

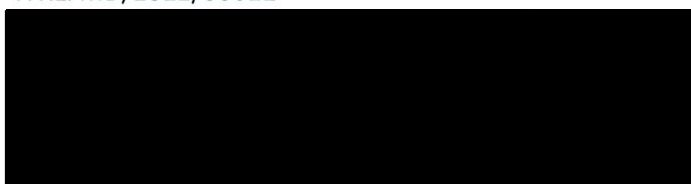


INSTITUTE FOR ANIMAL HEALTH
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00012

Sender Details:



Date Received: 24th February 2012

Country of Origin: IRAN

Date Reported: 4th April 2012

Dear Dr Darab Abdollahi

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Results Approved By: 

Official Stamp: 

Date: 4/4/12

A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: gareth.shimmon@iah.ac.uk. IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

Genotyping Report

Report Date for this Batch: 3 April 2012

FMDV type O

Country: Iran

Period: 2011

No. of samples: 7

BATCH: WRLFMD/2012/00012



The contents of this report are copyright and should not be reproduced without permission

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/61/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-4 (33050033)	
Location: Unknown, Iran	Topotype: ME-SA
Date collected: 09/11/2011	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-61.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/70/2011	IRN11-70	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/78/2011	IRN11-78	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{ANT-10}
3	O/AFG/59/2010	AFG10-59	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
4	O/AFG/61/2010	AFG10-61	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
5	O/AFG/89/2010	AFG10-89	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
6	O/BAR/17/2011	BAR11-17	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
7	O/IRN/14/2010	IRN10-14	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
8	O/IRN/30/2010	IRN10-30	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
9	O/IRN/4/2010	IRN10-04	639	629	0	98.44	1.56	ME-SA	PanAsia-2 ^{ANT-10}
10	O/IRN/88/2010	IRN10-88	639	629	0	98.44	1.56	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	627	0	98.12	1.88	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	598	0	93.58	6.42	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	598	0	93.58	6.42	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	596	0	93.27	6.73	ME-SA	PanAsia-2 ^{TER-08}
5	O/IRN/18/2010	IRN10-18	639	591	0	92.49	7.51	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	591	0	92.49	7.51	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	588	0	92.02	7.98	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	579	0	90.61	9.39	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	567	0	88.73	11.27	ME-SA	Ind-2001a
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	566	1	88.71	11.29	ME-SA	Iran-2001

