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

## Genotyping Report

Report Date for this Batch: 7 August 2014

FMDV type O
Country: Laos
Period: 2013
No. of samples: 3

BATCH: WRLFMD/2014/00023

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: LAO/1/2013
Batch No: WRLFMD/2014/00023
Sender Ref: LAO 3/13 R4B4
Location: Luang Namtha Province, Laos
Date collected: 19/07/2013
Date received by WRLFMD: 19/06/2014
Date received for sequencing: 25/07/2014
Species: Cattle
Material used: BTy1 23/07/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 07/08/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: LAO13-01.SEQ
Date sequence last updated: 05/08/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3936
Min. no. of nt for comparison: 600
Total turn-around time: 49 days
Sequencing time: 13 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/LAO/2/2013 | LAO13-02 | 639 | 637 | 0 | 99.69 | 0.31 | SEA | Mya-98 |
| 2 | O/TAI/14/2012 | TAI12-14 | 639 | 634 | 0 | 99.22 | 0.78 | SEA | Mya-98 |
| 3 | O/TAI/18/2012 | TAI12-18 | 639 | 634 | 0 | 99.22 | 0.78 | SEA | Mya-98 |
| 4 | O/LAO/1/2010 | LAO10-01 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 5 | O/TAI/12/2009 (HQ116260) | TAI09-12 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 6 | O/TAI/13/2009 (HQ116261) | TAI09-13 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 7 | O/TAI/15/2009 (HQ116262) | TAI09-15 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 8 | O/TAI/16/2009 (HQ116263) | TAI09-16 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 9 | O/TAI/17/2009 (HQ116264) | TAI09-17 | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |
| 10 | O/VN/SL186/2009 (HM055505) | VIT09-AL | 639 | 612 | 0 | 95.77 | 4.23 | SEA | Mya-98 |

## Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd_genotyping/prototypes.htm](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/MYA/7/98 (DQ164925) | MYA98-07 | 639 | 581 | 0 | 90.92 | 9.08 | SEA | Mya-98 |
| 2 | O/TAI/189/87* (TRRL) | TAI87-AC | 639 | 564 | 0 | 88.26 | 11.74 | SEA | unnamed |
| 3 | O/PAK/16/2003 (DQ165068) | PAK03-16 | 639 | 552 | 0 | 86.38 | 13.62 | ME-SA | Pak-98 |
| 4 | O/CAM/3/98 (AJ294910) | CAM98-03 | 639 | 548 | 0 | 85.76 | 14.24 | SEA | Cam-94 |
| 5 | O/IND/R2/75* (AF204276) | IND75--A | 639 | 548 | 0 | 85.76 | 14.24 | ME-SA | unnamed |
| 6 | O1/Manisa/TUR/69 (AY593823) | TUR69--G | 639 | 545 | 0 | 85.29 | 14.71 | ME-SA | unnamed |
| 7 | O/UAE/4/2008 | UAE08-04 | 636 | 541 | 0 | 85.06 | 14.94 | ME-SA | Ind-2001c |
| 8 | O/IRN/31/2009 | IRN09-31 | 639 | 541 | 0 | 84.66 | 15.34 | ME-SA | PanAsia-2$^{\text{FAR-09}}$ |
| 9 | O/TUR/264/2009* (FMDI) | TUR09-AK | 639 | 541 | 0 | 84.66 | 15.34 | ME-SA | PanAsia-2$^{\text{SAN-09}}$ |
| 10 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 540 | 0 | 84.51 | 15.49 | ME-SA | Ind-2001a |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

# FAO World Reference Laboratory for FMD Genotyping Report

| | |
|---|---|
| Serotype: O | Report date: 07/08/2014 |
| WRLFMD Ref No: LAO/2/2013 | Reported by: N.J. Knowles |
| Batch No: WRLFMD/2014/00023 | Checked by: K. Bachanek-Bankowska |
| Sender Ref: LAO 5/13 R4B4 | |
| Location: Luang Namtha Province, Laos | Topotype: SEA |
| Date collected: 19/07/2013 | Genotype/strain: Mya-98 |
| Date received by WRLFMD: 19/06/2014 | Sequence filename: LAO13-02.SEQ |
| Date received for sequencing: 01/08/2014 | Date sequence last updated: 05/08/2014 |
| Species: Cattle | No. of Nt determined: 639 |
| Material used: BTy1 29/07/2014 | No. of ambiguities: 0 |
| Region sequenced: VP1 | Gene length: 639 |
| RT-PCR primers: O-1C244F/EUR-2B52R | Total no. of comparisons: 3936 |
| O-1C272F/EUR-2B52R | Min. no. of nt for comparison: 600 |
| | Total turn-around time: 49 days |
| | Sequencing time: 6 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/LAO/1/2013 | LAO13-01 | 639 | 637 | 0 | 99.69 | 0.31 | SEA | Mya-98 |
| 2 | O/TAI/14/2012 | TAI12-14 | 639 | 636 | 0 | 99.53 | 0.47 | SEA | Mya-98 |
| 3 | O/TAI/18/2012 | TAI12-18 | 639 | 636 | 0 | 99.53 | 0.47 | SEA | Mya-98 |
| 4 | O/LAO/1/2010 | LAO10-01 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 5 | O/TAI/12/2009 (HQ116260) | TAI09-12 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 6 | O/TAI/13/2009 (HQ116261) | TAI09-13 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 7 | O/TAI/15/2009 (HQ116262) | TAI09-15 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 8 | O/TAI/16/2009 (HQ116263) | TAI09-16 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 9 | O/TAI/17/2009 (HQ116264) | TAI09-17 | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |
| 10 | O/VN/SL186/2009 (HM055505) | VIT09-AL | 639 | 614 | 0 | 96.09 | 3.91 | SEA | Mya-98 |

