

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

## Genotyping Report

Report Date for this Batch: 8 June 2015

FMDV type SAT 2

Country: Oman

Period: 2015

No. of samples: 3

BATCH: WRLFMD/2015/00007



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# FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: SAT2	Report date: 04/06/2015
WRLFMD Ref No: OMN/2/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00007	Checked by: K. Bachanek-Bankowska
Sender Ref: 2	
Location: Rumais, Muscat, Oman	Topotype: VII
Date collected: 23/04/2015	Genotype/strain: Alx-12
Date received by WRLFMD: 01/05/2015	Sequence filename: OMN15-02.SEQ
Date received for sequencing: 28/05/2015	Date sequence last updated: 03/06/2015
Species: Cattle	No. of Nt determined: 648
Material used: BTY1 07/05/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 694
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 34 days
	Sequencing time: 7 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/OMN/3/2015	OMN15-03	648	647	0	99.85	0.15	VII	Alx-12
2	SAT2/OMN/4/2015	OMN15-04	648	647	0	99.85	0.15	VII	Alx-12
3	SAT2/ETH/19/2014	ETH14-19	648	636	0	98.15	1.85	VII	Alx-12
4	SAT2/ETH/21/2014	ETH14-21	648	636	0	98.15	1.85	VII	Alx-12
5	SAT2/ETH/2/2015	ETH15-02	648	634	0	97.84	2.16	VII	Alx-12
6	SAT2/ETH/22/2014	ETH14-22	648	628	0	96.91	3.09	VII	Alx-12
7	SAT2/EGY/20/2014	EGY14-20	648	622	0	95.99	4.01	VII	Alx-12
8	SAT2/EGY/22/2014	EGY14-22	648	622	0	95.99	4.01	VII	Alx-12
9	SAT2/EGY/24/2014	EGY14-24	648	622	0	95.99	4.01	VII	Alx-12
10	SAT2/EGY/11/2014	EGY14-11	648	620	0	95.68	4.32	VII	Alx-12
<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/SAU/6/2000 (AF367135)	SAU00A06	647	588	1	90.88	9.12	VII	unnamed
2	SAT2/CAR/8/2005 (JX570616)	CAR05-08	648	568	0	87.65	12.35	VII	unnamed
3	SAT2/KEN/3/57 (AJ251473)	KEN57G03	648	484	0	74.69	25.31	IX	unnamed
4	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	478	0	73.77	26.23	IX	unnamed
5	SAT2/ZAI/1/82 (AF367100)	ZAI82-01	647	475	1	73.42	26.58	X	unnamed
6	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	471	0	73.36	26.64	VIII	unnamed
7	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	472	0	72.84	27.16	XIV	unnamed
8	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	472	0	72.84	27.16	X	unnamed
9	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	471	0	72.69	27.31	XIII	unnamed
10	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	466	0	71.91	28.09	XII	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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Serotype: SAT2	Report date: 04/06/2015
WRLFMD Ref No: OMN/3/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00007	Checked by: K. Bachanek-Bankowska
Sender Ref: 3	
Location: Rumais, Muscat, Oman	Topotype: VII
Date collected: 23/04/2015	Genotype/strain: Alx-12
Date received by WRLFMD: 01/05/2015	Sequence filename: OMN15-03.SEQ
Date received for sequencing: 28/05/2015	Date sequence last updated: 03/06/2015
Species: Cattle	No. of Nt determined: 648
Material used: BTY1 08/05/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 694
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 34 days
	Sequencing time: 7 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/OMN/4/2015	OMN15-04	648	648	0	100.00	0.00	VII	Alx-12
2	SAT2/OMN/2/2015	OMN15-02	648	647	0	99.85	0.15	VII	Alx-12
3	SAT2/ETH/19/2014	ETH14-19	648	637	0	98.30	1.70	VII	Alx-12
4	SAT2/ETH/21/2014	ETH14-21	648	637	0	98.30	1.70	VII	Alx-12
5	SAT2/ETH/2/2015	ETH15-02	648	635	0	97.99	2.01	VII	Alx-12
6	SAT2/ETH/22/2014	ETH14-22	648	629	0	97.07	2.93	VII	Alx-12
7	SAT2/EGY/20/2014	EGY14-20	648	623	0	96.14	3.86	VII	Alx-12
8	SAT2/EGY/22/2014	EGY14-22	648	623	0	96.14	3.86	VII	Alx-12
9	SAT2/EGY/24/2014	EGY14-24	648	623	0	96.14	3.86	VII	Alx-12
10	SAT2/EGY/11/2014	EGY14-11	648	621	0	95.83	4.17	VII	Alx-12

## Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](http://www.wrlfmd.org/fmd_genotyping/prototypes.htm))

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2	SAT2/CAR/8/2005 (JX570616)	CAR05-08	648	569	0	87.81	12.19	VII	unnamed
3	SAT2/KEN/3/57 (AJ251473)	KEN57G03	648	485	0	74.85	25.15	IX	unnamed
4	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	478	0	73.77	26.23	IX	unnamed
5	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	472	0	73.52	26.48	VIII	unnamed
6	SAT2/ZAI/1/82 (AF367100)	ZAI82-01	647	475	1	73.42	26.58	X	unnamed
7	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	473	0	72.99	27.01	XIV	unnamed
8	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	473	0	72.99	27.01	X	unnamed
9	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	471	0	72.69	27.31	XIII	unnamed
10	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	467	0	72.07	27.93	XII	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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Batch No: WRLFMD/2015/00007	Checked by: K. Bachanek-Bankowska
Sender Ref: 4	
Location: Rumais, Muscat, Oman	Topotype: VII
Date collected: 23/04/2015	Genotype/strain: Alx-12
Date received by WRLFMD: 01/05/2015	Sequence filename: OMN15-04.SEQ
Date received for sequencing: 28/05/2015	Date sequence last updated: 03/06/2015
Species: Cattle	No. of Nt determined: 648
Material used: BTY1 07/05/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 694
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9	SAT2/SUD/6/77 (AY343939)	SUD77-AA	648	471	0	72.69	27.31	XIII	unnamed
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# Report on FMDV SAT 2 in Oman in 2015

Batch: WRLFMD/2015/00007

◆ 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,  
04 June 2015

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