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/62/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-8 (160040062)	
Location: Kerman, Iran	Topotype: ME-SA
Date collected: 12/11/2011	Genotype/strain: PanAsia-2 ^{FAR-09}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-62.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/77/2011	IRN11-77	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/31/2009	IRN09-31	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/60/2009	IRN09-60	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/71/2011	IRN11-71	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
5	O/SAU/1/2009	SAU09-01	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
6	O/SAU/2/2009	SAU09-02	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/41/2009	IRN09-41	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
8	O/IRN/42/2009	IRN09-42	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
9	O/IRN/43/2009	IRN09-43	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
10	O/IRN/49/2009	IRN09-49	639	636	0	99.53	0.47	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	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/18/2010	IRN10-18	639	609	0	95.31	4.69	ME-SA	PanAsia-2 ^{BAL-09}
3	O/IRN/8/2005	IRN05-08	639	609	0	95.31	4.69	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	609	0	95.31	4.69	ME-SA	PanAsia-2 ^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	605	0	94.68	5.32	ME-SA	PanAsia-2 ^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	602	0	94.21	5.79	ME-SA	PanAsia-2 ^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	597	0	93.43	6.57	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	579	0	90.61	9.39	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/66/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-16 (14230082)	
Location: Fars, Iran	Topotype: ME-SA
Date collected: 19/11/2011	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-66.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Sheep	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/UAE/1/2011	UAE11-01	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/194/2010	IRN10194	639	633	0	99.06	0.94	ME-SA	PanAsia-2 ^{ANT-10}
3	O/IRN/217/2010	IRN10217	639	632	0	98.90	1.10	ME-SA	PanAsia-2 ^{ANT-10}
4	O/IRN/83/2010	IRN10-83	639	631	0	98.75	1.25	ME-SA	PanAsia-2 ^{ANT-10}
5	O/AFG/110/2010	AFG10110	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
6	O/AFG/121/2010	AFG10121	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
7	O/AFG/142/2010	AFG10142	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
8	O/AFG/164/2010	AFG10164	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
9	O/IRN/209/2010	IRN10209	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
10	O/IRN/62/2010	IRN10-62	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	625	0	97.81	2.19	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	598	0	93.58	6.42	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	598	0	93.58	6.42	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	594	0	92.96	7.04	ME-SA	PanAsia-2 ^{TER-08}
5	O/IRN/18/2010	IRN10-18	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	588	0	92.02	7.98	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/KUW/3/97 (DQ164904)	KUW97-03	639	566	0	88.58	11.42	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	566	0	88.58	11.42	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/70/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-15 (34170315)	
Location: Esfahan, Iran	Topotype: ME-SA
Date collected: 23/11/2011	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-70.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Sheep	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/61/2011	IRN11-61	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/78/2011	IRN11-78	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{ANT-10}
3	O/AFG/59/2010	AFG10-59	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
4	O/AFG/61/2010	AFG10-61	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
5	O/AFG/89/2010	AFG10-89	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
6	O/BAR/17/2011	BAR11-17	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
7	O/IRN/14/2010	IRN10-14	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
8	O/IRN/30/2010	IRN10-30	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
9	O/IRN/4/2010	IRN10-04	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
10	O/IRN/88/2010	IRN10-88	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	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	599	0	93.74	6.26	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	599	0	93.74	6.26	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/IRN/18/2010	IRN10-18	639	592	0	92.64	7.36	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	592	0	92.64	7.36	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	589	0	92.18	7.82	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	580	0	90.77	9.23	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	568	0	88.89	11.11	ME-SA	Ind-2001a
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	567	1	88.87	11.13	ME-SA	Iran-2001

