



**INSTITUTE FOR ANIMAL HEALTH**  
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath  
PIRBRIGHT LABORATORY  
Ash Road,  
Pirbright,  
Surrey,  
GU24 0NF  
Intn Tel: 00 44 1483 232441  
Tel: 01483 232441 Fax: 01483 232621

## FMD Sequencing Report

Lab Reference WRL Batch Number: none  
Sender Details: [REDACTED]

Date Received: 29<sup>th</sup> August 2011  
Country of Origin: South Ossetia / Georgia  
Date Reported: 1<sup>st</sup> September 2011

Dear Svetlana Kremenchugskaya,

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: [REDACTED]

Official Stamp:



Date: 2/9/11

[REDACTED]

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: [elizabeth.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.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: 29 August 2011

FMDV type O

Country: South Ossetia / Georgia (disputed)

Period: 2011

No. of sequences: 1

Originator: FGI-ARRIAH, Vladimir, Russian Federation



The contents of this report are copyright and should not be reproduced without permission

© Institute for Animal Health

# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: none Batch No: WRLMEG/2011/00023 Sender Ref: O/South Ossetia/2011 Location: Dzauskom region, South Ossetia / Tskhinvali Region Georgia (disputed) Date collected (estimated): 05/08/2011 Date received by WRLFMD: 29/08/2011 Date received for sequencing: n/a Species: Cattle Material used: Not known Region sequenced: VP1 RT-PCR primers: Not known	Report date: 29/08/2011 Reported by: N.J. Knowles Checked by: J.M. Hammond  Topotype: ME-SA Genotype/strain: PanAsia-2 <sup>ANT-10</sup> Sequence filename: GRG11-AA.SEQ Date sequence last updated: 29/08/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3090 Min. no. of nt for comparison: 600 Total turn-around time: 0 days Sequencing time: n/a
Comments: VP1 sequence received from FGI-ARRIAH, Vladimir, Russian Federation	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/92/2010	IRN10-92	639	634	0	99.22	0.78	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/IRN/180/2010	IRN10180	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
3	O/IRN/60/2010	IRN10-60	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
4	O/IRN/64/2010	IRN10-64	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
5	O/TUR/153/2010* (FMDI)	TUR10-AR	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
6	O/TUR/154/2010* (FMDI)	TUR10-AS	639	633	0	99.06	0.94	ME-SA	PanAsia-2 <sup>ANT-10</sup>
7	O/IRN/132/2010	IRN10132	639	632	0	98.90	1.10	ME-SA	PanAsia-2 <sup>ANT-10</sup>
8	O/IRN/139/2010	IRN10139	639	632	0	98.90	1.10	ME-SA	PanAsia-2 <sup>ANT-10</sup>
9	O/IRN/150/2010	IRN10150	639	632	0	98.90	1.10	ME-SA	PanAsia-2 <sup>ANT-10</sup>
10	O/IRN/66/2010	IRN10-66	639	632	0	98.90	1.10	ME-SA	PanAsia-2 <sup>ANT-10</sup>
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	O/IRN/88/2009	IRN09-88	639	627	0	98.12	1.88	ME-SA	PanAsia-2 <sup>ANT-10</sup>
2	O/IRN/31/2009	IRN09-31	639	604	0	94.52	5.48	ME-SA	PanAsia-2 <sup>FAR-09</sup>
3	O/IRN/8/2005	IRN05-08	639	604	0	94.52	5.48	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	600	0	93.90	6.10	ME-SA	PanAsia-2 <sup>TER-08</sup>
5	O/IRN/18/2010	IRN10-18	639	599	0	93.74	6.26	ME-SA	PanAsia-2 <sup>BAL-09</sup>
6	O/PAK/16/2010	PAK10-16	639	598	0	93.58	6.42	ME-SA	PanAsia-2 <sup>PUN-10</sup>
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	595	0	93.11	6.89	ME-SA	PanAsia-2 <sup>SAN-09</sup>
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	585	0	91.55	8.45	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	574	1	89.97	10.03	ME-SA	Irn-2001
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	574	0	89.83	10.17	ME-SA	Ind-2001a

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

# Report on FMDV O in South Ossetia in 2011

VP1 sequence submitted by FGI-ARRIAH

◆ 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 : 642

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 29 August 2011

© Institute for Animal Health

(not to be reproduced without permission)

