# FAO World Reference Laboratory for Foot-and-Mouth Disease

## Genotyping Report

**Report date for this batch: 04-Apr-2014**

**FMDV type: O**

**Country: SAUDI ARABIA**

**Year: 2014**

**WRL BATCH: WRLFMD/2014/00014**

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

## Genotyping Report

Report Date for this Batch: 4 April 2014

FMDV type O
Country: Saudi Arabia
Period: 2014
No. of samples: 3

BATCH: WRLFMD/2014/00014

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: SAU/2/2014
Batch No: WRLFMD/2014/00014
Sender Ref: Danah sample#2
Location: Haradh Rd, Al Kharj, Central, Saudi Arabia
Date collected: 02/03/2014
Date received by WRLFMD: 25/03/2014
Date received for sequencing: 02/04/2014
Species: Cattle
Material used: BTy1 26/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 04/04/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: Ind-2001d
Sequence filename: SAU14-02.SEQ
Date sequence last updated: 03/04/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3820
Min. no. of nt for comparison: 600
Total turn-around time: 10 days
Sequencing time: 2 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/SAU/3/2014 | SAU14-03 | 639 | 639 | 0 | 100.00 | 0.00 | ME-SA | Ind-2001d |
| 2 | O/SAU/1/2014 | SAU14-01 | 639 | 638 | 0 | 99.84 | 0.16 | ME-SA | Ind-2001d |
| 3 | O/SAU/6/2013 | SAU13-06 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 4 | O/SAU/7/2013 | SAU13-07 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 5 | O/SAU/8/2013 | SAU13-08 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 6 | O/SAU/3/2013 | SAU13-03 | 639 | 633 | 0 | 99.06 | 0.94 | ME-SA | Ind-2001d |
| 7 | O/SAU/4/2013 | SAU13-04 | 639 | 633 | 0 | 99.06 | 0.94 | ME-SA | Ind-2001d |
| 8 | O/IND127/2013* (PD-FMD) | IND13-AC | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 9 | O/SAU/1/2013 | SAU13-01 | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 10 | O/IND179/2013* (PD-FMD) | IND13-AD | 639 | 631 | 0 | 98.75 | 1.25 | 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 | BHU09-03 | 639 | 612 | 0 | 95.77 | 4.23 | ME-SA | Ind-2001d |
| 2 | O/OMN/7/2001 (DQ164941) | OMN01-07 | 639 | 585 | 0 | 91.55 | 8.45 | ME-SA | Ind-2001b |
| 3 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 582 | 0 | 91.08 | 8.92 | ME-SA | Ind-2001a |
| 4 | O/UAE/4/2008 | UAE08-04 | 636 | 574 | 0 | 90.25 | 9.75 | ME-SA | Ind-2001c |
| 5 | O/IRN/31/2009 | IRN09-31 | 639 | 573 | 0 | 89.67 | 10.33 | ME-SA | PanAsia-2$^{\text{FAR-09}}$ |
| 6 | O/IRN/8/2005 | IRN05-08 | 639 | 571 | 0 | 89.36 | 10.64 | ME-SA | PanAsia-2 |
| 7 | O/PAK/16/2010 | PAK10-16 | 639 | 570 | 0 | 89.20 | 10.80 | ME-SA | PanAsia-2$^{\text{PUN-10}}$ |
| 8 | O/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 569 | 0 | 89.05 | 10.95 | ME-SA | PanAsia |
| 9 | O/IRN/18/2010 | IRN10-18 | 639 | 567 | 0 | 88.73 | 11.27 | ME-SA | PanAsia-2$^{\text{BAL-09}}$ |
| 10 | O/IRN/61/2001 (DQ164896) | IRN01-61 | 638 | 566 | 1 | 88.71 | 11.29 | ME-SA | Irn-2001 |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: SAU/3/2014
Batch No: WRLFMD/2014/00014
Sender Ref: Danah sample #3
Location: Haradh Rd, Al Kharj, Central, Saudi Arabia
Date collected: 02/03/2014
Date received by WRLFMD: 25/03/2014
Date received for sequencing: 02/04/2014
Species: Cattle
Material used: BTy1 26/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 04/04/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: Ind-2001d
Sequence filename: SAU14-03.SEQ
Date sequence last updated: 03/04/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3820
Min. no. of nt for comparison: 600
Total turn-around time: 10 days
Sequencing time: 2 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/SAU/2/2014 | SAU14-02 | 639 | 639 | 0 | 100.00 | 0.00 | ME-SA | Ind-2001d |
| 2 | O/SAU/1/2014 | SAU14-01 | 639 | 638 | 0 | 99.84 | 0.16 | ME-SA | Ind-2001d |
| 3 | O/SAU/6/2013 | SAU13-06 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 4 | O/SAU/7/2013 | SAU13-07 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 5 | O/SAU/8/2013 | SAU13-08 | 639 | 635 | 0 | 99.37 | 0.63 | ME-SA | Ind-2001d |