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O WRLFMD Ref No: IRN/71/2011 Batch No: WRLFMD/2012/00012 Sender Ref: IR-90-18 (33120014) Location: Esfahan, Iran Date collected: 28/11/2011 Date received by WRLFMD: 24/02/2012 Date received for sequencing: 29/03/2012 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 03/04/2012 Reported by: N.J. Knowles Checked by: V. Mioulet Topotype: ME-SA Genotype/strain: PanAsia-2 ^{FAR-09} Sequence filename: IRN11-71.SEQ Date sequence last updated: 02/04/2012 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3240 Min. no. of nt for comparison: 600 Total turn-around time: 39 days Sequencing time: 5 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/62/2011	IRN11-62	639	637	0	99.69	0.31	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/77/2011	IRN11-77	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/31/2009	IRN09-31	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/60/2009	IRN09-60	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
5	O/SAU/1/2009	SAU09-01	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
6	O/SAU/2/2009	SAU09-02	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/41/2009	IRN09-41	639	634	0	99.22	0.78	ME-SA	PanAsia-2 ^{FAR-09}
8	O/IRN/42/2009	IRN09-42	639	634	0	99.22	0.78	ME-SA	PanAsia-2 ^{FAR-09}
9	O/IRN/43/2009	IRN09-43	639	634	0	99.22	0.78	ME-SA	PanAsia-2 ^{FAR-09}
10	O/IRN/49/2009	IRN09-49	639	634	0	99.22	0.78	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	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
2	O/TUR/257/2008* (FMDI)	TUR08-AD	639	609	0	95.31	4.69	ME-SA	PanAsia-2 ^{TER-08}
3	O/IRN/18/2010	IRN10-18	639	607	0	94.99	5.01	ME-SA	PanAsia-2 ^{BAL-09}
4	O/IRN/8/2005	IRN05-08	639	607	0	94.99	5.01	ME-SA	PanAsia-2
5	O/PAK/16/2010	PAK10-16	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	600	0	93.90	6.10	ME-SA	PanAsia-2 ^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	595	0	93.11	6.89	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	579	0	90.61	9.39	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/77/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-37 (32060045)	
Location: Makou, West Azerbaijan, Iran	Topotype: ME-SA
Date collected: 27/12/2011	Genotype/strain: PanAsia-2 ^{FAR-09}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-77.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/62/2011	IRN11-62	639	638	0	99.84	0.16	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/31/2009	IRN09-31	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/60/2009	IRN09-60	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/71/2011	IRN11-71	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
5	O/SAU/1/2009	SAU09-01	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
6	O/SAU/2/2009	SAU09-02	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/41/2009	IRN09-41	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
8	O/IRN/42/2009	IRN09-42	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
9	O/IRN/43/2009	IRN09-43	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{FAR-09}
10	O/IRN/49/2009	IRN09-49	639	635	0	99.37	0.63	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	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{FAR-09}
2	O/IRN/8/2005	IRN05-08	639	610	0	95.46	4.54	ME-SA	PanAsia-2
3	O/IRN/18/2010	IRN10-18	639	608	0	95.15	4.85	ME-SA	PanAsia-2 ^{BAL-09}
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	608	0	95.15	4.85	ME-SA	PanAsia-2 ^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	604	0	94.52	5.48	ME-SA	PanAsia-2 ^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	603	0	94.37	5.63	ME-SA	PanAsia-2 ^{SAN-09}
7	O/IRN/88/2009	IRN09-88	639	601	0	94.05	5.95	ME-SA	PanAsia-2 ^{ANT-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	598	0	93.58	6.42	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	580	0	90.77	9.23	ME-SA	Ind-2001a
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	578	0	90.45	9.55	ME-SA	Ind-2001b

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

Page 1 of 1

Serotype: O	Report date: 03/04/2012
WRLFMD Ref No: IRN/78/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00012	Checked by: V. Mioulet
Sender Ref: IR-90-21 (33020989)	
Location: Esfahan, Esfahan, Iran	Topotype: ME-SA
Date collected: 31/12/2011	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 24/02/2012	Sequence filename: IRN11-78.SEQ
Date received for sequencing: 29/03/2012	Date sequence last updated: 02/04/2012
Species: Sheep	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3240
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 39 days
	Sequencing time: 5 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/61/2011	IRN11-61	639	636	0	99.53	0.47	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/70/2011	IRN11-70	639	635	0	99.37	0.63	ME-SA	PanAsia-2 ^{ANT-10}
3	O/AFG/59/2010	AFG10-59	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
4	O/AFG/61/2010	AFG10-61	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
5	O/AFG/89/2010	AFG10-89	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
6	O/BAR/17/2011	BAR11-17	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
7	O/IRN/14/2010	IRN10-14	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
8	O/IRN/30/2010	IRN10-30	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
9	O/IRN/4/2010	IRN10-04	639	628	0	98.28	1.72	ME-SA	PanAsia-2 ^{ANT-10}
10	O/IRN/88/2010	IRN10-88	639	628	0	98.28	1.72	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	626	0	97.97	2.03	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	597	0	93.43	6.57	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	597	0	93.43	6.57	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	595	0	93.11	6.89	ME-SA	PanAsia-2 ^{TER-08}
5	O/IRN/18/2010	IRN10-18	639	590	0	92.33	7.67	ME-SA	PanAsia-2 ^{BAL-09}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	590	0	92.33	7.67	ME-SA	PanAsia-2 ^{SAN-09}
7	O/PAK/16/2010	PAK10-16	639	587	0	91.86	8.14	ME-SA	PanAsia-2 ^{PUN-10}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	580	0	90.77	9.23	ME-SA	PanAsia
9	O/KUW/3/97 (DQ164904)	KUW97-03	639	568	0	88.89	11.11	ME-SA	Ind-2001a
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	567	1	88.87	11.13	ME-SA	Iran-2001

