

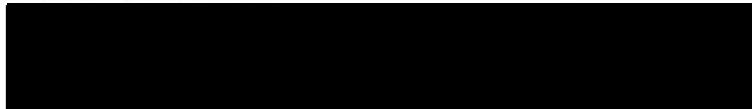


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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00007

Sender Details:



Date Received: 2nd February 2012

Country of Origin: Turkey

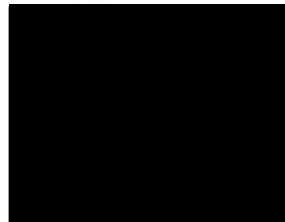
Date Reported: 6th March 2012

Dear Dr Musa Alkan

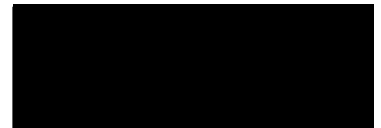
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date:

6/3/12 ✓

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: 5 March 2012

FMDV type O

Country: Turkey

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2012/00007



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: TUR/71/2011 Batch No: WRLFMD/2012/00007 Sender Ref: 1712/2011 Location: Soguk Pinar, Sivrice, Elazig, East Anatolia, Turkey Date collected: 08/12/2011 Date received by WRLFMD: 02/02/2012 Date received for sequencing: 23/02/2012 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 05/03/2012 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ME-SA Genotype/strain: PanAsia-2 ^{ANT-10} Sequence filename: TUR11-71.SEQ Date sequence last updated: 01/03/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3229 Min. no. of nt for comparison: 600 Total turn-around time: 32 days Sequencing time: 11 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/ISR/6/2011	ISR11-06	639	632	0	98.90	1.10	ME-SA	PanAsia-2 ^{ANT-10}
2	O/ISR/11/2011	ISR11-11	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
3	O/ISR/12/2011	ISR11-12	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
4	O/ISR/13/2011	ISR11-13	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
5	O/ISR/17/2011	ISR11-17	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
6	O/ISR/22/2011	ISR11-22	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
7	O/ISR/26/2011	ISR11-26	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
8	O/ISR/5/2011	ISR11-05	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
9	O/ISR/7/2011	ISR11-07	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
10	O/ISR/9/2011	ISR11-09	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
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/IRN/88/2009	IRN09-88	639	626	0	97.97	2.03	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/8/2005	IRN05-08	639	605	0	94.68	5.32	ME-SA	PanAsia-2
3	O/IRN/31/2009	IRN09-31	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{FAR-09}
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{TER-08}
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	599	0	93.74	6.26	ME-SA	PanAsia-2 ^{SAN-09}
6	O/PAK/16/2010	PAK10-16	639	598	0	93.58	6.42	ME-SA	PanAsia-2 ^{PUN-10}
7	O/IRN/18/2010	IRN10-18	639	597	0	93.43	6.57	ME-SA	PanAsia-2 ^{BAL-09}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	586	0	91.71	8.29	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	569	0	89.05	10.95	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	569	0	89.05	10.95	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV O in Turkey in 2011

Batch: WRLFMD/2012/00007

◆ 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, 05 March 2012

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