## 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/MYA/7/98 (DQ164925) | MYA98-07 | 639 | 583 | 0 | 91.24 | 8.76 | SEA | Mya-98 |
| 2 | O/TAI/189/87* (TRRL) | TAI87-AC | 639 | 566 | 0 | 88.58 | 11.42 | SEA | unnamed |
| 3 | O/PAK/16/2003 (DQ165068) | PAK03-16 | 639 | 554 | 0 | 86.70 | 13.30 | ME-SA | Pak-98 |
| 4 | O/CAM/3/98 (AJ294910) | CAM98-03 | 639 | 550 | 0 | 86.07 | 13.93 | SEA | Cam-94 |
| 5 | O/IND/R2/75* (AF204276) | IND75--A | 639 | 550 | 0 | 86.07 | 13.93 | ME-SA | unnamed |
| 6 | O1/Manisa/TUR/69 (AY593823) | TUR69--G | 639 | 547 | 0 | 85.60 | 14.40 | ME-SA | unnamed |
| 7 | O/UAE/4/2008 | UAE08-04 | 636 | 543 | 0 | 85.38 | 14.62 | ME-SA | Ind-2001c |
| 8 | O/IRN/31/2009 | IRN09-31 | 639 | 543 | 0 | 84.98 | 15.02 | ME-SA | PanAsia-2$^{\text{FAR-09}}$ |
| 9 | O/TUR/264/2009* (FMDI) | TUR09-AK | 639 | 543 | 0 | 84.98 | 15.02 | ME-SA | PanAsia-2$^{\text{SAN-09}}$ |
| 10 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 542 | 0 | 84.82 | 15.18 | ME-SA | Ind-2001a |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: LAO/3/2013
Batch No: WRLFMD/2014/00023
Sender Ref: LAO 8/13 R4B4
Location: Sainyabuli Province (Xayaboury), Laos
Date collected: 19/07/2013
Date received by WRLFMD: 19/06/2014
Date received for sequencing: 01/08/2014
Species: Cattle
Material used: BTy1 29/07/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 07/08/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: SEA
Genotype/strain: Mya-98
Sequence filename: LAO13-03.SEQ
Date sequence last updated: 05/08/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3936
Min. no. of nt for comparison: 600
Total turn-around time: 49 days
Sequencing time: 6 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/MAY/4/2007 (HQ116208) | MAY07-04 | 639 | 610 | 0 | 95.46 | 4.54 | SEA | Mya-98 |
| 2 | O/MAY/6/2007 (HQ116210) | MAY07-06 | 639 | 609 | 0 | 95.31 | 4.69 | SEA | Mya-98 |
| 3 | O/LAO/061/2007* | LAO07-AA | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 4 | O/LAO/064/2007* | LAO07-AC | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 5 | O/LAO/067/2007* | LAO07-AD | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 6 | O/LAO/078/2008* | LAO08-AF | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 7 | O/LAO/080/2008* | LAO08-AH | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 8 | O/LAO/1/2007 (HQ116175) | LAO07-01 | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 9 | O/MAY/7/2007 (HQ116211) | MAY07-07 | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |
| 10 | O/TAI/7/2007 (HQ116243) | TAI07-07 | 639 | 608 | 0 | 95.15 | 4.85 | SEA | Mya-98 |

## 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/MYA/7/98 (DQ164925) | MYA98-07 | 639 | 578 | 0 | 90.45 | 9.55 | SEA | Mya-98 |
| 2 | O/TAI/189/87* (TRRL) | TAI87-AC | 639 | 558 | 0 | 87.32 | 12.68 | SEA | unnamed |
| 3 | O/IND/R2/75* (AF204276) | IND75--A | 639 | 542 | 0 | 84.82 | 15.18 | ME-SA | unnamed |
| 4 | O/TUR/257/2008* (FMDI) | TUR08-AD | 639 | 540 | 0 | 84.51 | 15.49 | ME-SA | PanAsia-2$^{\text{TER-08}}$ |
| 5 | O/PAK/16/2003 (DQ165068) | PAK03-16 | 639 | 539 | 0 | 84.35 | 15.65 | ME-SA | Pak-98 |
| 6 | O/TUR/264/2009* (FMDI) | TUR09-AK | 639 | 539 | 0 | 84.35 | 15.65 | ME-SA | PanAsia-2$^{\text{SAN-09}}$ |
| 7 | O/IRN/31/2009 | IRN09-31 | 639 | 538 | 0 | 84.19 | 15.81 | ME-SA | PanAsia-2$^{\text{FAR-09}}$ |
| 8 | O/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 538 | 0 | 84.19 | 15.81 | ME-SA | PanAsia |
| 9 | O1/Manisa/TUR/69 (AY593823) | TUR69--G | 639 | 538 | 0 | 84.19 | 15.81 | ME-SA | unnamed |
| 10 | O/PAK/16/2010 | PAK10-16 | 639 | 537 | 0 | 84.04 | 15.96 | ME-SA | PanAsia-2$^{\text{PUN-10}}$ |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

# Report on FMDV O in Laos in 2013

Batch: WRLFMD/2014/00023

◆ 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 August 2014