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

Genotyping Report

Report Date for this Batch: 4 April 2014

FMDV type O
Country: Iran
Period: 2013-2014
No. of samples: 7

BATCH: WRLFMD/2014/000006

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 04/04/2014
WRLFMD Ref No: IRN/17/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00006	Checked by: K. Bachanek-Bankowska
Sender Ref: IR-92 A-18	
Location: Esfahan, Iran	Topotype: ME-SA
Date collected: 07/10/2013	Genotype/strain: PanAsia-2^{FAR-09}
Date received by WRLFMD: 05/02/2014	Sequence filename: IRN13-17.SEQ
Date received for sequencing: 11/03/2014	Date sequence last updated: 17/03/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 26/02/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3820
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 58 days
	Sequencing time: 24 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/IRN/22/2013	IRN13-22	639	635	0	99.37	0.63	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/23/2013	IRN13-23	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{FAR-09}
3	O/IRN/30/2013	IRN13-30	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{FAR-09}
4	O/IRN/29/2013	IRN13-29	639	630	0	98.59	1.41	ME-SA	PanAsia-2^{FAR-09}
5	O/IRN 3917/2012*	IRN12-AM	639	624	0	97.65	2.35	ME-SA	PanAsia-2^{FAR-09}
6	O/IRN 12463/2012*	IRN12-AQ	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{FAR-09}
7	O/IRN 3921/2012*	IRN12-AN	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{FAR-09}
8	O/IRN 3922/2012*	IRN12-AO	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{FAR-09}
9	O/SAU/1/2009	SAU09-01	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{FAR-09}
10	O/SAU/2/2009	SAU09-02	639	623	0	97.50	2.50	ME-SA	PanAsia-2^{FAR-09}

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/31/2009	IRN09-31	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/18/2010	IRN10-18	639	607	0	94.99	5.01	ME-SA	PanAsia-2^{BAL-09}
3	O/IRN/8/2005	IRN05-08	639	601	0	94.05	5.95	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	600	0	93.90	6.10	ME-SA	PanAsia-2^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	597	0	93.43	6.57	ME-SA	PanAsia-2^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	595	0	93.11	6.89	ME-SA	PanAsia-2^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	593	0	92.80	7.20	ME-SA	PanAsia-2^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	591	0	92.49	7.51	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	575	0	89.98	10.02	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	572	0	89.51	10.49	ME-SA	Ind-2001b

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: IRN/22/2013
Batch No: WRLFMD/2014/00006
Sender Ref: IR-92 A19
Location: Esfahan, Iran
Date collected: 04/12/2013
Date received by WRLFMD: 05/02/2014
Date received for sequencing: 07/03/2014
Species: Cattle
Material used: BTy1 26/02/2014 & BTy2 27/02/2014
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: PanAsia-2$^{\text{FAR-09}}$
Sequence filename: IRN13-22.SEQ
Date sequence last updated: 17/03/2014
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: 58 days
Sequencing time: 28 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/IRN/17/2013	IRN13-17	639	635	0	99.37	0.63	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/IRN/30/2013	IRN13-30	639	635	0	99.37	0.63	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/IRN/23/2013	IRN13-23	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{FAR-09}}$
4	O/IRN/29/2013	IRN13-29	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{FAR-09}}$
5	O/IRN 3917/2012*	IRN12-AM	639	626	0	97.97	2.03	ME-SA	PanAsia-2$^{\text{FAR-09}}$
6	O/IRN 12463/2012*	IRN12-AQ	639	625	0	97.81	2.19	ME-SA	PanAsia-2$^{\text{FAR-09}}$
7	O/IRN 3921/2012*	IRN12-AN	639	625	0	97.81	2.19	ME-SA	PanAsia-2$^{\text{FAR-09}}$
8	O/IRN 3922/2012*	IRN12-AO	639	625	0	97.81	2.19	ME-SA	PanAsia-2$^{\text{FAR-09}}$
9	O/SAU/1/2009	SAU09-01	639	625	0	97.81	2.19	ME-SA	PanAsia-2$^{\text{FAR-09}}$
10	O/SAU/2/2009	SAU09-02	639	625	0	97.81	2.19	ME-SA	PanAsia-2$^{\text{FAR-09}}$

