

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

Genotyping Report

Report Date for this Batch: 15 December 2015

FMDV type SAT 1

Country: Zimbabwe

Period: 2015

No. of samples: 4

BATCH: WRLFMD/2015/000027



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Notes:

- 1) Sample ZIM/7/2015 (935/15) was typed as both SAT1 and SAT 2. RT-PCR amplification of the VP1 region detected both serotypes, but the sequence data was of poor quality and is not reported here.
- 2) The phylogenetic tree indicates that the SAT 1 outbreak viruses are closely related to each other and are most closely related to viruses from African buffalo sampled in the 1990's in southeast Zimbabwe (Gonarezhou NP and Lone Star and Hippo Valley Ranches). This may indicate an origin for this epidemic.

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Serotype: SAT1 WRLFMD Ref No: ZIM/10/2015 Batch No: WRLFMD/2015/00027 Sender Ref: 1045/15 Location: Masondy Diptank, Gokwe, Midlands, Zimbabwe Date collected: 20/06/2015 Date received by WRLFMD: 03/09/2015 Date received for sequencing: 26/11/2015 Species: Bovine Material used: BTY1 12/11/2015 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 14/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: II (SEZ) Genotype/strain: unnamed Sequence filename: ZIM15-10.SEQ Date sequence last updated: 14/12/2015 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 506 Min. no. of nt for comparison: 600 Total turn-around time: 102 days Sequencing time: 18 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT1/ZIM/17/2015	ZIM15-17	663	663	0	100.00	0.00	II (SEZ)	unnamed
2	SAT1/ZIM/19/2015	ZIM15-19	663	662	0	99.85	0.15	II (SEZ)	unnamed
3	SAT1/ZIM/14/2015	ZIM15-14	663	659	0	99.40	0.60	II (SEZ)	unnamed
4	SAT1/ZIM/P18/91 GN-11 buffalo	ZIM91B08	663	599	0	90.35	9.65	II (SEZ)	unnamed
5	SAT1/ZIM/P26/90 HV-3 buffalo	ZIM90B08	663	599	0	90.35	9.65	II (SEZ)	unnamed
6	SAT1/ZIM/P18/91 GN-30 buffalo	ZIM91B17	663	596	0	89.89	10.11	II (SEZ)	unnamed
7	SAT1/ZIM/P1/93 LS-9 buffalo	ZIM93B02	663	595	0	89.74	10.26	II (SEZ)	unnamed
8	SAT1/ZIM/P18/91 GN-16 buffalo	ZIM91B12	663	594	0	89.59	10.41	II (SEZ)	unnamed
9	SAT1/ZIM/P18/91 GN-19 buffalo	ZIM91B13	663	594	0	89.59	10.41	II (SEZ)	unnamed
10	SAT1/ZIM/P7/94 MT-5 buffalo	ZIM94B03	663	594	0	89.59	10.41	II (SEZ)	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	SAT1/RV/11/37 (AY593839)	RHO37-11	663	561	0	84.62	15.38	II (SEZ)	unnamed
2	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	540	0	81.45	18.55	II (SEZ)	unnamed
3	SAT1/ZIM/23/2003 (KF219690)	ZIM03-23	663	525	0	79.19	20.81	I (NWZ)	unnamed
4	SAT1/T155/71 (KF561706)	TAN71155	663	515	0	77.68	22.32	I (NWZ)	unnamed
5	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	507	0	76.47	23.53	III (WZ)	unnamed
6	SAT1/BOT/1/77 (KF219686)	BOT77-01	663	499	0	75.26	24.74	III (WZ)	unnamed
7	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	496	0	74.81	25.19	III (WZ)	unnamed
8	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	494	0	74.51	25.49	IV (EA-1)	unnamed
9	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	470	0	70.89	29.11	VIII (EA-3)	unnamed
10	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	462	0	70.00	30.00	V	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: SAT1 WRLFMD Ref No: ZIM/14/2015 Batch No: WRLFMD/2015/00027 Sender Ref: 1156/15 Location: Torkie Rockwood Farm, Masvingo, Masvingo, Zimbabwe Date collected: 14/07/2015 Date received by WRLFMD: 03/09/2015 Date received for sequencing: 26/11/2015 Species: Bovine Material used: BTY1 18/11/2015 Region sequenced: VPI RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 14/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: II (SEZ) Genotype/strain: unnamed Sequence filename: ZIM15-14.SEQ Date sequence last updated: 14/12/2015 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 506 Min. no. of nt for comparison: 600 Total turn-around time: 102 days Sequencing time: 18 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	SAT1/ZIM/19/2015	ZIM15-19	663	660	0	99.55	0.45	II (SEZ)	unnamed
2	SAT1/ZIM/10/2015	ZIM15-10	663	659	0	99.40	0.60	II (SEZ)	unnamed
3	SAT1/ZIM/17/2015	ZIM15-17	663	659	0	99.40	0.60	II (SEZ)	unnamed
4	SAT1/ZIM/P26/90 HV-3 buffalo	ZIM90B08	663	600	0	90.50	9.50	II (SEZ)	unnamed
5	SAT1/ZIM/P18/91 GN-11 buffalo	ZIM91B08	663	598	0	90.20	9.80	II (SEZ)	unnamed
6	SAT1/ZIM/P18/91 GN-30 buffalo	ZIM91B17	663	597	0	90.05	9.95	II (SEZ)	unnamed
7	SAT1/ZIM/P1/93 LS-9 buffalo	ZIM93B02	663	596	0	89.89	10.11	II (SEZ)	unnamed
8	SAT1/ZIM/P18/91 GN-16 buffalo	ZIM91B12	663	595	0	89.74	10.26	II (SEZ)	unnamed
9	SAT1/ZIM/P18/91 GN-19 buffalo	ZIM91B13	663	595	0	89.74	10.26	II (SEZ)	unnamed
10	SAT1/ZIM/P1/93 LS-7 buffalo	ZIM93B01	663	594	0	89.59	10.41	II (SEZ)	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	SAT1/RV/11/37 (AY593839)	RHO37-11	663	564	0	85.07	14.93	II (SEZ)	unnamed
2	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	541	0	81.60	18.40	II (SEZ)	unnamed
3	SAT1/ZIM/23/2003 (KF219690)	ZIM03-23	663	527	0	79.49	20.51	I (NWZ)	unnamed
4	SAT1/T155/71 (KF561706)	TAN71155	663	515	0	77.68	22.32	I (NWZ)	unnamed
5	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	506	0	76.32	23.68	III (WZ)	unnamed
6	SAT1/BOT/1/77 (KF219686)	BOT77-01	663	498	0	75.11	24.89	III (WZ)	unnamed
7	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	496	0	74.81	25.19	III (WZ)	unnamed
8	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	494	0	74.51	25.49	IV (EA-1)	unnamed
9	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	472	0	71.19	28.81	VIII (EA-3)	unnamed
10	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	463	0	70.15	29.85	V	unnamed

