received for sequencing: 13/10/2015	Date sequence last updated: 19/10/2015
Species: Bovine	No. of Nt determined: 648
Material used: BTy1 11/09/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 705
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 67 days
	Sequencing time: 6 days
Comments:	

<b>Most Closely Related Viruses</b>									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/ZIM/1/2015* (BVI)	ZIM15-AA	648	648	0	100.00	0.00	II	unnamed
2	SAT2/ZIM/1/2015a* (BVI)	ZIM15-AB	640	638	8	99.69	0.31	II	unnamed
3	SAT2/ZIM/1/2014	ZIM14-01	648	641	0	98.92	1.08	II	unnamed
4	SAT2/ZIM/11/2014 (BVI)	ZIM14-AA	628	621	0	98.89	1.11	II	unnamed
5	SAT2/ZIM/14/13* (BVI)	ZIM13-AB	636	626	0	98.43	1.57	II	unnamed
6	SAT2/ZIM/18/13* (BVI)	ZIM13-AD	626	616	0	98.40	1.60	II	unnamed
7	SAT2/ZIM/16/13* (BVI)	ZIM13-AC	613	603	0	98.37	1.63	II	unnamed
8	SAT2/BOT-BUFF/170/74 (buffalo)	BOT74B170	648	596	0	91.98	8.02	II	unnamed
9	SAT2/ZIM/8/89 (KF112975)	ZIM89-08	648	588	0	90.74	9.26	II	unnamed
10	SAT2/ZIM/2/2010	ZIM10-02	648	587	0	90.59	9.41	II	Unnamed
<b>Most Closely Related Reference Viruses</b>									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT2/ZIM/7/83 (AF136607)	ZIM83A07	648	584	0	90.12	9.88	II	unnamed
2	SAT2/ZIM/5/81 (EF134951)	ZIM81-AA	648	527	0	81.33	18.67	II	unnamed
3	SAT2/SA/106/59 (AY593848)	RSA59--A	648	499	0	77.01	22.99	I	unnamed
4	SAT2/RHO/1/48 (AY593847)	ZAM48B01	648	497	0	76.70	23.30	III	unnamed
5	SAT2/ZIM/14/2002 (KF219689)	ZIM02-14	648	491	0	75.77	24.23	I	unnamed
6	SAT2/BOT/P3/98 (buffalo 29) (AF367124)	BOT98-AC	647	490	1	75.73	24.27	III	unnamed
7	SAT2/ETH/1/90 (1989)(AY343935)	ETH90-AA	648	489	0	75.46	24.54	IV	unnamed
8	SAT2/MAL/1/2003	MAL03-01	648	489	0	75.46	24.54	I	unnamed
9	SAT2/KEN/1/84 (K7/84) (AY344505)	KEN84-AB	648	486	0	75.00	25.00	IV	unnamed
10	SAT2/ANG/4/74 (AF479417)	ANG74-04	648	482	0	74.38	25.62	XI	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.3

© The Pirbright Institute (not to be reproduced without permission)

# Report on FMDV SAT 2 in Zimbabwe in 2015

Batch: WRLFMD/2015/00022

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

----- Phylogeny Reconstruction

----- All Selected Taxa

----- Neighbor-joining

Phylogeny Test

----- Bootstrap method

----- 1000

Substitution Model

----- Nucleotide

----- Kimura 2-parameter model

----- d: Transitions + Transversions

Rates and Patterns

----- Uniform rates

----- Same (Homogeneous)

Data Subset to Use

----- Pairwise deletion

----- 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

© The Pirbright Institute

(not to be reproduced without permission)

