FAO World Reference Laboratory for Foot-and-Mouth Disease

Genotyping Report

Report date for this batch: 27-Mar-2014

FMDV type: A, SAT 1
Country: TANZANIA
Year: 2014

WRL BATCH: WRLFMD/2014/00002

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

Genotyping Report

Report Date for this Batch: 25 March 2014

FMDV type SAT 1
Country: Tanzania
Period: 2013
No. of samples: 2 (in addition to 9 reported on 14 Feb 2014)

BATCH: WRLFMD/2014/00002

FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: SAT1	Report date: 15/03/2014
WRLFMD Ref No: TAN/23/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: 9034	
Location: Makundusi, Tanzania	Topotype: I (NWZ)
Date collected: 15/08/2013	Genotype/strain: unnamed
Date received by WRLFMD: 27/01/2014	Sequence filename: TAN13-23.SEQ
Date received for sequencing: 07/03/2014	Date sequence last updated: 15/03/2014
Species: Cattle	No. of Nt determined: 663
Material used: BTy2 06/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 663
RT-PCR primers: SAT1-1C559F/SAT-2B208R	Total no. of comparisons: 455
SAT1U-OS/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 47 days
	Sequencing time: 8 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/TAN/30/2013	TAN13-30	663	662	0	99.85	0.15	I (NWZ)	unnamed
2	SAT1/TAN/31/2013	TAN13-31	663	662	0	99.85	0.15	I (NWZ)	unnamed
3	SAT1/TAN/32/2013	TAN13-32	663	662	0	99.85	0.15	I (NWZ)	unnamed
4	SAT1/TAN/20/2013	TAN13-20	663	661	0	99.70	0.30	I (NWZ)	unnamed
5	SAT1/TAN/21/2013	TAN13-21	663	661	0	99.70	0.30	I (NWZ)	unnamed
6	SAT1/TAN/24/2013	TAN13-24	663	661	0	99.70	0.30	I (NWZ)	unnamed
7	SAT1/TAN/25/2013	TAN13-25	663	661	0	99.70	0.30	I (NWZ)	unnamed
8	SAT1/TAN/27/2013	TAN13-27	663	661	0	99.70	0.30	I (NWZ)	unnamed
9	SAT1/TAN/22/2013	TAN13-22	663	659	0	99.40	0.60	I (NWZ)	unnamed
10	SAT1/TAN/29/2013	TAN13-29	663	658	0	99.25	0.75	I (NWZ)	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/T155/71 (KF561706)	TAN71155	663	589	0	88.84	11.16	I (NWZ)	unnamed
2	SAT1/ZIM/23/2003 (KF219690)	ZIM03-23	663	526	0	79.34	20.66	I (NWZ)	unnamed
3	SAT1/RV/11/37 (AY593839)	RHO37-11	663	510	0	76.92	23.08	II (SEZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	501	0	75.57	24.43	II (SEZ)	unnamed
5	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	498	0	75.11	24.89	IV (EA-1)	unnamed
6	SAT1/BOT/1/77 (KF219686)	BOT77-01	663	495	0	74.66	25.34	III (WZ)	unnamed
7	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	494	0	74.51	25.49	III (WZ)	unnamed
8	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	488	0	73.60	26.40	III (WZ)	unnamed
9	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	475	0	71.64	28.36	VIII (EA-3)	unnamed
10	SAT1/UGA/13/74 (AY442010)	UGA74S13	663	470	0	70.89	29.11	VII (EA-2)	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: SAT1	Report date: 01/03/2014
WRLFMD Ref No: TAN/29/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: 9115	
Location: Motukeri, Tanzania	Topotype: I (NWZ)
Date collected: 26/09/2013	Genotype/strain: unnamed
Date received by WRLFMD: 27/01/2014	Sequence filename: TAN13-29.SEQ
Date received for sequencing: 27/02/2014	Date sequence last updated: 01/03/2014
Species: Cattle	No. of Nt determined: 663
Material used: BTy2 25/02/2002	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 663
RT-PCR primers: SAT1-1C559F/SAT-2B208R	Total no. of comparisons: 454
SAT1U-OS/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 33 days
	Sequencing time: 2 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/TAN/27/2013	TAN13-27	663	660	0	99.55	0.45	I (NWZ)	unnamed
2	SAT1/TAN/30/2013	TAN13-30	663	659	0	99.40	0.60	I (NWZ)	unnamed
3	SAT1/TAN/31/2013	TAN13-31	663	659	0	99.40	0.60	I (NWZ)	unnamed
4	SAT1/TAN/32/2013	TAN13-32	663	659	0	99.40	0.60	I (NWZ)	unnamed
5	SAT1/TAN/20/2013	TAN13-20	663	658	0	99.25	0.75	I (NWZ)	unnamed
6	SAT1/TAN/21/2013	TAN13-21	663	658	0	99.25	0.75	I (NWZ)	unnamed
7	SAT1/TAN/24/2013	TAN13-24	663	658	0	99.25	0.75	I (NWZ)	unnamed
8	SAT1/TAN/25/2013	TAN13-25	663	658	0	99.25	0.75	I (NWZ)	unnamed
9	SAT1/TAN/22/2013	TAN13-22	663	656	0	98.94	1.06	I (NWZ)	unnamed
10	SAT1/TAN/25/2012	TAN12-25	663	608	0	91.70	8.30	I (NWZ)	unnamed

Most Closely Related Reference Viruses

(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)

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3	SAT1/RV/11/37 (AY593839)	RHO37-11	663	510	0	76.92	23.08	II (SEZ)	unnamed
4	SAT1/RHO/5/66 (AY593846)	RHO66-05	663	503	0	75.87	24.13	II (SEZ)	unnamed
5	SAT1/UGA BUFF/21/70 (KF219682)	UGA70-21	663	501	0	75.57	24.43	IV (EA-1)	unnamed
6	SAT1/BEC/1/48 (AY593838)	BEC48-01	663	495	0	74.66	25.34	III (WZ)	unnamed
7	SAT1/BOT/1/77 (KF219686)	BOT77-01	663	494	0	74.51	25.49	III (WZ)	unnamed
8	SAT1/BOT/1/68 (AY593845)	BOT68-C1	663	491	0	74.06	25.94	III (WZ)	unnamed
9	SAT1/UGA/1/97 (AY442012)	UGA97S01	663	473	0	71.34	28.66	VIII (EA-3)	unnamed
10	SAT1/SUD/3/76 (DQ009725)	SUD76M03	657	466	0	70.93	29.07	VI	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

Report on FMDV SAT 1 in Tanzania in 2013

Batch: WRLFMD/2014/00002

◆ indicates viruses in this batch for which new sequence data has been obtained

◆ indicates viruses in the same batch which were reported earlier

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,
25 March 2014