nt, nucleotides

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Serotype: SAT1 WRLFMD Ref No: ZIM/17/2015 Batch No: WRLFMD/2015/00027 Sender Ref: 1416(10) Location: Chipinge, Manicaland, Zimbabwe Date collected: 07/08/2015 Date received by WRLFMD: 03/09/2015 Date received for sequencing: 26/11/2015 Species: Bovine Material used: BTY1 20/11/2015 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 14/12/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: II (SEZ) Genotype/strain: unnamed Sequence filename: ZIM15-17.SEQ Date sequence last updated: 14/12/2015 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 506 Min. no. of nt for comparison: 600 Total turn-around time: 102 days Sequencing time: 18 days
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2	SAT1/ZIM/19/2015	ZIM15-19	663	662	0	99.85	0.15	II (SEZ)	unnamed
3	SAT1/ZIM/14/2015	ZIM15-14	663	659	0	99.40	0.60	II (SEZ)	unnamed
4	SAT1/ZIM/P18/91 GN-11 buffalo	ZIM91B08	663	599	0	90.35	9.65	II (SEZ)	unnamed
5	SAT1/ZIM/P26/90 HV-3 buffalo	ZIM90B08	663	599	0	90.35	9.65	II (SEZ)	unnamed
6	SAT1/ZIM/P18/91 GN-30 buffalo	ZIM91B17	663	596	0	89.89	10.11	II (SEZ)	unnamed
7	SAT1/ZIM/P1/93 LS-9 buffalo	ZIM93B02	663	595	0	89.74	10.26	II (SEZ)	unnamed
8	SAT1/ZIM/P18/91 GN-16 buffalo	ZIM91B12	663	594	0	89.59	10.41	II (SEZ)	unnamed
9	SAT1/ZIM/P18/91 GN-19 buffalo	ZIM91B13	663	594	0	89.59	10.41	II (SEZ)	unnamed
10	SAT1/ZIM/P7/94 MT-5 buffalo	ZIM94B03	663	594	0	89.59	10.41	II (SEZ)	unnamed
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8	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	494	0	74.51	25.49	IV (EA-1)	unnamed
9	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	470	0	70.89	29.11	VIII (EA-3)	unnamed
10	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	462	0	70.00	30.00	V	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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Report on FMDV SAT 1 in Zimbabwe in 2015

