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

Genotyping Report

Report Date for this Batch: 16 June 2014

FMDV type SAT 2
Country: Ethiopia
Period: 2010
No. of samples: 2

BATCH: WRLFMD/2014/00013

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: SAT2
WRLFMD Ref No: ETH/23/2010
Batch No: WRLFMD/2014/00013
Sender Ref: 12a ETH 12/13
Location: Debre Berhan, North Shewa, Amhara, Ethiopia
Date collected: 2009/2010
Date received by WRLFMD: 27/02/2014
Date received for sequencing: 19/05/2014
Species: Swine
Material used: BTy1 20/03/2014
Region sequenced: VP1
RT-PCR primers: SAT2-1C445F/SAT-2B208R
SAT2-P1-1223F/SAT-2B208R

Report date: 16/06/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: XIII
Genotype/strain: unnamed
Sequence filename: ETH10-23.SEQ
Date sequence last updated: 22/05/2014
No. of Nt determined: 648
No. of ambiguities: 0
Gene length: 648
Total no. of comparisons: 648
Min. no. of nt for comparison: 600
Total turn-around time: 109 days
Sequencing time: 28 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/ETH/64/2009 (KF112944)	ETH09-64	648	648	0	100.00	0.00	XIII	unnamed
2	SAT2/ETH/65/2009 (KF112945)	ETH09-65	648	648	0	100.00	0.00	XIII	unnamed
3	SAT2/ETH/67/2009 (KF112946)	ETH09-67	648	648	0	100.00	0.00	XIII	unnamed
4	SAT2/ETH/68/2009 (KF112947)	ETH09-68	648	648	0	100.00	0.00	XIII	unnamed
5	SAT2/ETH/69/2009 (KF112948)	ETH09-69	648	648	0	100.00	0.00	XIII	unnamed
6	SAT2/ETH/70/2009 (KF112949)	ETH09-70	648	648	0	100.00	0.00	XIII	unnamed
7	SAT2/ETH/72/2009 (KF112950)	ETH09-72	648	648	0	100.00	0.00	XIII	unnamed
8	SAT2/ETH/73/2009 (KF112951)	ETH09-73	648	648	0	100.00	0.00	XIII	unnamed
9	SAT2/ETH/74/2009 (KF112952)	ETH09-74	648	648	0	100.00	0.00	XIII	unnamed
10	SAT2/ETH/24/2010	ETH10-24	648	647	0	99.85	0.15	XIII	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/ETH/2/2007 (FJ798161)	ETH07-02	648	633	0	97.69	2.31	XIII	unnamed
2	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	526	0	81.17	18.83	XIII	unnamed
3	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	497	0	76.70	23.30	XIV	unnamed
4	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	488	0	76.01	23.99	VIII	unnamed
5	SAT2/RWA/1/2000* (AF367134)	RWA00-01	648	491	0	75.77	24.23	VIII	unnamed
6	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	477	0	73.61	26.39	XII	unnamed
7	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	476	0	73.46	26.54	IX	unnamed
8	SAT2/SAU/6/2000 (AF367135)	SAU00A06	647	474	1	73.26	26.74	VII	unnamed
9	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	473	0	72.99	27.01	X	unnamed
10	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	470	0	72.53	27.47	V	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: SAT2	Report date: 16/06/2014
WRLFMD Ref No: ETH/24/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00013	Checked by: K. Bachanek-Bankowska
Sender Ref: 12b ETH 12/13	
Location: Debre Berhan, North Shewa, Amhara, Ethiopia	Topotype: XIII
Date collected: 2009/2010	Genotype/strain: unnamed
Date received by WRLFMD: 27/02/2014	Sequence filename: ETH10-24.SEQ
Date received for sequencing: 19/05/2014	Date sequence last updated: 22/05/2014
Species: Swine	No. of Nt determined: 648
Material used: BTy1 20/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 648
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 109 days
	Sequencing time: 28 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/ETH/23/2010	ETH10-23	648	647	0	99.85	0.15	XIII	unnamed
2	SAT2/ETH/64/2009 (KF112944)	ETH09-64	648	647	0	99.85	0.15	XIII	unnamed
3	SAT2/ETH/65/2009 (KF112945)	ETH09-65	648	647	0	99.85	0.15	XIII	unnamed
4	SAT2/ETH/67/2009 (KF112946)	ETH09-67	648	647	0	99.85	0.15	XIII	unnamed
5	SAT2/ETH/68/2009 (KF112947)	ETH09-68	648	647	0	99.85	0.15	XIII	unnamed
6	SAT2/ETH/69/2009 (KF112948)	ETH09-69	648	647	0	99.85	0.15	XIII	unnamed
7	SAT2/ETH/70/2009 (KF112949)	ETH09-70	648	647	0	99.85	0.15	XIII	unnamed
8	SAT2/ETH/72/2009 (KF112950)	ETH09-72	648	647	0	99.85	0.15	XIII	unnamed
9	SAT2/ETH/73/2009 (KF112951)	ETH09-73	648	647	0	99.85	0.15	XIII	unnamed
10	SAT2/ETH/74/2009 (KF112952)	ETH09-74	648	647	0	99.85	0.15	XIII	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/ETH/2/2007 (FJ798161)	ETH07-02	648	632	0	97.53	2.47	XIII	unnamed
2	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	525	0	81.02	18.98	XIII	unnamed
3	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	496	0	76.54	23.46	XIV	unnamed
4	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	487	0	75.86	24.14	VIII	unnamed
5	SAT2/RWA/1/2000* (AF367134)	RWA00-01	648	490	0	75.62	24.38	VIII	unnamed
6	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	476	0	73.46	26.54	XII	unnamed
7	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	475	0	73.30	26.70	IX	unnamed
8	SAT2/SAU/6/2000 (AF367135)	SAU00A06	647	473	1	73.11	26.89	VII	unnamed
9	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	472	0	72.84	27.16	X	unnamed
10	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	469	0	72.38	27.62	V	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV SAT 2 in Ethiopia in 2010

Batch: WRLFMD/2014/00013

◆ 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 : 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,
16 June 2014