

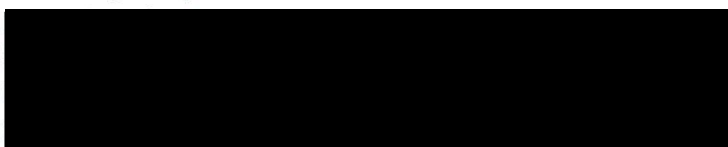


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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00017

Sender Details:



Date Received:

21st April 2012

Country of Origin:

PALESTINIAN AUTONOMOUS TERRITORIES

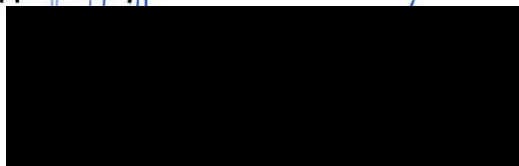
Date Reported:

25th April 2012

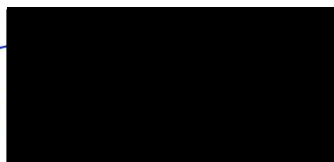
Dear Dr Gelman,

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:

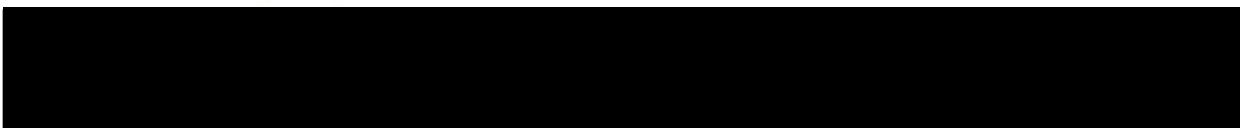


Official Stamp:



Date:

25/4/12



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: gareth.shimmon@iah.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: 24 April 2012

FMDV type SAT 2

Country: Palestinian Autonomous Territories

Period: 2012

No. of samples: 1

BATCH: WRLFMD/2012/00017



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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 WRLFMD Ref No: PAT/1/2012 Batch No: WRLFMD/2012/00017 Sender Ref: 135048 - EPI-2 Location: Rafa, Gaza Strip, Palestinian Autonomous Territories Date collected: 16/04/2012 Date received by WRLFMD: 21/04/2012 Date received for sequencing: 23/04/2012 Species: Cattle Material used: BTy2 Region sequenced: VP1 RT-PCR primers: SAT2-1C445F/SAT-2B208R SAT2-P1-1223F/SAT-2B208R	Report date: 24/04/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: VII Genotype/strain: unnamed Sequence filename: PAT12-01.SEQ Date sequence last updated: 24/04/2012 No. of Nt determined: 648 No. of ambiguities: 0 Gene length: 648 Total no. of comparisons: 519 Min. no. of nt for comparison: 600 Total turn-around time: 3 days Sequencing time: 1 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/10/2012	EGY12-10	648	648	0	100.00	0.00	VII	unnamed
2	SAT2/EGY/14/2012	EGY12-14	648	648	0	100.00	0.00	VII	unnamed
3	SAT2/EGY/15/2012	EGY12-15	648	648	0	100.00	0.00	VII	unnamed
4	SAT2/EGY/6/2012	EGY12-06	648	648	0	100.00	0.00	VII	unnamed
5	SAT2/EGY/11/2012	EGY12-11	648	647	0	99.85	0.15	VII	unnamed
6	SAT2/EGY/13/2012	EGY12-13	648	647	0	99.85	0.15	VII	unnamed
7	SAT2/EGY/4/2012	EGY12-04	648	647	0	99.85	0.15	VII	unnamed
8	SAT2/EGY/5/2012	EGY12-05	648	647	0	99.85	0.15	VII	unnamed
9	SAT2/EGY/9/2012	EGY12-09	648	647	0	99.85	0.15	VII	unnamed
10	SAT2/EGY/3/2012	EGY12-03	648	646	0	99.69	0.31	VII	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/CAR/8/2005	CAR05-08	648	582	0	89.81	10.19	VII	unnamed
2	SAT2/SAU/6/2000 (AF367135)	SAU00A06	647	580	1	89.64	10.36	VII	unnamed
3	SAT2/KEN/2/84 (AY343941)	KEN84-AC	648	489	0	75.46	24.54	IX	unnamed
4	SAT2/KEN/3/57 (AJ251473)	KEN57G03	648	484	0	74.69	25.31	IX	unnamed
5	SAT2/ZAI/1/74 (DQ009737)	ZAI74-AA	642	478	0	74.45	25.55	VIII	unnamed
6	SAT2/RWA/1/2000* (AF367134)	RWA00-01	648	476	0	73.46	26.54	VIII	unnamed
7	SAT2/UGA/19/98 (AY343969)	UGA98-AA	648	476	0	73.46	26.54	X	unnamed
8	SAT2/UGA/51/75 (AY343963)	UGA75-AA	648	472	0	72.84	27.16	XII	unnamed
9	SAT2/ZAI/1/82 (AF367100)	ZAI82-01	647	471	1	72.80	27.20	X	unnamed
10	SAT2/ETH/2/91 (AY343938)	ETH91-AB	648	471	0	72.69	27.31	XIV	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV SAT 2 in the Palestinian Autonomous Territories in 2012

Batch: WRLFMD/2012/00017

◆ indicates viruses in this batch

Software: MEGA 5.0

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, B. Valdazo-González & J. Wadsworth, 24 April 2012

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