

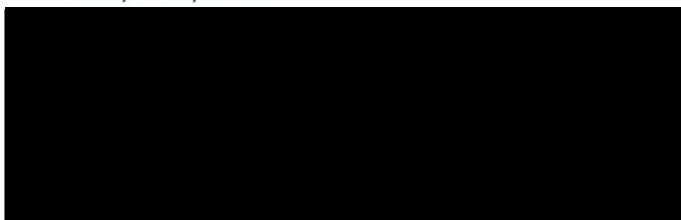


INSTITUTE FOR ANIMAL HEALTH
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441, Fax: 01483 232621

FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00036

Sender Details:



Date Received: 28th September 2012

Country of Origin: ZAMBIA

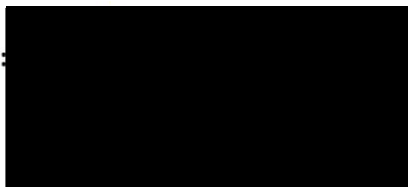
Date Reported: 22nd January 2013

Dear Dr Thobokwe,

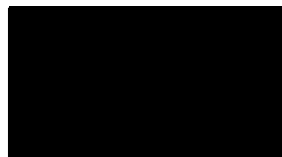
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date:

22/1/13



A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: trish.ryder@p.ac.uk. IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

