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

Genotyping Report

Report Date for this Batch: 20 April 2014

FMDV type O
Country: Afghanistan
Period: 2013
No. of samples: 4

BATCH: WRLFMD/2014/00004

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 10/04/2014
WRLFMD Ref No: AFG/1/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00004	Checked by: K. Bachanek-Bankowska
Sender Ref: 5935	
Location: Hirat province, Afghanistan	Topotype: ME-SA
Date collected: 10/09/2013	Genotype/strain: PanAsia-2$^{\text{ANT-10}}$
Date received by WRLFMD: 10/02/2014	Sequence filename: AFG13-01.SEQ
Date received for sequencing: 08/04/2014	Date sequence last updated: 10/04/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 13/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3830
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 59 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/AFG/110/2010	AFG10110	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/AFG/40/2010	AFG10-40	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
3	O/AFG/41/2010	AFG10-41	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/AFG/42/2010	AFG10-42	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/IRN/62/2010	IRN10-62	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{ANT-10}}$
6	O/AFG/120/2010	AFG10120	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
7	O/AFG/126/2010	AFG10126	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/AFG/145/2010	AFG10145	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/AFG/39/2010	AFG10-39	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/AFG/43/2010	AFG10-43	639	632	0	98.90	1.10	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	628	0	98.28	1.72	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/IRN/8/2005	IRN05-08	639	603	0	94.37	5.63	ME-SA	PanAsia-2
3	O/IRN/31/2009	IRN09-31	639	601	0	94.05	5.95	ME-SA	PanAsia-2$^{\text{FAR-09}}$
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	599	0	93.74	6.26	ME-SA	PanAsia-2$^{\text{TER-08}}$
5	O/IRN/18/2010	IRN10-18	639	596	0	93.27	6.73	ME-SA	PanAsia-2$^{\text{BAL-09}}$
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	594	0	92.96	7.04	ME-SA	PanAsia-2$^{\text{SAN-09}}$
7	O/PAK/16/2010	PAK10-16	639	591	0	92.49	7.51	ME-SA	PanAsia-2$^{\text{PUN-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	580	0	90.77	9.23	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	569	1	89.18	10.82	ME-SA	Irn-2001
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	569	0	89.05	10.95	ME-SA	Ind-2001a

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.2

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: AFG/4/2013
Batch No: WRLFMD/2014/00004
Sender Ref: 5914
Location: Khaer Abad, Enjeil, Hirat province, Afghanistan
Date collected: 27/09/2013
Date received by WRLFMD: 10/02/2014
Date received for sequencing: 08/04/2014
Species: Cattle
Material used: BTy1 15/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 10/04/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: PanAsia-2$^{\text{ANT-10}}$
Sequence filename: AFG13-04.SEQ
Date sequence last updated: 10/04/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3830
Min. no. of nt for comparison: 600
Total turn-around time: 59 days
Sequencing time: 2 days

Comments: FMDV type A was also detected in this sample.

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/AFG/17/2013	AFG13-17	639	639	0	100.00	0.00	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/AFG/21/2013	AFG13-21	639	639	0	100.00	0.00	ME-SA	PanAsia-2$^{\text{ANT-10}}$
3	O/AFG/253/2010	AFG10253	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/PAK/112/2010	PAK10112	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/PAK/74/2011	PAK11-74	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
6	O/PAK/77/2010	PAK10-77	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
7	O/PAK/78/2010	PAK10-78	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/PAK/79/2010	PAK10-79	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/PAK/80/2010	PAK10-80	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/PAK/88/2010	PAK10-88	639	623	0	97.50	2.50	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	617	0	96.56	3.44	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/IRN/31/2009	IRN09-31	639	595	0	93.11	6.89	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	594	0	92.96	7.04	ME-SA	PanAsia-2$^{\text{TER-08}}$
4	O/IRN/8/2005	IRN05-08	639	593	0	92.80	7.20	ME-SA	PanAsia-2
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	589	0	92.18	7.82	ME-SA	PanAsia-2$^{\text{SAN-09}}$
6	O/IRN/18/2010	IRN10-18	639	586	0	91.71	8.29	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/PAK/16/2010	PAK10-16	639	585	0	91.55	8.45	ME-SA	PanAsia-2$^{\text{PUN-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	577	0	90.30	9.70	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	567	1	88.87	11.13	ME-SA	Irn-2001
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	565	0	88.42	11.58	ME-SA	Ind-2001b