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/31/2009	IRN09-31	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/IRN/18/2010	IRN10-18	639	608	0	95.15	4.85	ME-SA	PanAsia-2$^{\text{BAL-09}}$
3	O/IRN/8/2005	IRN05-08	639	603	0	94.37	5.63	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	602	0	94.21	5.79	ME-SA	PanAsia-2$^{\text{TER-08}}$
5	O/PAK/16/2010	PAK10-16	639	599	0	93.74	6.26	ME-SA	PanAsia-2$^{\text{PUN-10}}$
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	597	0	93.43	6.57	ME-SA	PanAsia-2$^{\text{SAN-09}}$
7	O/IRN/88/2009	IRN09-88	639	595	0	93.11	6.89	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	593	0	92.80	7.20	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	577	0	90.30	9.70	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	574	0	89.83	10.17	ME-SA	Ind-2001b

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 04/04/2014
WRLFMD Ref No: IRN/23/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00006	Checked by: K. Bachanek-Bankowska
Sender Ref: IR-92 A-3	
Location: Gillan, Iran	Topotype: ME-SA
Date collected: 05/12/2013	Genotype/strain: PanAsia-2$^{\text{FAR-09}}$
Date received by WRLFMD: 05/02/2014	Sequence filename: IRN13-23.SEQ
Date received for sequencing: 07/03/2014	Date sequence last updated: 17/03/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 27/02/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3820
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 58 days
	Sequencing time: 28 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/IRN/22/2013	IRN13-22	639	633	0	99.06	0.94	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/IRN/29/2013	IRN13-29	639	632	0	98.90	1.10	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/IRN/17/2013	IRN13-17	639	631	0	98.75	1.25	ME-SA	PanAsia-2$^{\text{FAR-09}}$
4	O/IRN/30/2013	IRN13-30	639	629	0	98.44	1.56	ME-SA	PanAsia-2$^{\text{FAR-09}}$
5	O/IRN 3917/2012*	IRN12-AM	639	624	0	97.65	2.35	ME-SA	PanAsia-2$^{\text{FAR-09}}$
6	O/IRN 12463/2012*	IRN12-AQ	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$
7	O/IRN 3921/2012*	IRN12-AN	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$
8	O/IRN 3922/2012*	IRN12-AO	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$
9	O/SAU/1/2009	SAU09-01	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$
10	O/SAU/2/2009	SAU09-02	639	623	0	97.50	2.50	ME-SA	PanAsia-2$^{\text{FAR-09}}$

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/31/2009	IRN09-31	639	621	0	97.18	2.82	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/IRN/18/2010	IRN10-18	639	606	0	94.84	5.16	ME-SA	PanAsia-2$^{\text{BAL-09}}$
3	O/IRN/8/2005	IRN05-08	639	601	0	94.05	5.95	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	600	0	93.90	6.10	ME-SA	PanAsia-2$^{\text{TER-08}}$
5	O/PAK/16/2010	PAK10-16	639	597	0	93.43	6.57	ME-SA	PanAsia-2$^{\text{PUN-10}}$
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	595	0	93.11	6.89	ME-SA	PanAsia-2$^{\text{SAN-09}}$
7	O/IRN/88/2009	IRN09-88	639	593	0	92.80	7.20	ME-SA	PanAsia-2$^{\text{ANT-10}}$
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	591	0	92.49	7.51	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	575	0	89.98	10.02	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	572	0	89.51	10.49	ME-SA	Ind-2001b

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: IRN/29/2013
Batch No: WRLFMD/2014/00006
Sender Ref: IR-92 A-31
Location: Qom, Iran
Date collected: 18/12/2013
Date received by WRLFMD: 05/02/2014
Date received for sequencing: 14/03/2014
Species: Cattle
Material used: BTy2 11/03/2014
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: PanAsia-2^{FAR-09}
Sequence filename: IRN13-29.SEQ
Date sequence last updated: 18/03/2014
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: 58 days
Sequencing time: 21 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/IRN/22/2013	IRN13-22	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/23/2013	IRN13-23	639	632	0	98.90	1.10	ME-SA	PanAsia-2^{FAR-09}
3	O/IRN/17/2013	IRN13-17	639	630	0	98.59	1.41	ME-SA	PanAsia-2^{FAR-09}
4	O/IRN/30/2013	IRN13-30	639	628	0	98.28	1.72	ME-SA	PanAsia-2^{FAR-09}
5	O/IRN 3917/2012*	IRN12-AM	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
6	O/IRN 12463/2012*	IRN12-AQ	639	620	0	97.03	2.97	ME-SA	PanAsia-2^{FAR-09}
7	O/IRN 3921/2012*	IRN12-AN	639	620	0	97.03	2.97	ME-SA	PanAsia-2^{FAR-09}
8	O/IRN 3922/2012*	IRN12-AO	639	620	0	97.03	2.97	ME-SA	PanAsia-2^{FAR-09}
9	O/SAU/1/2009	SAU09-01	639	620	0	97.03	2.97	ME-SA	PanAsia-2^{FAR-09}
10	O/SAU/2/2009	SAU09-02	639	620	0	97.03	2.97	ME-SA	PanAsia-2^{FAR-09}

