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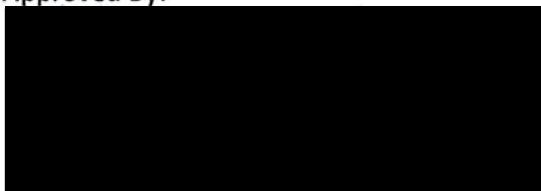
FMD Sequencing Report

Lab Reference WRL Batch Number: none
Sender Details: [REDACTED]
Date Received: 29th August 2011
Country of Origin: Kazakhstan
Date Reported: 1st September 2011

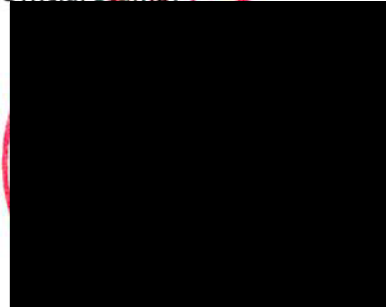
Dear Svetlana Kremenchugskaya,

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:



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). 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: Kazakhstan

Period: 2011

No. of sequences: 1

Originator: FGI-ARRIAH, Vladimir, Russian Federation



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O WRLFMD Ref No: none Batch No: WRLMEG/2011/00023 Sender Ref: O/Kazakhstan/Aug2011 Location: Karashilik, Kurchumskiy, Kazakhstan Date collected (estimated): 12/08/2011 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 Sequence filename: KAZ11-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/VIT/17/2011	VIT11-17	639	637	0	99.69	0.31	ME-SA	PanAsia
2	O/VIT/16/2011	VIT11-16	639	635	0	99.37	0.63	ME-SA	PanAsia
3	O/VIT/5/2011	VIT11-05	639	635	0	99.37	0.63	ME-SA	PanAsia
4	O/VIT/6/2011	VIT11-06	639	635	0	99.37	0.63	ME-SA	PanAsia
5	O/VIT/12/2011	VIT11-12	639	634	0	99.22	0.78	ME-SA	PanAsia
6	O/VIT/37/2011	VIT11-37	639	634	0	99.22	0.78	ME-SA	PanAsia
7	O/VIT/4/2011	VIT11-04	639	634	0	99.22	0.78	ME-SA	PanAsia
8	O/VIT/9/2011	VIT11-09	639	634	0	99.22	0.78	ME-SA	PanAsia
9	O/LAO/2/2010	LAO10-02	639	633	0	99.06	0.94	ME-SA	PanAsia
10	O/VIT/13/2011	VIT11-13	639	633	0	99.06	0.94	ME-SA	PanAsia
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	O/UKG/35/2001 (AJ539141)	UKG01-35	639	597	0	93.43	6.57	ME-SA	PanAsia
2	O/IRN/31/2009	IRN09-31	639	584	0	91.39	8.61	ME-SA	PanAsia-2 ^{FAR-09}
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	584	0	91.39	8.61	ME-SA	Ind-2001a
4	O/IRN/8/2005	IRN05-08	639	580	0	90.77	9.23	ME-SA	PanAsia-2
5	O/IRN/18/2010	IRN10-18	639	579	0	90.61	9.39	ME-SA	PanAsia-2 ^{BAL-09}
6	O/OMN/7/2001 (DQ164941)	OMN01-07	639	578	0	90.45	9.55	ME-SA	Ind-2001b
7	O/BHU/3/2009	BHU09-03	639	576	0	90.14	9.86	ME-SA	Ind-2001d
8	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
9	O/PAK/16/2010	PAK10-16	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{PUN-10}
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{TER-08}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Kazakhstan 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

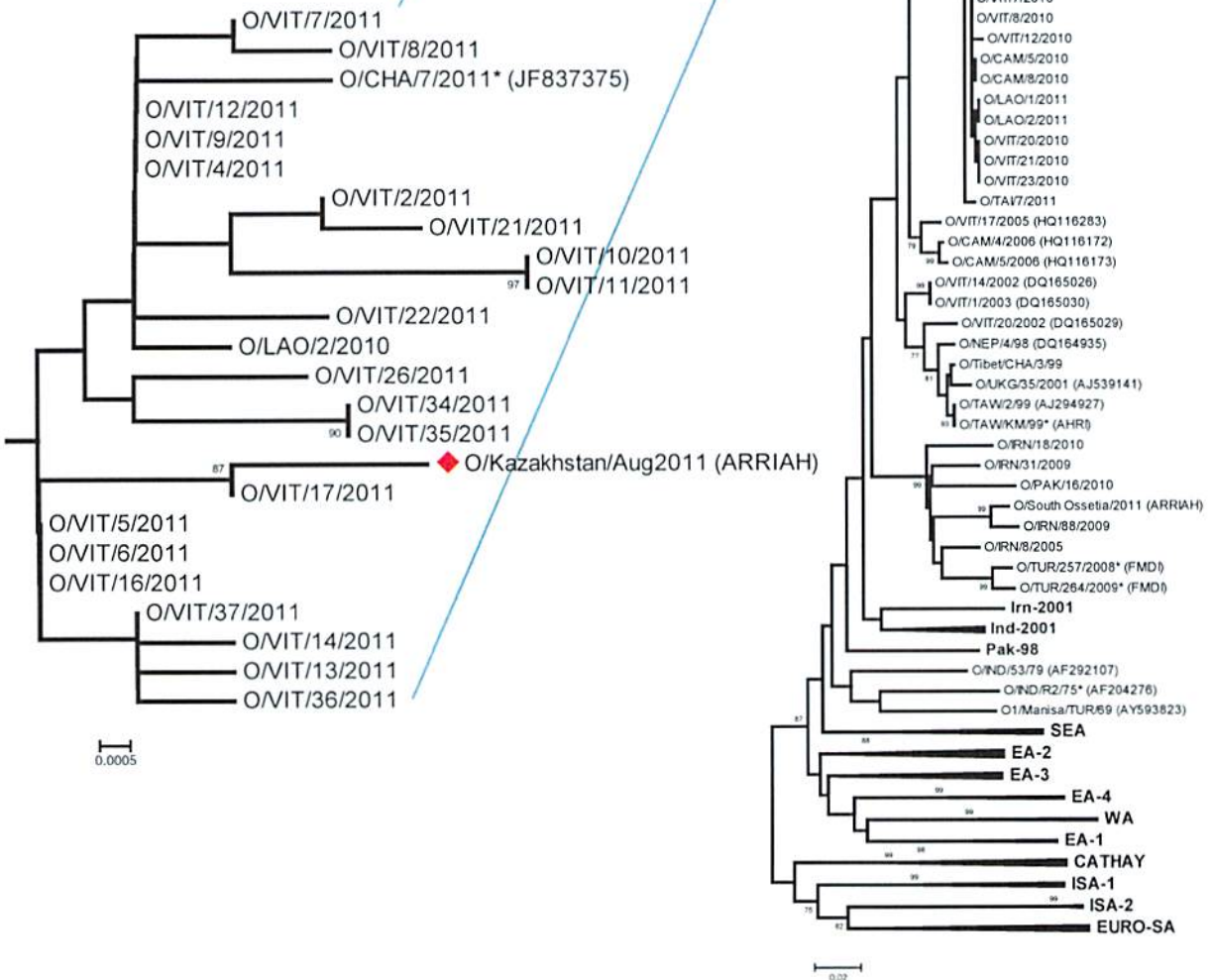
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

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

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PanAsia

ME-SA

PanAsia-2