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.2

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 10/04/2014
WRLFMD Ref No: AFG/17/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00004	Checked by: K. Bachanek-Bankowska
Sender Ref: 5899	
Location: Qalaemosa, Guldara, Kabul province, Afghanistan	Topotype: ME-SA
Date collected: 24/10/2013	Genotype/strain: PanAsia-2^{ANT-10}
Date received by WRLFMD: 10/02/2014	Sequence filename: AFG13-17.SEQ
Date received for sequencing: 08/04/2014	Date sequence last updated: 10/04/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 25/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3830
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 59 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/AFG/21/2013	AFG13-21	639	639	0	100.00	0.00	ME-SA	PanAsia-2^{ANT-10}
2	O/AFG/4/2013	AFG13-04	639	639	0	100.00	0.00	ME-SA	PanAsia-2^{ANT-10}
3	O/AFG/253/2010	AFG10253	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
4	O/PAK/112/2010	PAK10112	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
5	O/PAK/74/2011	PAK11-74	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
6	O/PAK/77/2010	PAK10-77	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
7	O/PAK/78/2010	PAK10-78	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
8	O/PAK/79/2010	PAK10-79	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
9	O/PAK/80/2010	PAK10-80	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{ANT-10}
10	O/PAK/88/2010	PAK10-88	639	623	0	97.50	2.50	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	617	0	96.56	3.44	ME-SA	PanAsia-2^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	595	0	93.11	6.89	ME-SA	PanAsia-2^{FAR-09}
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	594	0	92.96	7.04	ME-SA	PanAsia-2^{TER-08}
4	O/IRN/8/2005	IRN05-08	639	593	0	92.80	7.20	ME-SA	PanAsia-2
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	589	0	92.18	7.82	ME-SA	PanAsia-2^{SAN-09}
6	O/IRN/18/2010	IRN10-18	639	586	0	91.71	8.29	ME-SA	PanAsia-2^{BAL-09}
7	O/PAK/16/2010	PAK10-16	639	585	0	91.55	8.45	ME-SA	PanAsia-2^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	577	0	90.30	9.70	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	567	1	88.87	11.13	ME-SA	Irn-2001
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	565	0	88.42	11.58	ME-SA	Ind-2001b

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.2

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: AFG/21/2013
Batch No: WRLFMD/2014/00004
Sender Ref: 5900
Location: Chenar, Srobie, Kabul province, Afghanistan
Date collected: 29/10/2013
Date received by WRLFMD: 10/02/2014
Date received for sequencing: 08/04/2014
Species: Cattle
Material used: BTy1 28/03/2014
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 10/04/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: PanAsia-2$^{\text{ANT-10}}$
Sequence filename: AFG13-21.SEQ
Date sequence last updated: 10/04/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3830
Min. no. of nt for comparison: 600
Total turn-around time: 59 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/AFG/17/2013	AFG13-17	639	639	0	100.00	0.00	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/AFG/4/2013	AFG13-04	639	639	0	100.00	0.00	ME-SA	PanAsia-2$^{\text{ANT-10}}$
3	O/AFG/253/2010	AFG10253	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/PAK/112/2010	PAK10112	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/PAK/74/2011	PAK11-74	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
6	O/PAK/77/2010	PAK10-77	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
7	O/PAK/78/2010	PAK10-78	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/PAK/79/2010	PAK10-79	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/PAK/80/2010	PAK10-80	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/PAK/88/2010	PAK10-88	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{ANT-10}}$

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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	617	0	96.56	3.44	ME-SA	PanAsia-2$^{\text{ANT-10}}$
2	O/IRN/31/2009	IRN09-31	639	595	0	93.11	6.89	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	594	0	92.96	7.04	ME-SA	PanAsia-2$^{\text{TER-08}}$
4	O/IRN/8/2005	IRN05-08	639	593	0	92.80	7.20	ME-SA	PanAsia-2
5	O/TUR/264/2009* (FMDI)	TUR09-AK	639	589	0	92.18	7.82	ME-SA	PanAsia-2$^{\text{SAN-09}}$
6	O/IRN/18/2010	IRN10-18	639	586	0	91.71	8.29	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/PAK/16/2010	PAK10-16	639	585	0	91.55	8.45	ME-SA	PanAsia-2$^{\text{PUN-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	577	0	90.30	9.70	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	567	1	88.87	11.13	ME-SA	Irn-2001
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	565	0	88.42	11.58	ME-SA	Ind-2001b

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.2

Report on FMDV O in Afghanistan in 2013

Batch: WRLFMD/2014/00004

◆ 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,
20 April 2014