| 6 | O/SAU/3/2013 | SAU13-03 | 639 | 633 | 0 | 99.06 | 0.94 | ME-SA | Ind-2001d |
| 7 | O/SAU/4/2013 | SAU13-04 | 639 | 633 | 0 | 99.06 | 0.94 | ME-SA | Ind-2001d |
| 8 | O/IND127/2013* (PD-FMD) | IND13-AC | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 9 | O/SAU/1/2013 | SAU13-01 | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 10 | O/IND179/2013* (PD-FMD) | IND13-AD | 639 | 631 | 0 | 98.75 | 1.25 | 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 | BHU09-03 | 639 | 612 | 0 | 95.77 | 4.23 | ME-SA | Ind-2001d |
| 2 | O/OMN/7/2001 (DQ164941) | OMN01-07 | 639 | 585 | 0 | 91.55 | 8.45 | ME-SA | Ind-2001b |
| 3 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 582 | 0 | 91.08 | 8.92 | ME-SA | Ind-2001a |
| 4 | O/UAE/4/2008 | UAE08-04 | 636 | 574 | 0 | 90.25 | 9.75 | ME-SA | Ind-2001c |
| 5 | O/IRN/31/2009 | IRN09-31 | 639 | 573 | 0 | 89.67 | 10.33 | ME-SA | PanAsia-2$^{\text{FAR-09}}$ |
| 6 | O/IRN/8/2005 | IRN05-08 | 639 | 571 | 0 | 89.36 | 10.64 | ME-SA | PanAsia-2 |
| 7 | O/PAK/16/2010 | PAK10-16 | 639 | 570 | 0 | 89.20 | 10.80 | ME-SA | PanAsia-2$^{\text{PUN-10}}$ |
| 8 | O/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 569 | 0 | 89.05 | 10.95 | ME-SA | PanAsia |
| 9 | O/IRN/18/2010 | IRN10-18 | 639 | 567 | 0 | 88.73 | 11.27 | ME-SA | PanAsia-2$^{\text{BAL-09}}$ |
| 10 | O/IRN/61/2001 (DQ164896) | IRN01-61 | 638 | 566 | 1 | 88.71 | 11.29 | ME-SA | Irn-2001 |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: SAU/4/2014
Batch No: WRLFMD/2014/00014
Sender Ref: Nakeel sample #1
Location: Durma, Riyadh, Central, Saudi Arabia
Date collected: 09/03/2014
Date received by WRLFMD: 25/03/2014
Date received for sequencing: 02/04/2014
Species: Cattle
Material used: BTy1 27/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 04/04/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: Ind-2001d
Sequence filename: SAU14-04.SEQ
Date sequence last updated: 03/04/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3820
Min. no. of nt for comparison: 600
Total turn-around time: 10 days
Sequencing time: 2 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/SAU/6/2013 | SAU13-06 | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 2 | O/SAU/7/2013 | SAU13-07 | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 3 | O/SAU/8/2013 | SAU13-08 | 639 | 632 | 0 | 98.90 | 1.10 | ME-SA | Ind-2001d |
| 4 | O/SAU/1/2014 | SAU14-01 | 639 | 631 | 0 | 98.75 | 1.25 | ME-SA | Ind-2001d |
| 5 | O/SAU/2/2014 | SAU14-02 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | Ind-2001d |
| 6 | O/SAU/3/2013 | SAU13-03 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | Ind-2001d |
| 7 | O/SAU/3/2014 | SAU14-03 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | Ind-2001d |
| 8 | O/SAU/4/2013 | SAU13-04 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | Ind-2001d |
| 9 | O/IND127/2013* (PD-FMD) | IND13-AC | 639 | 629 | 0 | 98.44 | 1.56 | ME-SA | Ind-2001d |
| 10 | O/SAU/1/2013 | SAU13-01 | 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 | BHU09-03 | 639 | 609 | 0 | 95.31 | 4.69 | ME-SA | Ind-2001d |
| 2 | O/OMN/7/2001 (DQ164941) | OMN01-07 | 639 | 586 | 0 | 91.71 | 8.29 | ME-SA | Ind-2001b |
| 3 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 585 | 0 | 91.55 | 8.45 | ME-SA | Ind-2001a |
| 4 | O/UAE/4/2008 | UAE08-04 | 636 | 572 | 0 | 89.94 | 10.06 | ME-SA | Ind-2001c |
| 5 | O/IRN/31/2009 | IRN09-31 | 639 | 574 | 0 | 89.83 | 10.17 | ME-SA | PanAsia-2$^{FAR-09}$ |
| 6 | O/IRN/8/2005 | IRN05-08 | 639 | 572 | 0 | 89.51 | 10.49 | ME-SA | PanAsia-2 |
| 7 | O/PAK/16/2010 | PAK10-16 | 639 | 571 | 0 | 89.36 | 10.64 | ME-SA | PanAsia-2$^{PUN-10}$ |
| 8 | O/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 569 | 0 | 89.05 | 10.95 | ME-SA | PanAsia |
| 9 | O/IRN/18/2010 | IRN10-18 | 639 | 568 | 0 | 88.89 | 11.11 | ME-SA | PanAsia-2$^{BAL-09}$ |
| 10 | O/IRN/61/2001 (DQ164896) | IRN01-61 | 638 | 567 | 1 | 88.87 | 11.13 | ME-SA | Irn-2001 |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

# Report on FMDV O in Saudi Arabia in 2014

Batch: WRLFMD/2014/00014

◆ 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,
04 April 2014