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/31/2009	IRN09-31	639	618	0	96.71	3.29	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/18/2010	IRN10-18	639	603	0	94.37	5.63	ME-SA	PanAsia-2^{BAL-09}
3	O/IRN/8/2005	IRN05-08	639	600	0	93.90	6.10	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	597	0	93.43	6.57	ME-SA	PanAsia-2^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	594	0	92.96	7.04	ME-SA	PanAsia-2^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	592	0	92.64	7.36	ME-SA	PanAsia-2^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	591	0	92.49	7.51	ME-SA	PanAsia-2^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	590	0	92.33	7.67	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	576	0	90.14	9.86	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	571	0	89.36	10.64	ME-SA	Ind-2001b

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: IRN/30/2013
Batch No: WRLFMD/2014/00006
Sender Ref: IR-92 A-10
Location: Yazd, Iran
Date collected: 25/12/2013
Date received by WRLFMD: 05/02/2014
Date received for sequencing: 13/03/2014
Species: Cattle
Material used: BTy1 08/03/2014
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: PanAsia-2^{FAR-09}
Sequence filename: IRN13-30.SEQ
Date sequence last updated: 17/03/2014
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: 58 days
Sequencing time: 22 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/IRN/22/2013	IRN13-22	639	635	0	99.37	0.63	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/17/2013	IRN13-17	639	631	0	98.75	1.25	ME-SA	PanAsia-2^{FAR-09}
3	O/IRN/23/2013	IRN13-23	639	629	0	98.44	1.56	ME-SA	PanAsia-2^{FAR-09}
4	O/IRN/29/2013	IRN13-29	639	628	0	98.28	1.72	ME-SA	PanAsia-2^{FAR-09}
5	O/IRN 3917/2012*	IRN12-AM	639	622	0	97.34	2.66	ME-SA	PanAsia-2^{FAR-09}
6	O/IRN 12463/2012*	IRN12-AQ	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
7	O/IRN 3921/2012*	IRN12-AN	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
8	O/IRN 3922/2012*	IRN12-AO	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
9	O/SAU/1/2009	SAU09-01	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}
10	O/SAU/2/2009	SAU09-02	639	621	0	97.18	2.82	ME-SA	PanAsia-2^{FAR-09}

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/31/2009	IRN09-31	639	619	0	96.87	3.13	ME-SA	PanAsia-2^{FAR-09}
2	O/IRN/18/2010	IRN10-18	639	606	0	94.84	5.16	ME-SA	PanAsia-2^{BAL-09}
3	O/IRN/8/2005	IRN05-08	639	599	0	93.74	6.26	ME-SA	PanAsia-2
4	O/PAK/16/2010	PAK10-16	639	598	0	93.58	6.42	ME-SA	PanAsia-2^{PUN-10}
5	O/TUR/257/2008* (FMDI)	TUR08-AD	639	598	0	93.58	6.42	ME-SA	PanAsia-2^{TER-08}
6	O/IRN/88/2009	IRN09-88	639	593	0	92.80	7.20	ME-SA	PanAsia-2^{ANT-10}
7	O/TUR/264/2009* (FMDI)	TUR09-AK	639	593	0	92.80	7.20	ME-SA	PanAsia-2^{SAN-09}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	589	0	92.18	7.82	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	577	0	90.30	9.70	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	574	0	89.83	10.17	ME-SA	Ind-2001b

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 04/04/2014
WRLFMD Ref No: IRN/31/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00006	Checked by: K. Bachanek-Bankowska
Sender Ref: IR-92 A-27	
Location: Fars, Iran	Topotype: ME-SA
Date collected: 26/12/2013	Genotype/strain: unnamed
Date received by WRLFMD: 05/02/2014	Sequence filename: IRN13-31.SEQ
Date received for sequencing: 14/03/2014	Date sequence last updated: 18/03/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy2 11/03/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3820
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 58 days
	Sequencing time: 21 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/IRN/1/2014	IRN14-01	639	638	0	99.84	0.16	ME-SA	unnamed
2	O/PAK/40/2012	PAK12-40	639	629	0	98.44	1.56	ME-SA	unnamed
3	O/PAK/41/2012	PAK12-41	639	629	0	98.44	1.56	ME-SA	unnamed
4	O/PAK/51/2012	PAK12-51	639	629	0	98.44	1.56	ME-SA	unnamed
5	O/PAK/22/2013	PAK13-22	639	627	0	98.12	1.88	ME-SA	unnamed
6	O/PAK/53/2012	PAK12-53	639	626	0	97.97	2.03	ME-SA	unnamed
7	O/PAK/55/2012	PAK12-55	639	625	0	97.81	2.19	ME-SA	unnamed
8	O/IRN/11/2006	IRN06-11	639	602	0	94.21	5.79	ME-SA	PanAsia-2
9	O/IRN/29/2006	IRN06-29	639	602	0	94.21	5.79	ME-SA	PanAsia-2
10	O/IRN/43/2006	IRN06-43	639	602	0	94.21	5.79	ME-SA	PanAsia-2