Batch: WRLFMD/2015/00027

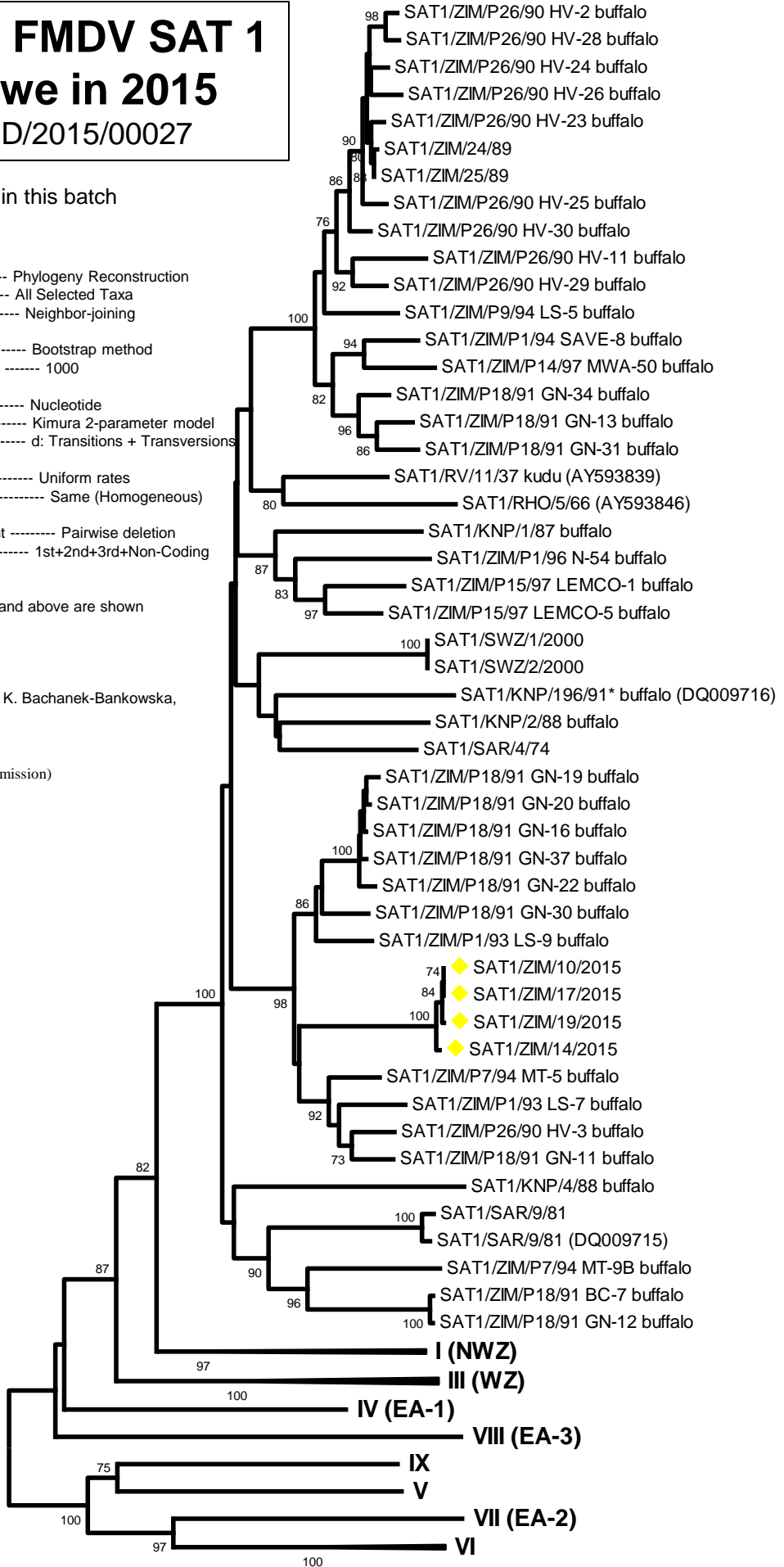
◆ indicates viruses in this batch

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 : 663
 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,
 14 December 2015

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II (SEZ)

0.05