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

## Genotyping Report

Report Date for this Batch: 18 February 2014

FMDV type O
Country: Russian Federation
Period: 2014
No. of sequences: 1 (VP1)
Originator: [redacted] Federal Centre for Animal Health (FGI ARRIAH), Yur’evets, Vladimir, 600900, Russia, 600900 Yur'evets.

# FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: Zabaikalsky/RUS/2014*
Batch No: WRLMEG/2014/00003
Sender Ref: O/Zabaikalsky/RUS/2014
Location: Starotsuruhaitui, Priargunsky, Zabaikalsky krai, Russia
Date collected: 09/02/2013
Date received by WRLFMD: 18/02/2014
Date received for sequencing: n/a
Species: Cattle
Material used: epithelium
Region sequenced: VP1
RT-PCR primers: Not known

Report date: 18/02/2014
Reported by: N.J. Knowles
Checked by: B. Valdazo-Gonzalez

Topotype: ME-SA
Genotype/strain: PanAsia
Sequence filename: RUS14-AB.SEQ
Date sequence last updated: 18/02/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3765
Min. no. of nt for comparison: 600
Total turn-around time: 0 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/VIT/13/2013 | VIT13-13 | 639 | 631 | 0 | 98.75 | 1.25 | ME-SA | PanAsia |
| 2 | O/VIT/15/2013 | VIT13-15 | 639 | 631 | 0 | 98.75 | 1.25 | ME-SA | PanAsia |
| 3 | O/VIT/32/2013 | VIT13-32 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 4 | O/VIT/33/2013 | VIT13-33 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 5 | O/VIT/40/2013 | VIT13-40 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 6 | O/VIT/46/2013 | VIT13-46 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 7 | O/VIT/47/2013 | VIT13-47 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 8 | O/VIT/51/2013 | VIT13-51 | 639 | 630 | 0 | 98.59 | 1.41 | ME-SA | PanAsia |
| 9 | O/VIT/11/2013 | VIT13-11 | 639 | 629 | 0 | 98.44 | 1.56 | ME-SA | PanAsia |
| 10 | O/VIT/12/2013 | VIT13-12 | 639 | 629 | 0 | 98.44 | 1.56 | ME-SA | PanAsia |

## 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/UKG/35/2001 (AJ539141) | UKG01-35 | 639 | 588 | 0 | 92.02 | 7.98 | ME-SA | PanAsia |
| 2 | O/KUW/3/97 (DQ164904) | KUW97-03 | 639 | 580 | 0 | 90.77 | 9.23 | ME-SA | Ind-2001a |
| 3 | O/IRN/8/2005 | IRN05-08 | 639 | 576 | 0 | 90.14 | 9.86 | ME-SA | PanAsia-2 |
| 4 | O/BHU/3/2009 | BHU09-03 | 639 | 575 | 0 | 89.98 | 10.02 | ME-SA | Ind-2001d |
| 5 | O/OMN/7/2001 (DQ164941) | OMN01-07 | 639 | 575 | 0 | 89.98 | 10.02 | ME-SA | Ind-2001b |
| 6 | O/UAE/4/2008 | UAE08-04 | 636 | 572 | 0 | 89.94 | 10.06 | ME-SA | Ind-2001c |
| 7 | O/BHU/1/2013 | BHU13-01 | 639 | 572 | 0 | 89.51 | 10.49 | ME-SA | Ind-2001$^{KAR-13}$ |
| 8 | O/IRN/61/2001 (DQ164896) | IRN01-61 | 638 | 570 | 1 | 89.34 | 10.66 | ME-SA | Irn-2001 |
| 9 | O/IRN/31/2009 | IRN09-31 | 639 | 570 | 0 | 89.20 | 10.80 | ME-SA | PanAsia-2$^{FAR-09}$ |
| 10 | O/IRN/18/2010 | IRN10-18 | 639 | 568 | 0 | 88.89 | 11.11 | ME-SA | PanAsia-2$^{BAL-09}$ |

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

# Report on FMDV O in the Russian Federation in 2014

Batch: WRLMEG/2014/00003

◆ 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,
18 February 2014