Genotyping Report

Report Date for this Batch: 15 January 2013

FMDV type SAT 1

Country: Zambia

Period: 2012

No. of samples: 4

BATCH: WRLFMD/2012/00036



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT1	Report date: 11/01/2013
WRLFMD Ref No: ZAM/6/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00036	Checked by: D.P. King
Sender Ref: ZAM 06/12	
Location: Livinstone, Kazungula, Zambia	Topotype: III (WZ)
Date collected: 01/06/2012	Genotype/strain: unnamed
Date received by WRLFMD: 28/09/2012	Sequence filename: ZAM12-06.SEQ
Date received for sequencing: 07/01/2013	Date sequence last updated: 11/01/2013
Species: Bovine	No. of Nt determined: 663
Material used: BTy1 08/12/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 663
RT-PCR primers: SAT1-1C559F/SAT-2B208R	Total no. of comparisons: 426
SAT1U-OS/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 105 days
	Sequencing 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	SAT1/ZAM/7/2012	ZAM12-07	663	663	0	100.00	0.00	III (WZ)	unnamed
2	SAT1/ZAM/8/2012	ZAM12-08	663	663	0	100.00	0.00	III (WZ)	unnamed
3	SAT1/ZAM/9/2012	ZAM12-09	663	663	0	100.00	0.00	III (WZ)	unnamed
4	SAT1/ZAM/7/2012* (BVI)	ZAM12-AA	622	621	0	99.84	0.16	III (WZ)	unnamed
5	SAT1/ZIM/P12/90 A-10 buffalo	ZIM90B03	663	615	0	92.76	7.24	III (WZ)	unnamed
6	SAT1/ZIM/P45/91 MT-6 buffalo	ZIM91B72	663	612	0	92.31	7.69	III (WZ)	unnamed
7	SAT1/ZIM/P45/91 MT-9 buffalo	ZIM91B73	663	611	0	92.16	7.84	III (WZ)	unnamed
8	SAT1/ZAM/4/2000	ZAM00-04	663	609	0	91.86	8.14	III (WZ)	unnamed
9	SAT1/ZIM/12/90 A-5 buffalo	ZIM90B01	663	609	0	91.86	8.14	III (WZ)	unnamed
10	SAT1/ZIM/P12/90 A-7 buffalo	ZIM90B02	663	609	0	91.86	8.14	III (WZ)	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/BOT/1/77	BOT77-01	663	583	0	87.93	12.07	III (WZ)	unnamed
2	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	575	0	86.73	13.27	III (WZ)	unnamed
3	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	562	0	84.77	15.23	III (WZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	507	0	76.47	23.53	II (SEZ)	unnamed
5	SAT1/T155/71	TAN71155	663	506	0	76.32	23.68	I (NWZ)	unnamed
6	SAT1/RV/11/37 (AY593839)	RHO37-11	663	501	0	75.57	24.43	II (SEZ)	unnamed
7	SAT1/UGA BUFF/21/70 buffalo	UGA70-21	663	493	0	74.36	25.64	IV (EA-1)	unnamed
8	SAT1/ZIM/23/2003	ZIM03-23	663	493	0	74.36	25.64	I (NWZ)	unnamed
9	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	470	0	71.21	28.79	V	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	472	0	71.19	28.81	VII (EA-2)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT1	Report date: 11/01/2013
WRLFMD Ref No: ZAM/7/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00036	Checked by: D.P. King
Sender Ref: ZAM 08/12	
Location: Livinstone, Kazungula, Zambia	Topotype: III (WZ)
Date collected: 01/06/2012	Genotype/strain: unnamed
Date received by WRLFMD: 28/09/2012	Sequence filename: ZAM12-07.SEQ
Date received for sequencing: 07/01/2013	Date sequence last updated: 11/01/2013
Species: Bovine	No. of Nt determined: 663
Material used: BTy1 10/12/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 663
RT-PCR primers: SAT1-1C559F/SAT-2B208R	Total no. of comparisons: 426
SAT1U-OS/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 105 days
	Sequencing 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	SAT1/ZAM/6/2012	ZAM12-06	663	663	0	100.00	0.00	III (WZ)	unnamed
2	SAT1/ZAM/8/2012	ZAM12-08	663	663	0	100.00	0.00	III (WZ)	unnamed
3	SAT1/ZAM/9/2012	ZAM12-09	663	663	0	100.00	0.00	III (WZ)	unnamed
4	SAT1/ZAM/7/2012* (BVI)	ZAM12-AA	622	621	0	99.84	0.16	III (WZ)	unnamed
5	SAT1/ZIM/P12/90 A-10 buffalo	ZIM90B03	663	615	0	92.76	7.24	III (WZ)	unnamed
6	SAT1/ZIM/P45/91 MT-6 buffalo	ZIM91B72	663	612	0	92.31	7.69	III (WZ)	unnamed
7	SAT1/ZIM/P45/91 MT-9 buffalo	ZIM91B73	663	611	0	92.16	7.84	III (WZ)	unnamed
8	SAT1/ZAM/4/2000	ZAM00-04	663	609	0	91.86	8.14	III (WZ)	unnamed
9	SAT1/ZIM/12/90 A-5 buffalo	ZIM90B01	663	609	0	91.86	8.14	III (WZ)	unnamed
10	SAT1/ZIM/P12/90 A-7 buffalo	ZIM90B02	663	609	0	91.86	8.14	III (WZ)	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/BOT/1/77	BOT77-01	663	583	0	87.93	12.07	III (WZ)	unnamed
2	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	575	0	86.73	13.27	III (WZ)	unnamed
3	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	562	0	84.77	15.23	III (WZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	507	0	76.47	23.53	II (SEZ)	unnamed
5	SAT1/T155/71	TAN71155	663	506	0	76.32	23.68	I (NWZ)	unnamed
6	SAT1/RV/11/37 (AY593839)	RHO37-11	663	501	0	75.57	24.43	II (SEZ)	unnamed
7	SAT1/UGA BUFF/21/70 buffalo	UGA70-21	663	493	0	74.36	25.64	IV (EA-1)	unnamed
8	SAT1/ZIM/23/2003	ZIM03-23	663	493	0	74.36	25.64	I (NWZ)	unnamed
9	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	470	0	71.21	28.79	V	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	472	0	71.19	28.81	VII (EA-2)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT1 WRLFMD Ref No: ZAM/8/2012 Batch No: WRLFMD/2012/00036 Sender Ref: ZAM 09/12 Location: Kazungula, Kazungula, Zambia Date collected: 11/06/2012 Date received by WRLFMD: 28/09/2012 Date received for sequencing: 07/01/2013 Species: Bovine Material used: BTy1 10/12/2012 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 11/01/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: III (WZ) Genotype/strain: unnamed Sequence filename: ZAM12-08.SEQ Date sequence last updated: 11/01/2013 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 426 Min. no. of nt for comparison: 600 Total turn-around time: 105 days Sequencing 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	SAT1/ZAM/6/2012	ZAM12-06	663	663	0	100.00	0.00	III (WZ)	unnamed
2	SAT1/ZAM/7/2012	ZAM12-07	663	663	0	100.00	0.00	III (WZ)	unnamed
3	SAT1/ZAM/9/2012	ZAM12-09	663	663	0	100.00	0.00	III (WZ)	unnamed
4	SAT1/ZAM/7/2012* (BVI)	ZAM12-AA	622	621	0	99.84	0.16	III (WZ)	unnamed
5	SAT1/ZIM/P12/90 A-10 buffalo	ZIM90B03	663	615	0	92.76	7.24	III (WZ)	unnamed
6	SAT1/ZIM/P45/91 MT-6 buffalo	ZIM91B72	663	612	0	92.31	7.69	III (WZ)	unnamed
7	SAT1/ZIM/P45/91 MT-9 buffalo	ZIM91B73	663	611	0	92.16	7.84	III (WZ)	unnamed
8	SAT1/ZAM/4/2000	ZAM00-04	663	609	0	91.86	8.14	III (WZ)	unnamed
9	SAT1/ZIM/12/90 A-5 buffalo	ZIM90B01	663	609	0	91.86	8.14	III (WZ)	unnamed
10	SAT1/ZIM/P12/90 A-7 buffalo	ZIM90B02	663	609	0	91.86	8.14	III (WZ)	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/BOT/1/77	BOT77-01	663	583	0	87.93	12.07	III (WZ)	unnamed
2	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	575	0	86.73	13.27	III (WZ)	unnamed
3	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	562	0	84.77	15.23	III (WZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	507	0	76.47	23.53	II (SEZ)	unnamed
5	SAT1/T155/71	TAN71155	663	506	0	76.32	23.68	I (NWZ)	unnamed
6	SAT1/RV/11/37 (AY593839)	RHO37-11	663	501	0	75.57	24.43	II (SEZ)	unnamed
7	SAT1/UGA BUFF/21/70 buffalo	UGA70-21	663	493	0	74.36	25.64	IV (EA-1)	unnamed
8	SAT1/ZIM/23/2003	ZIM03-23	663	493	0	74.36	25.64	I (NWZ)	unnamed
9	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	470	0	71.21	28.79	V	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	472	0	71.19	28.81	VII (EA-2)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