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/31/2009	IRN09-31	639	596	0	93.27	6.73	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/TUR/264/2009* (FMDI)	TUR09-AK	639	593	0	92.80	7.20	ME-SA	PanAsia-2$^{\text{SAN-09}}$
3	O/IRN/88/2009	IRN09-88	639	592	0	92.64	7.36	ME-SA	PanAsia-2$^{\text{ANT-10}}$
4	O/PAK/16/2010	PAK10-16	639	592	0	92.64	7.36	ME-SA	PanAsia-2$^{\text{PUN-10}}$
5	O/TUR/257/2008* (FMDI)	TUR08-AD	639	592	0	92.64	7.36	ME-SA	PanAsia-2$^{\text{TER-08}}$
6	O/IRN/18/2010	IRN10-18	639	591	0	92.49	7.51	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/IRN/8/2005	IRN05-08	639	590	0	92.33	7.67	ME-SA	PanAsia-2
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	584	0	91.39	8.61	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	578	0	90.45	9.55	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	576	0	90.14	9.86	ME-SA	Ind-2001b

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: IRN/1/2014
Batch No: WRLFMD/2014/00006
Sender Ref: IR-92 A-22
Location: Qom, Iran
Date collected: 01/01/2014
Date received by WRLFMD: 05/02/2014
Date received for sequencing: 18/03/2014
Species: Bovine
Material used: BTy1 13/03/2014
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: unnamed
Sequence filename: IRN14-01.SEQ
Date sequence last updated: 19/03/2014
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: 58 days
Sequencing time: 17 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/IRN/31/2013	IRN13-31	639	638	0	99.84	0.16	ME-SA	unnamed
2	O/PAK/40/2012	PAK12-40	639	630	0	98.59	1.41	ME-SA	unnamed
3	O/PAK/41/2012	PAK12-41	639	630	0	98.59	1.41	ME-SA	unnamed
4	O/PAK/51/2012	PAK12-51	639	630	0	98.59	1.41	ME-SA	unnamed
5	O/PAK/22/2013	PAK13-22	639	628	0	98.28	1.72	ME-SA	unnamed
6	O/PAK/53/2012	PAK12-53	639	627	0	98.12	1.88	ME-SA	unnamed
7	O/PAK/55/2012	PAK12-55	639	626	0	97.97	2.03	ME-SA	unnamed
8	O/PAK/31/2007	PAK07-31	639	602	0	94.21	5.79	ME-SA	PanAsia-2
9	O/PAK 23.1 8 (EF494490)	PAK06-AI	627	590	0	94.10	5.90	ME-SA	PanAsia-2
10	O/IRN/11/2006	IRN06-11	639	601	0	94.05	5.95	ME-SA	PanAsia-2

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/31/2009	IRN09-31	639	595	0	93.11	6.89	ME-SA	PanAsia-2$^{\text{FAR-09}}$
2	O/TUR/264/2009* (FMDI)	TUR09-AK	639	594	0	92.96	7.04	ME-SA	PanAsia-2$^{\text{SAN-09}}$
3	O/TUR/257/2008* (FMDI)	TUR08-AD	639	593	0	92.80	7.20	ME-SA	PanAsia-2$^{\text{TER-08}}$
4	O/IRN/88/2009	IRN09-88	639	591	0	92.49	7.51	ME-SA	PanAsia-2$^{\text{ANT-10}}$
5	O/PAK/16/2010	PAK10-16	639	591	0	92.49	7.51	ME-SA	PanAsia-2$^{\text{PUN-10}}$
6	O/IRN/18/2010	IRN10-18	639	590	0	92.33	7.67	ME-SA	PanAsia-2$^{\text{BAL-09}}$
7	O/IRN/8/2005	IRN05-08	639	589	0	92.18	7.82	ME-SA	PanAsia-2
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	583	0	91.24	8.76	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	577	0	90.30	9.70	ME-SA	Ind-2001a
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	575	1	90.13	9.87	ME-SA	Irn-2001

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

Report on FMDV O in Iran in 2013-2014

Batch: WRLFMD/2014/00006

◆ 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