

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

## Genotyping Report

Report Date for this Batch: 4 December 2014

FMDV type SAT 2

Country: Egypt

Period: 2012 & 2014

No. of samples: 2

BATCH: WRLFMD/2014/000037



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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: SAT2	Report date: 04/12/2014
WRLFMD Ref No: EGY/43/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00037	Checked by: K. Bachanek-Bankowska
Sender Ref: SUR/16, sample #7	
Location: Dakahlia, Egypt	Topotype: VII
Date collected: 21/05/2012	Genotype/strain: Ghb-12
Date received by WRLFMD: 04/11/2014	Sequence filename: EGY12-43.SEQ
Date received for sequencing: 17/11/2014	Date sequence last updated: 20/11/2014
Species: Cattle	No. of Nt determined: 648
Material used: BTy1 13/11/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 687
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 30 days
	Sequencing time: 17 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/EGY/28/2012 (KF112935)	EGY12-28	648	647	0	99.85	0.15	VII	Ghb-12
2	SAT2/EGY/10/2012 (JX570623)	EGY12-10	648	645	0	99.54	0.46	VII	Ghb-12
3	SAT2/EGY/14/2012 (JX570626)	EGY12-14	648	645	0	99.54	0.46	VII	Ghb-12
4	SAT2/EGY/15/2012 (JX570627)	EGY12-15	648	645	0	99.54	0.46	VII	Ghb-12
5	SAT2/EGY/21/2012 (KF112933)	EGY12-21	648	645	0	99.54	0.46	VII	Ghb-12
6	SAT2/EGY/22/2012 (KF112934)	EGY12-22	648	645	0	99.54	0.46	VII	Ghb-12
7	SAT2/EGY/31/2012 (KF112937)	EGY12-31	648	645	0	99.54	0.46	VII	Ghb-12
8	SAT2/EGY/6/2012 (JX570621)	EGY12-06	648	645	0	99.54	0.46	VII	Ghb-12
9	SAT2/EGY/7/2012* (JX013978)	EGY12-AB	648	645	0	99.54	0.46	VII	Ghb-12
10	SAT2/PAT/1/2012 (JX570637)	PAT12-01	648	645	0	99.54	0.46	VII	Ghb-12
Most Closely Related Reference Viruses									
(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	579	1	89.49	10.51	VII	unnamed
2	SAT2/CAR/8/2005 (JX570616)	CAR05-08	648	579	0	89.35	10.65	VII	unnamed
3	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	487	0	75.15	24.85	IX	unnamed
4	SAT2/KEN/3/57 (AJ251473)	KEN57G03	648	482	0	74.38	25.62	IX	unnamed
5	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	475	0	73.99	26.01	VIII	unnamed
6	SAT2/RWA/1/2000* (AF367134)	RWA00-01	648	474	0	73.15	26.85	VIII	unnamed
7	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	474	0	73.15	26.85	X	unnamed
8	SAT2/NIG/2/75 (AF367139)	NIG75-02	648	470	0	72.53	27.47	V	unnamed
9	SAT2/SA/106/59 (AY593848)	RSA59--A	648	470	0	72.53	27.47	I	unnamed
10	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	470	0	72.53	27.47	XII	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: SAT2	Report date: 04/12/2014
WRLFMD Ref No: EGY/24/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00037	Checked by: K. Bachanek-Bankowska
Sender Ref: RL/1431, sample #9	
Location: Elsalam, Kafr Skhr, Kalubia, Egypt	Topotype: VII
Date collected: 17/04/2014	Genotype/strain: Alx-12
Date received by WRLFMD: 04/11/2014	Sequence filename: EGY14-24.SEQ
Date received for sequencing: 17/11/2014	Date sequence last updated: 20/11/2014
Species: Cattle	No. of Nt determined: 648
Material used: BTy1 12/11/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 648
RT-PCR primers: SAT2-1C445F/SAT-2B208R	Total no. of comparisons: 687
SAT2-P1-1223F/SAT-2B208R	Min. no. of nt for comparison: 600
	Total turn-around time: 30 days
	Sequencing time: 17 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/EGY/20/2014	EGY14-20	648	646	0	99.69	0.31	VII	Alx-12
2	SAT2/EGY/22/2014	EGY14-22	648	646	0	99.69	0.31	VII	Alx-12
3	SAT2/EGY/11/2014	EGY14-11	648	644	0	99.38	0.62	VII	Alx-12
4	SAT2/SUD/4/2010 (KF112968)	SUD10-04	648	623	0	96.14	3.86	VII	Alx-12
5	SAT2/EGY/2/2012 (JX570617)	EGY12-02	648	607	0	93.67	6.33	VII	Alx-12
6	SAT2/SAU/6/2000 (AF367135)	SAU00A06	647	593	1	91.65	8.35	VII	unnamed
7	SAT2/CAR/24/2013	CAR13-24	648	577	0	89.04	10.96	VII	unnamed
8	SAT2/CAR/29/2013	CAR13-29	648	577	0	89.04	10.96	VII	unnamed
9	SAT2/CAR/42/2013	CAR13-42	648	577	0	89.04	10.96	VII	unnamed
10	SAT2/EGY/11/2012 (JX570624)	EGY12-11	648	576	0	88.89	11.11	VII	Ghb-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	593	1	91.65	8.35	VII	unnamed
2	SAT2/CAR/8/2005 (JX570616)	CAR05-08	648	570	0	87.96	12.04	VII	unnamed
3	SAT2/KEN/3/57 (AJ251473)	KEN57G03	648	492	0	75.93	24.07	IX	unnamed
4	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	483	0	74.54	25.46	IX	unnamed
5	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	476	0	74.14	25.86	VIII	unnamed
6	SAT2/ZAI/1/82 (AF367100)	ZAI82-01	647	479	1	74.03	25.97	X	unnamed
7	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	476	0	73.46	26.54	X	unnamed
8	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	475	0	73.30	26.70	XIV	unnamed
9	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	475	0	73.30	26.70	XII	unnamed
10	SAT2/RWA/1/2000* (AF367134)	RWA00-01	648	469	0	72.38	27.62	VIII	unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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# Report on FMDV SAT 2 in Egypt in 2012 & 2014

Batch: WRLFMD/2014/00037

◆ 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 December 2014

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