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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 WRLFMD Ref No: ZAM/9/2012 Batch No: WRLFMD/2012/00036 Sender Ref: ZAM 10/12 Location: Kazungula, Kazungula, Zambia Date collected: 11/06/2012 Date received by WRLFMD: 28/09/2012 Date received for sequencing: 07/01/2013 Species: Bovine Material used: BTy1 10/12/2012 Region sequenced: VP1 RT-PCR primers: SAT1-1C559F/SAT-2B208R SAT1U-OS/SAT-2B208R	Report date: 11/01/2013 Reported by: N.J. Knowles Checked by: D.P. King Topotype: III (WZ) Genotype/strain: unnamed Sequence filename: ZAM12-09.SEQ Date sequence last updated: 11/01/2013 No. of Nt determined: 663 No. of ambiguities: 0 Gene length: 663 Total no. of comparisons: 426 Min. no. of nt for comparison: 600 Total turn-around time: 105 days Sequencing 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	SAT1/ZAM/6/2012	ZAM12-06	663	663	0	100.00	0.00	III (WZ)	unnamed
2	SAT1/ZAM/7/2012	ZAM12-07	663	663	0	100.00	0.00	III (WZ)	unnamed
3	SAT1/ZAM/8/2012	ZAM12-08	663	663	0	100.00	0.00	III (WZ)	unnamed
4	SAT1/ZAM/7/2012* (BVI)	ZAM12-AA	622	621	0	99.84	0.16	III (WZ)	unnamed
5	SAT1/ZIM/P12/90 A-10 buffalo	ZIM90B03	663	615	0	92.76	7.24	III (WZ)	unnamed
6	SAT1/ZIM/P45/91 MT-6 buffalo	ZIM91B72	663	612	0	92.31	7.69	III (WZ)	unnamed
7	SAT1/ZIM/P45/91 MT-9 buffalo	ZIM91B73	663	611	0	92.16	7.84	III (WZ)	unnamed
8	SAT1/ZAM/4/2000	ZAM00-04	663	609	0	91.86	8.14	III (WZ)	unnamed
9	SAT1/ZIM/12/90 A-5 buffalo	ZIM90B01	663	609	0	91.86	8.14	III (WZ)	unnamed
10	SAT1/ZIM/P12/90 A-7 buffalo	ZIM90B02	663	609	0	91.86	8.14	III (WZ)	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/BOT/1/77	BOT77-01	663	583	0	87.93	12.07	III (WZ)	unnamed
2	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	575	0	86.73	13.27	III (WZ)	unnamed
3	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	562	0	84.77	15.23	III (WZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	507	0	76.47	23.53	II (SEZ)	unnamed
5	SAT1/T155/71	TAN71155	663	506	0	76.32	23.68	I (NWZ)	unnamed
6	SAT1/RV/11/37 (AY593839)	RHO37-11	663	501	0	75.57	24.43	II (SEZ)	unnamed
7	SAT1/UGA BUFF/21/70 buffalo	UGA70-21	663	493	0	74.36	25.64	IV (EA-1)	unnamed
8	SAT1/ZIM/23/2003	ZIM03-23	663	493	0	74.36	25.64	I (NWZ)	unnamed
9	SAT1/NIG/11/75 (AF431711)	NIG75-AA	660	470	0	71.21	28.79	V	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	472	0	71.19	28.81	VII (EA-2)	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV SAT 1 in Zambia in 2012