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

© Institute for Animal Health (not to be reproduced without permission)

Report on FMDV O in Iran in 2011

Batch: WRLFMD/2012/00012

◆ indicates viruses in this batch

Software: MEGA 5.0

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

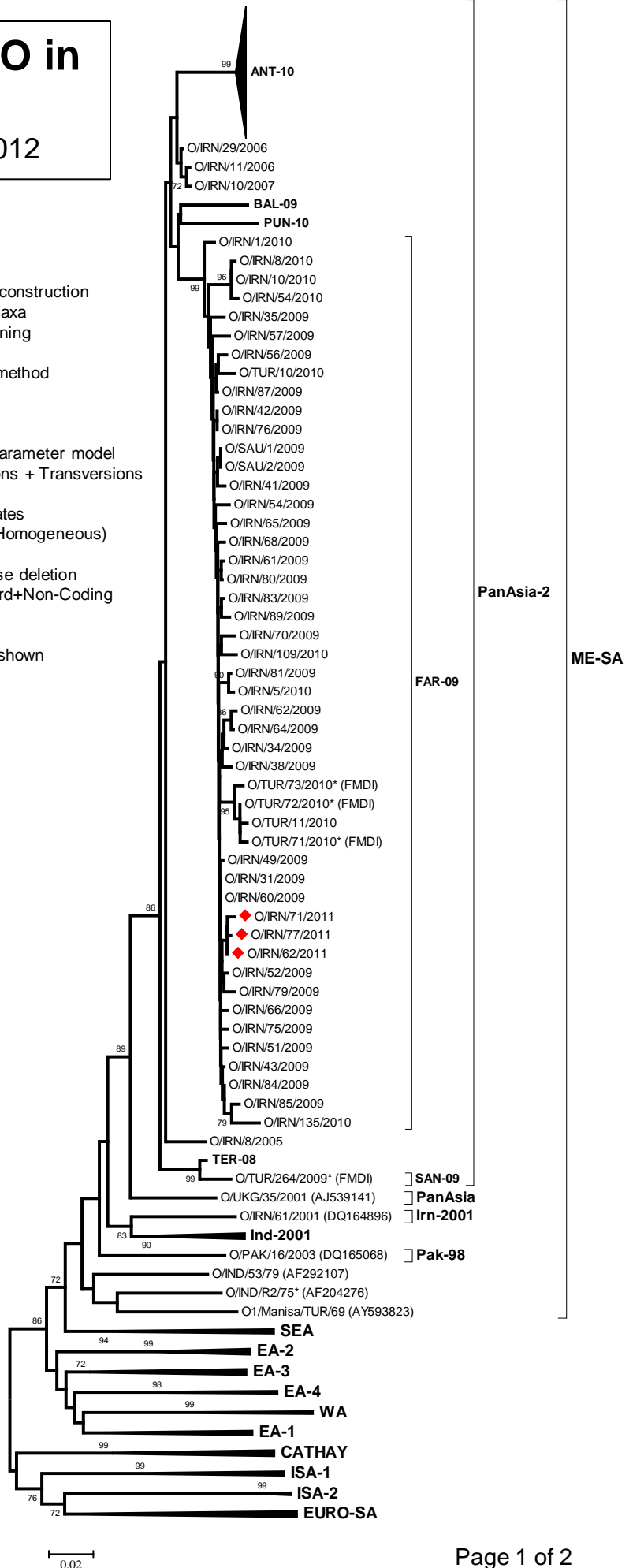
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 03 April 2012

© Institute for Animal Health

(not to be reproduced without permission)



0.02

Report on FMDV O in Iran in 2011

Batch: WRLFMD/2012/00012

◆ indicates viruses in this batch

Software: MEGA 5.0

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, 03 April 2012

© Institute for Animal Health

(not to be reproduced without permission)

