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

Genotyping Report

Report Date for this Batch: 17 December 2014

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

BATCH: WRLFMD/2014/00036

Serotype: O	Report date: 17/12/2014
WRLFMD Ref No: BAR/1/2014	Reported by: K. Bachanek-Bankowska
Batch No: WRLFMD/2014/00036	Checked by: N.J. Knowles
Sender Ref: A	
Location: North Governate, Bahrain	Topotype: ME-SA
Date collected: 16/10/2014	Genotype/strain: PanAsia-2^{ANT-10}
Date received by WRLFMD: 04/11/2014	Sequence filename: BAR14-01.SEQ
Date received for sequencing: 08/12/2014	Date sequence last updated: 09/12/2014
Species: Cow	No. of Nt determined: 639
Material used: BTy1 03/12/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4099
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 9 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/BAR/3/2014	BAR14-03	639	638	0	99.84	0.16	ME-SA	PanAsia-2^{ANT-10}
2	O/BAR/2/2014	BAR14-02	639	637	0	99.69	0.31	ME-SA	PanAsia-2^{ANT-10}
3	O/PAK/12/2014	PAK14-12	639	634	0	99.22	0.78	ME-SA	PanAsia-2^{ANT-10}
4	O/PAK/13/2014	PAK14-13	639	634	0	99.22	0.78	ME-SA	PanAsia-2^{ANT-10}
5	O/PAK/27/2013	PAK13-27	639	634	0	99.22	0.78	ME-SA	PanAsia-2^{ANT-10}
6	O/PAK/3/2014	PAK14-03	639	634	0	99.22	0.78	ME-SA	PanAsia-2^{ANT-10}
7	O/PAK/11/2014	PAK14-11	639	633	0	99.06	0.94	ME-SA	PanAsia-2^{ANT-10}
8	O/PAK/23/2014	PAK14-23	639	633	0	99.06	0.94	ME-SA	PanAsia-2^{ANT-10}
9	O/PAK/58/2012	PAK12-58	639	633	0	99.06	0.94	ME-SA	PanAsia-2^{ANT-10}
10	O/PAK/2/2014	PAK14-02	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{ANT-10}

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/IRN/88/2009	IRN09-88	639	608	0	95.15	4.85	ME-SA	PanAsia-2^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	593	0	92.80	7.20	ME-SA	PanAsia-2^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	586	0	91.71	8.29	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	585	0	91.55	8.45	ME-SA	PanAsia-2^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	583	0	91.24	8.76	ME-SA	PanAsia-2^{PUN-10}
6	O/IRN/18/2010	IRN10-18	639	582	0	91.08	8.92	ME-SA	PanAsia-2^{BAL-09}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	580	0	90.77	9.23	ME-SA	PanAsia-2^{SAN-09}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	577	0	90.30	9.70	ME-SA	PanAsia
9	O/OMN/7/2001 (DQ164941)	OMN01-07	639	568	0	88.89	11.11	ME-SA	Ind-2001b
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	566	0	88.58	11.42	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: 17/12/2014
WRLFMD Ref No: BAR/2/2014	Reported by: K. Bachanek-Bankowska
Batch No: WRLFMD/2014/00036	Checked by: N.J. Knowles
Sender Ref: B	
Location: North Governate, Bahrain	Topotype: ME-SA
Date collected: 16/10/2014	Genotype/strain: PanAsia-2^{ANT-10}
Date received by WRLFMD: 04/11/2014	Sequence filename: BAR14-02.SEQ
Date received for sequencing: 08/12/2014	Date sequence last updated: 09/12/2014
Species: Cow	No. of Nt determined: 639
Material used: BTy1 29/11/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4099
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 9 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/BAR/1/2014	BAR14-01	639	637	0	99.69	0.31	ME-SA	PanAsia-2^{ANT-10}
2	O/BAR/3/2014	BAR14-03	639	636	0	99.53	0.47	ME-SA	PanAsia-2^{ANT-10}
3	O/PAK/12/2014	PAK14-12	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{ANT-10}
4	O/PAK/13/2014	PAK14-13	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{ANT-10}
5	O/PAK/27/2013	PAK13-27	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{ANT-10}
6	O/PAK/3/2014	PAK14-03	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{ANT-10}
7	O/PAK/11/2014	PAK14-11	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{ANT-10}
8	O/PAK/23/2014	PAK14-23	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{ANT-10}
9	O/PAK/58/2012	PAK12-58	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{ANT-10}
10	O/PAK/2/2014	PAK14-02	639	630	0	98.59	1.41	ME-SA	PanAsia-2^{ANT-10}

