

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

Genotyping Report

Report Date for this Batch: 18 December 2013

FMDV type O

Country: Palestinian Autonomous Territories

Period: 2013

No. of samples: 2

BATCH: WRLFMD/2013/00029



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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	Report date: 18/12/2013
WRLFMD Ref No: PAT/13/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00029	Checked by: K. Bachanek-Bankowska
Sender Ref: 184392	
Location: Jericho, West Bank, Palestinian AT	Topotype: ME-SA
Date collected: 21/11/2013	Genotype/strain: PanAsia-2 ^{FAR-09}
Date received by WRLFMD: 04/12/2013	Sequence filename: PAT13-13.SEQ
Date received for sequencing: 13/12/2013	Date sequence last updated: 18/12/2013
Species: Sheep	No. of Nt determined: 639
Material used: BTy1 05/12/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3729
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 14 days
	Sequencing time: 5 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/PAT/14/2013	PAT13-14	639	639	0	100	0	ME-SA	PanAsia-2 ^{FAR-09}
2	O/TUR/12/2013	TUR13-12	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{FAR-09}
3	O/TUR/24/2013	TUR13-24	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{FAR-09}
4	O/TUR/26/2013	TUR13-26	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{FAR-09}
5	O/TUR/29/2013	TUR13-29	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{FAR-09}
6	O/TUR/38/2013	TUR13-38	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/49/2009	IRN09-49	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{FAR-09}
8	O/TUR/25/2013	TUR13-25	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{FAR-09}
9	O/TUR/33/2013	TUR13-33	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{FAR-09}
10	O/TUR/37/2013	TUR13-37	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{FAR-09}
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/31/2009	IRN09-31	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/18/2010	IRN10-18	639	602	0	94.21	5.79	ME-SA	PanAsia-2 ^{BAL-09}
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	602	0	94.21	5.79	ME-SA	PanAsia-2 ^{TER-08}
4	O/PAK/16/2010	PAK10-16	639	601	0	94.05	5.95	ME-SA	PanAsia-2 ^{PUN-10}
5	O/IRN/8/2005	IRN05-08	639	600	0	93.90	6.10	ME-SA	PanAsia-2
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	597	0	93.43	6.57	ME-SA	PanAsia-2 ^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	595	0	93.11	6.89	ME-SA	PanAsia-2 ^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	588	0	92.02	7.98	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	577	0	90.30	9.70	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	576	0	90.14	9.86	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: PAT/14/2013 Batch No: WRLFMD/2013/00029 Sender Ref: 184392 Location: Jericho, West Bank, Palestinian AT Date collected: 24/11/2013 Date received by WRLFMD: 04/12/2013 Date received for sequencing: 13/12/2013 Species: Sheep Material used: BTy1 05/12/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 18/12/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: PanAsia-2 ^{FAR-09} Sequence filename: PAT13-14.SEQ Date sequence last updated: 18/12/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3729 Min. no. of nt for comparison: 600 Total turn-around time: 14 days Sequencing time: 5 days
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Report on FMDV O in the Palestinian Autonomous Territories in 2013

Batch: WRLFMD/2013/00029

◆ indicates viruses in this batch

Software: MEGA 5.2

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

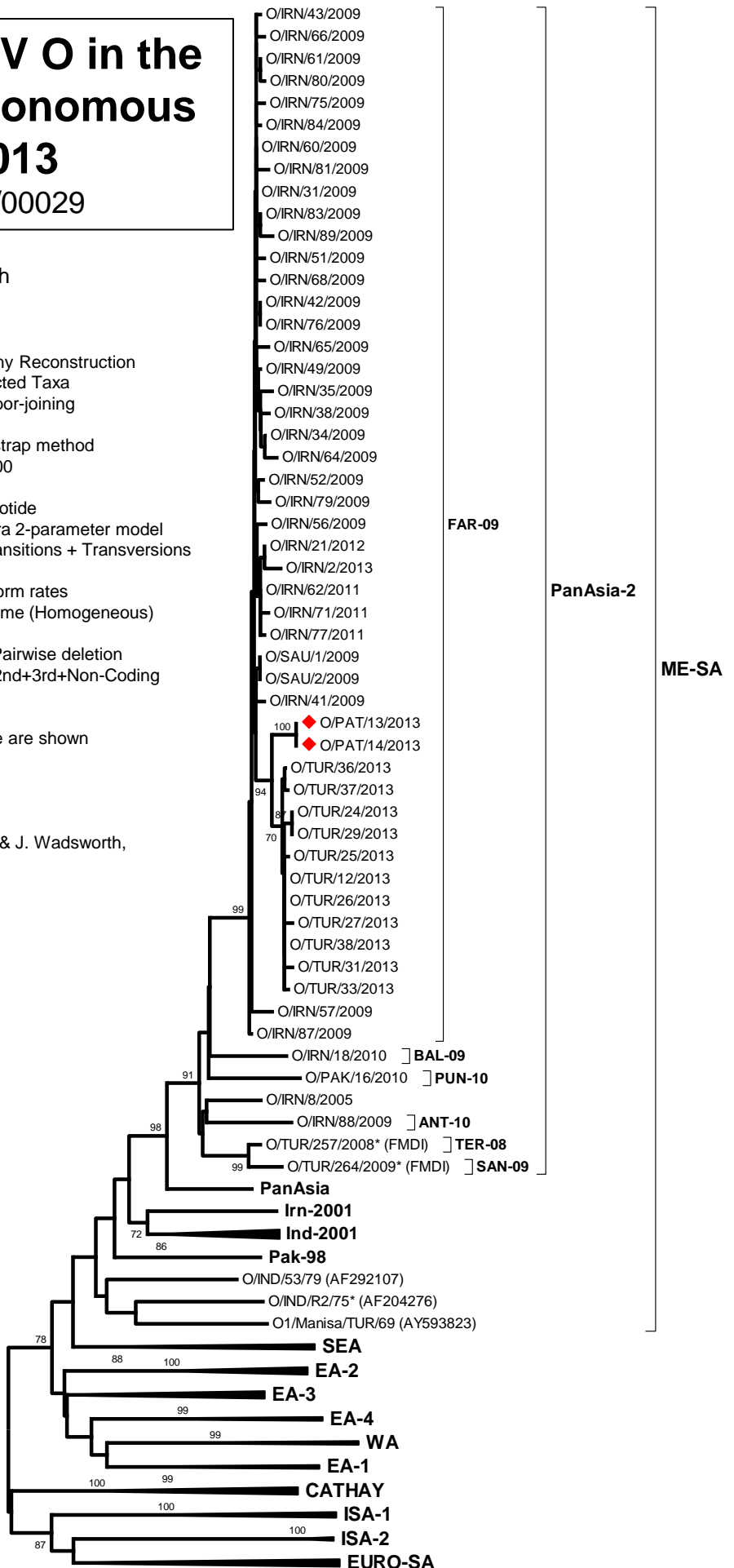
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Bachanek-Bankowska & J. Wadsworth,
18 December 2013

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