

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

Genotyping Report

Report Date for this Batch: 15 February 2016

FMDV type O

Country: United Arab Emirates

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2016/00005



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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: UAE/1/2015 Batch No: WRLFMD/2016/00005 Sender Ref: D07/16 Location: Barari Forest Management, Al Ain, Abu Dhabi, United Arab Emirates Date collected: 31/12/2015 Date received by WRLFMD: 26/01/2016 Date received for sequencing: 11/02/2016 Species: Mountain Gazelle Material used: BTY1 29/01/2016 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R | Report date: 15/02/2016 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ME-SA Genotype/strain: Ind-2001d Sequence filename: UAE15-01.SEQ Date sequence last updated: 15/02/2016 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4209 Min. no. of nt for comparison: 600 Total turn-around time: 20 days Sequencing time: 4 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/IND/69/2012* (KC506524) | IND12069 | 639 | 618 | 0 | 96.71 | 3.29 | ME-SA | Ind-2001d |
| 2 | O/IND/70/2012* (KC506525) | IND12070 | 639 | 618 | 0 | 96.71 | 3.29 | ME-SA | Ind-2001d |
| 3 | O/IND/95/2012* (KC506526) | IND12095 | 639 | 618 | 0 | 96.71 | 3.29 | ME-SA | Ind-2001d |
| 4 | O/BHU/12/2012 (KM921827) | BHU12-12 | 639 | 617 | 0 | 96.56 | 3.44 | ME-SA | Ind-2001d |
| 5 | O/IND/141/2012* (KC506527) | IND12141 | 639 | 617 | 0 | 96.56 | 3.44 | ME-SA | Ind-2001d |
| 6 | O/IND/150/2012* (KC506528) | IND12150 | 639 | 617 | 0 | 96.56 | 3.44 | ME-SA | Ind-2001d |
| 7 | O/IND/171/2012* (KC506529) | IND12171 | 639 | 617 | 0 | 96.56 | 3.44 | ME-SA | Ind-2001d |
| 8 | O/IND/193/2012* (KC506530) | IND12193 | 639 | 615 | 0 | 96.24 | 3.76 | ME-SA | Ind-2001d |
| 9 | O/NEP/4/2012 (KM921846) | NEP12-04 | 639 | 615 | 0 | 96.24 | 3.76 | ME-SA | Ind-2001d |
| 10 | O/NEP/6/2012 (KM921847) | NEP12-06 | 639 | 615 | 0 | 96.24 | 3.76 | 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 | 601 | 0 | 94.05 | 5.95 | ME-SA | Ind-2001d |
| 2 | O/OMN/7/2001 (DQ164941) | OMN01-07 | 639 | 590 | 0 | 92.33 | 7.67 | ME-SA | Ind-2001b |
| 3 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 584 | 0 | 91.39 | 8.61 | ME-SA | Ind-2001a |
| 4 | O/UAE/4/2008 (KM921876) | UAE08-04 | 636 | 574 | 0 | 90.25 | 9.75 | ME-SA | Ind-2001c |
| 5 | O/IRN/31/2009 | IRN09-31 | 639 | 567 | 0 | 88.73 | 11.27 | ME-SA | PanAsia-2 ^{FAR-09} |
| 6 | O/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 567 | 0 | 88.73 | 11.27 | ME-SA | PanAsia |
| 7 | O/PAK/16/2010 | PAK10-16 | 639 | 562 | 0 | 87.95 | 12.05 | ME-SA | PanAsia-2 ^{PUN-10} |
| 8 | O1/Manisa/TUR/69 (AY593823) | TUR69--G | 639 | 562 | 0 | 87.95 | 12.05 | ME-SA | unnamed |
| 9 | O/IRN/88/2009 | IRN09-88 | 639 | 560 | 0 | 87.64 | 12.36 | ME-SA | PanAsia-2 ^{ANT-10} |
| 10 | O/IRN/8/2005 | IRN05-08 | 639 | 559 | 0 | 87.48 | 12.52 | ME-SA | PanAsia-2 |

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV O in the United Arab Emirates in 2015

Batch: WRLFMD/2016/00005

◆ 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

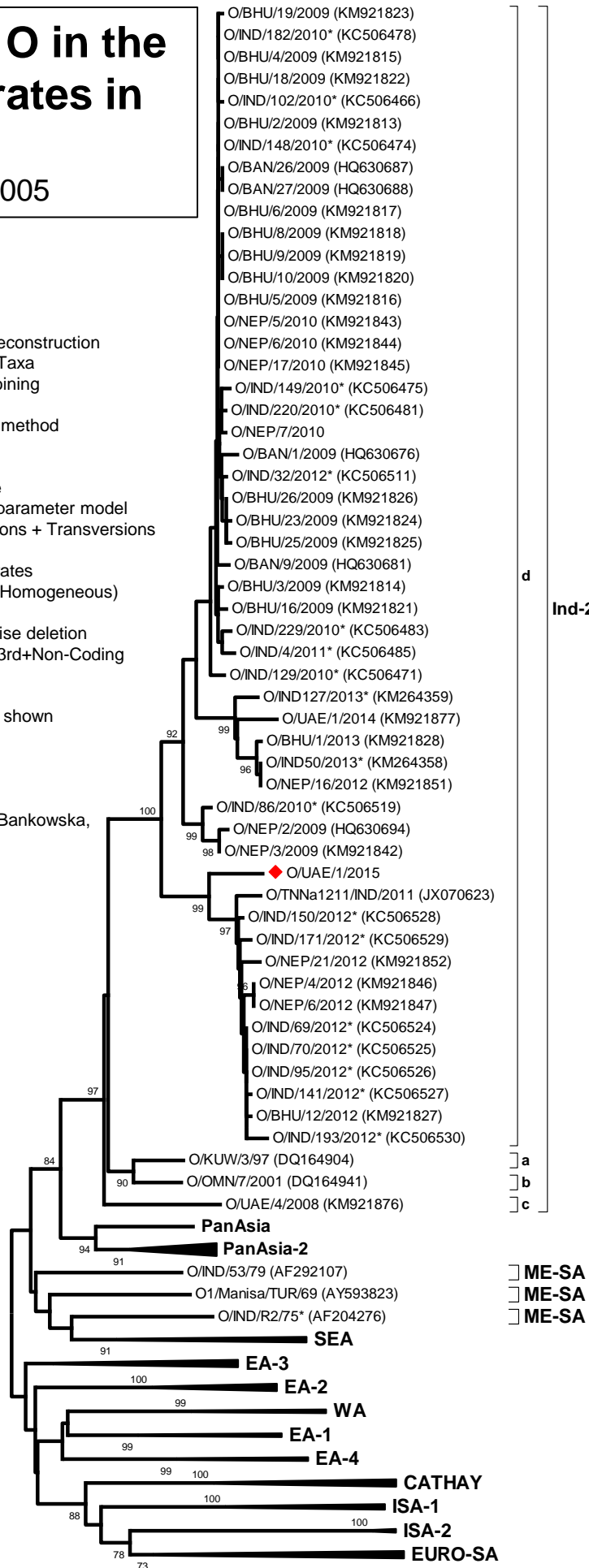
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
15 February 2016

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d

Ind-2001

ME-SA

a
b
c

ME-SA
ME-SA
ME-SA

0.02