Batch: WRLFMD/2012/00036

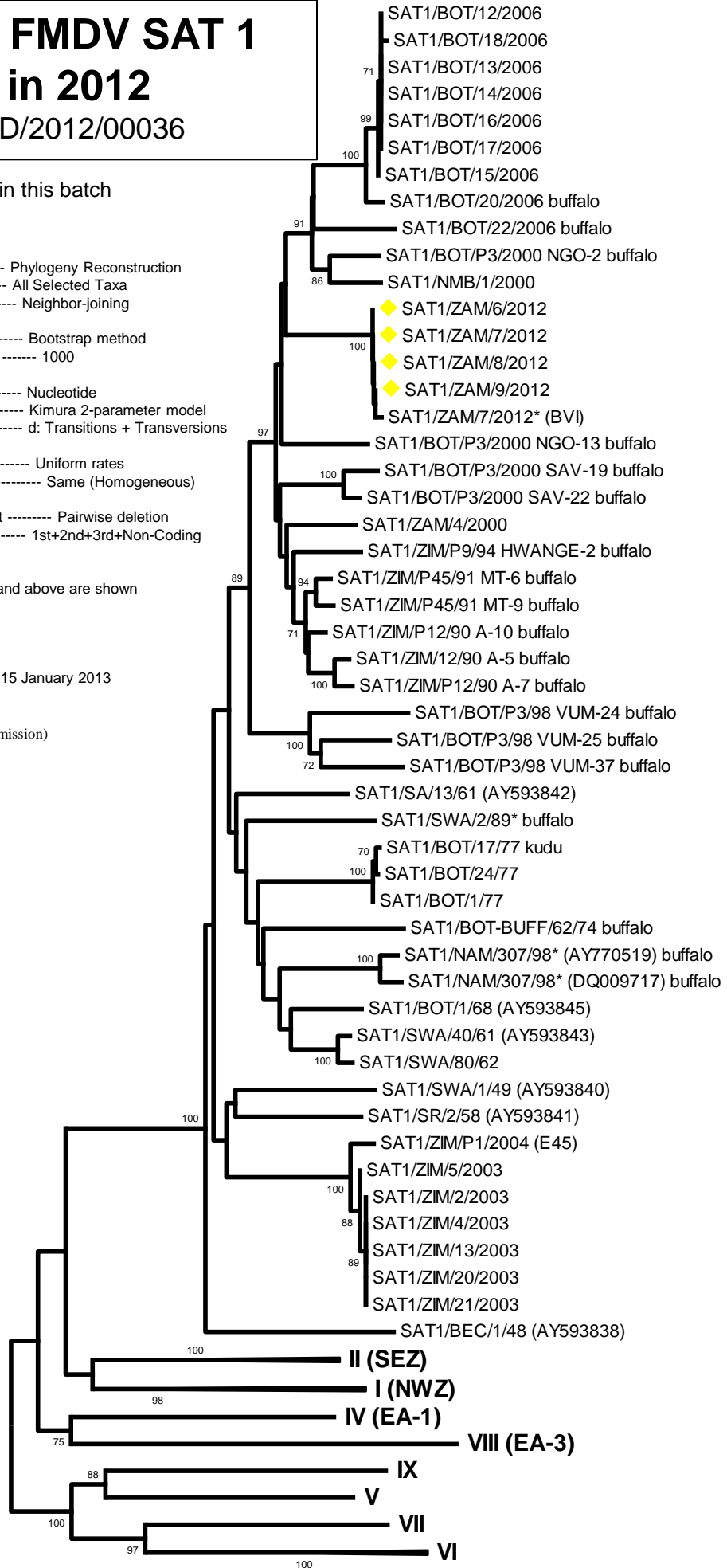
◆ indicates viruses in this batch

Software: MEGA 5.1
 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, 15 January 2013

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III (WZ)