

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

Genotyping Report

Report Date for this Batch: 5 July 2016

FMDV type O

Country: Saudi Arabia

Period: 2016

No. of samples: 1

BATCH: WRLFMD/2016/00015



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

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Serotype: O WRLFMD Ref No: SAU/17/2016 Batch No: WRLFMD/2016/00015 Sender Ref: #1 Location: Durma, Riyadh, Central Region, Saudi Arabia Date collected: 27/04/2016 Date received by WRLFMD: 17/05/2016 Date received for sequencing: 01/06/2016 Species: Cattle Material used: Orig fluid 17/05/2016 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R	Report date: 07/06/2016 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001d Sequence filename: SAU16-17.SEQ Date sequence last updated: 07/06/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4211 Min. no. of nt for comparison: 600 Total turn-around time: 21 days Sequencing time: 6 days
Comments: No virus was isolated in cell cultures. The sequence was determined from a single read on the negative strand of the PCR DNA product.	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/SAU/1/2016	SAU16-01	639	635	0	99.37	0.63	ME-SA	Ind-2001d
2	O/SAU/10/2016	SAU16-10	639	634	0	99.22	0.78	ME-SA	Ind-2001d
3	O/UAE/1/2015	UAE15-01	639	634	0	99.22	0.78	ME-SA	Ind-2001d
4	O/SAU/18/2015	SAU15-18	639	633	0	99.06	0.94	ME-SA	Ind-2001d
5	O/SAU/19/2015	SAU15-19	639	633	0	99.06	0.94	ME-SA	Ind-2001d
6	O/SAU/20/2015	SAU15-20	639	633	0	99.06	0.94	ME-SA	Ind-2001d
7	O/SAU/22/2015	SAU15-22	639	633	0	99.06	0.94	ME-SA	Ind-2001d
8	O/NEP/17/2015	NEP15-17	639	632	0	98.90	1.10	ME-SA	Ind-2001d
9	O/NEP/19/2015	NEP15-19	639	632	0	98.90	1.10	ME-SA	Ind-2001d
10	O/UAE/2/2016	UAE16-02	639	629	0	98.44	1.56	ME-SA	Ind-2001d
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/BHU/3/2009 (KM921814)	BHU09-03	639	599	0	93.74	6.26	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	589	0	92.18	7.82	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
4	O/UAE/4/2008 (KM921876)	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
5	O/UKG/35/2001 (AJ539141)	UKG01-35	639	566	0	88.58	11.42	ME-SA	PanAsia
6	O/IRN/31/2009	IRN09-31	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{FAR-09}
7	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	565	0	88.42	11.58	ME-SA	unnamed
8	O/PAK/16/2010	PAK10-16	639	560	0	87.64	12.36	ME-SA	PanAsia-2 ^{PUN-10}
9	O/IRN/8/2005	IRN05-08	639	558	0	87.32	12.68	ME-SA	PanAsia-2
10	O/IRN/88/2009	IRN09-88	639	558	0	87.32	12.68	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Report on FMDV O in Saudi Arabia in 2016

Batch: WRLFMD/2016/00015

◆ indicates viruses in this batch

Software: MEGA 6.06

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

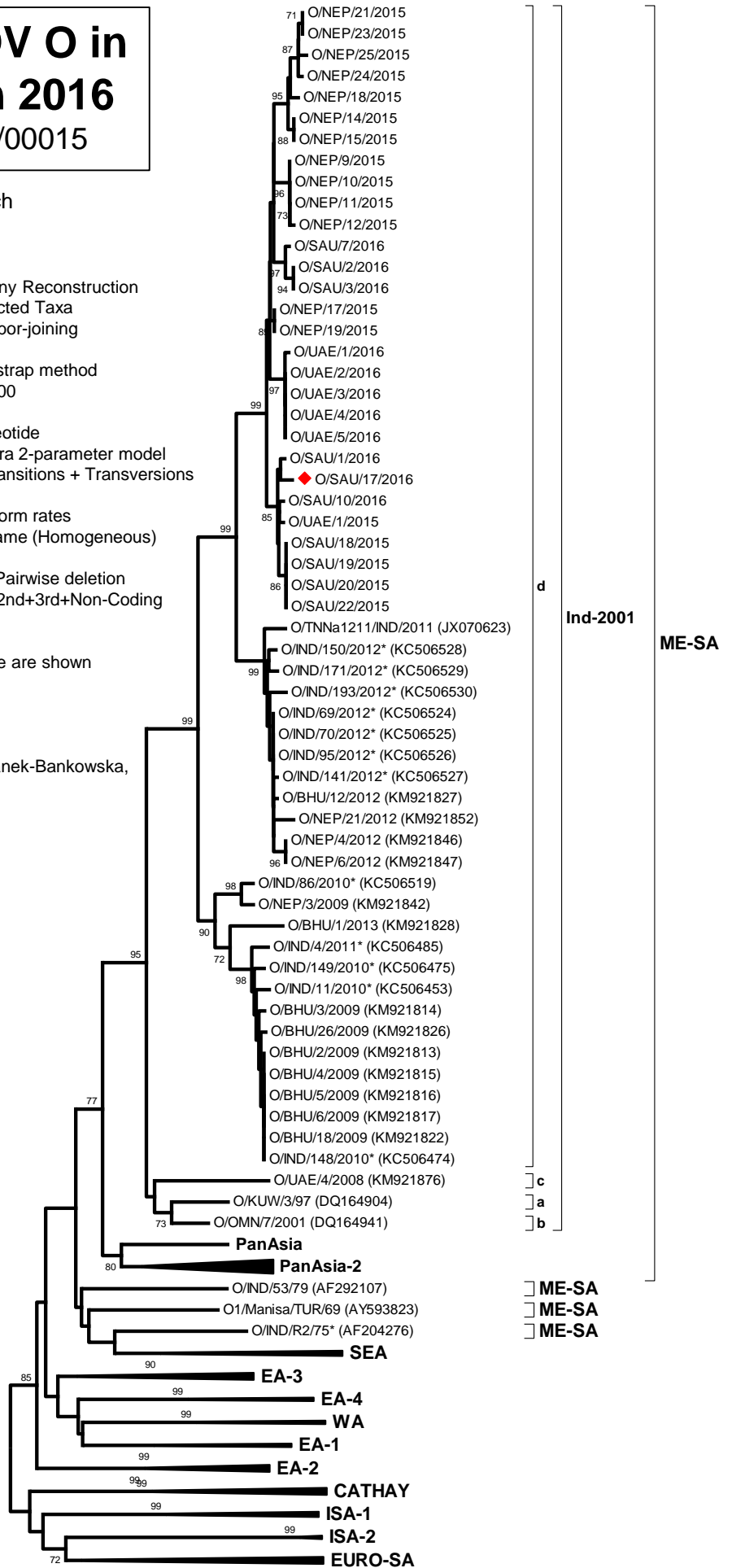
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
07 June 2016

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d
Ind-2001

ME-SA

c
a
b

ME-SA
ME-SA
ME-SA

0.02