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/IRN/88/2009	IRN09-88	639	608	0	95.15	4.85	ME-SA	PanAsia-2^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	591	0	92.49	7.51	ME-SA	PanAsia-2^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	584	0	91.39	8.61	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	583	0	91.24	8.76	ME-SA	PanAsia-2^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	581	0	90.92	9.08	ME-SA	PanAsia-2^{PUN-10}
6	O/IRN/18/2010	IRN10-18	639	580	0	90.77	9.23	ME-SA	PanAsia-2^{BAL-09}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	578	0	90.45	9.55	ME-SA	PanAsia-2^{SAN-09}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	575	0	89.98	10.02	ME-SA	PanAsia
9	O/OMN/7/2001 (DQ164941)	OMN01-07	639	566	0	88.58	11.42	ME-SA	Ind-2001b
10	O/UAE/4/2008 (KM921876)	UAE08-04	636	563	0	88.52	11.48	ME-SA	Ind-2001c

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: BAR/3/2014
Batch No: WRLFMD/2014/00036
Sender Ref: C
Location: North Governate, Bahrain
Date collected: 27/10/2014
Date received by WRLFMD: 04/11/2014
Date received for sequencing: 08/12/2014
Species: Cow
Material used: BTy1 30/11/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 17/12/2014
Reported by: K. Bachanek-Bankowska
Checked by: N.J. Knowles

Topotype: ME-SA
Genotype/strain: PanAsia-2$^{\text{ANT-10}}$
Sequence filename: BAR14-03.SEQ
Date sequence last updated: 11/12/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 4099
Min. no. of nt for comparison: 600
Total turn-around time: 43 days
Sequencing time: 9 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/BAR/1/2014	BAR14-01	639	638	0	99.84	0.16	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/BAR/2/2014	BAR14-02	639	636	0	99.53	0.47	ME-SA	PanAsia-2$^{\text{ANT-10}}$
3	O/PAK/12/2014	PAK14-12	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/PAK/13/2014	PAK14-13	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/PAK/27/2013	PAK13-27	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
6	O/PAK/3/2014	PAK14-03	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
7	O/PAK/11/2014	PAK14-11	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/PAK/23/2014	PAK14-23	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/PAK/58/2012	PAK12-58	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/PAK/2/2014	PAK14-02	639	631	0	98.75	1.25	ME-SA	PanAsia-2$^{\text{ANT-10}}$

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/IRN/88/2009	IRN09-88	639	607	0	94.99	5.01	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/IRN/31/2009	IRN09-31	639	592	0	92.64	7.36	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/IRN/8/2005	IRN05-08	639	585	0	91.55	8.45	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	584	0	91.39	8.61	ME-SA	PanAsia-2$^{\text{TER-08}}$
5	O/PAK/16/2010	PAK10-16	639	582	0	91.08	8.92	ME-SA	PanAsia-2$^{\text{PUN-10}}$
6	O/IRN/18/2010	IRN10-18	639	581	0	90.92	9.08	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	579	0	90.61	9.39	ME-SA	PanAsia-2$^{\text{SAN-09}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	576	0	90.14	9.86	ME-SA	PanAsia
9	O/OMN/7/2001 (DQ164941)	OMN01-07	639	567	0	88.73	11.27	ME-SA	Ind-2001b
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	565	0	88.42	11.58	ME-SA	Ind-2001a

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in Bahrain in 2014

Batch: WRLFMD/2014/00036

◆ 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,
17 December 2014