

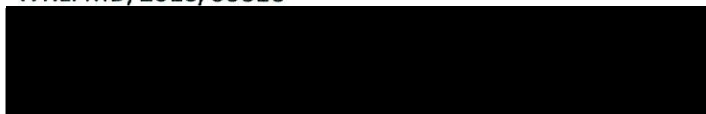


**INSTITUTE FOR ANIMAL HEALTH**  
Director: Professor Martin W. Shirley, PhD  
PIRBRIGHT LABORATORY  
Ash Road,  
Pirbright,  
Surrey,  
GU24 0NF  
Intn Tel: 00 44 1483 232441  
Tel: 01483 232441 Fax: 01483 232621

## **FMD Sequencing Report**

**Lab Reference WRL Batch Number:** WRLFMD/2010/00016

**Sender Details:**



**Date Received:** 28<sup>th</sup> April 2010

**Country of Origin:** United Arab Emirates

**Date Reported:** 21<sup>st</sup> May 2010

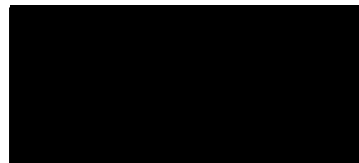
Dear Dr. Habil Ulrich Wernery,

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:** 21/05/2010



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: [elizabeth.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.ac.uk))

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

## Genotyping Report

Date: 20 May 2010

FMDV type O

Country: United Arab Emirates

Period: 2010

No. of isolates: 4

BATCH: WRLFMD/2010/00016



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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: UAE/1/2010 Batch No: WRLFMD/2010/00016 Sender Ref: D 758/10 Location: Al Ain Wildlife Park, United Arab Emirates Date collected: 29/03/2010 Date received by WRLFMD: 28/04/2010 Date received for sequencing: 10/05/2010 Species: Arabian Gazelle ( <i>Gazella arabica</i> ) Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 20/05/2010 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: UAE10-01.SEQ Date sequence last updated: 19/05/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2408 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 10 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/4/2010	UAE10-04	639	638	0	99.84	0.16	ME-SA	PanAsia-2
2	O/UAE/2/2010	UAE10-02	639	637	0	99.69	0.31	ME-SA	PanAsia-2
3	O/UAE/3/2010	UAE10-03	639	637	0	99.69	0.31	ME-SA	PanAsia-2
4	O/IRN/20/2010	IRN10-20	639	636	0	99.53	0.47	ME-SA	PanAsia-2
5	O/IRN/33/2010	IRN10-33	639	636	0	99.53	0.47	ME-SA	PanAsia-2
6	O/IRN/34/2010	IRN10-34	639	636	0	99.53	0.47	ME-SA	PanAsia-2
7	O/IRN/37/2010	IRN10-37	639	636	0	99.53	0.47	ME-SA	PanAsia-2
8	O/IRN/38/2010	IRN10-38	639	636	0	99.53	0.47	ME-SA	PanAsia-2
9	O/IRN/39/2010	IRN10-39	639	636	0	99.53	0.47	ME-SA	PanAsia-2
10	O/IRN/15/2010	IRN10-15	639	635	0	99.37	0.63	ME-SA	PanAsia-2
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/8/2005	IRN05-08	639	606	0	94.84	5.16	ME-SA	PanAsia-2
2	O/UKG/35/2001 (AJ539141)	UKG01-35	639	585	0	91.55	8.45	ME-SA	PanAsia
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	571	0	89.36	10.64	ME-SA	Ind-2001b
4	O/IRN/61/2001 (DQ164896)	IRN01-61	638	570	1	89.34	10.66	ME-SA	Irn-2001
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	570	0	89.20	10.80	ME-SA	Pak-98
6	O/UAE/4/2008	UAE08-04	636	567	0	89.15	10.85	ME-SA	Ind-2001c
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	569	0	89.05	10.95	ME-SA	Ind-2001a
8	O/IND/53/79 (AF292107)	IND79A53	639	566	0	88.58	11.42	ME-SA	unnamed
9	O/IND/R2/75* (AF204276)	IND75--A	639	566	0	88.58	11.42	ME-SA	unnamed
10	O/BHU/3/2009	BHU09-03	639	565	0	88.42	11.58	ME-SA	Ind-2001d

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: UAE/2/2010 Batch No: WRLFMD/2010/00016 Sender Ref: D 759/10 Location: Al Ain Wildlife Park, United Arab Emirates Date collected: 29/03/2010 Date received by WRLFMD: 28/04/2010 Date received for sequencing: 10/05/2010 Species: Arabian Gazelle ( <i>Gazella arabica</i> ) Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 20/05/2010 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: UAE10-02.SEQ Date sequence last updated: 19/05/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2408 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 10 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/3/2010	UAE10-03	639	639	0	100.00	0.00	ME-SA	PanAsia-2
2	O/UAE/4/2010	UAE10-04	639	638	0	99.84	0.16	ME-SA	PanAsia-2
3	O/UAE/1/2010	UAE10-01	639	637	0	99.69	0.31	ME-SA	PanAsia-2
4	O/IRN/20/2010	IRN10-20	639	636	0	99.53	0.47	ME-SA	PanAsia-2
5	O/IRN/33/2010	IRN10-33	639	636	0	99.53	0.47	ME-SA	PanAsia-2
6	O/IRN/34/2010	IRN10-34	639	636	0	99.53	0.47	ME-SA	PanAsia-2
7	O/IRN/37/2010	IRN10-37	639	636	0	99.53	0.47	ME-SA	PanAsia-2
8	O/IRN/38/2010	IRN10-38	639	636	0	99.53	0.47	ME-SA	PanAsia-2
9	O/IRN/39/2010	IRN10-39	639	636	0	99.53	0.47	ME-SA	PanAsia-2
10	O/IRN/15/2010	IRN10-15	639	635	0	99.37	0.63	ME-SA	PanAsia-2
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/8/2005	IRN05-08	639	604	0	94.52	5.48	ME-SA	PanAsia-2
2	O/UKG/35/2001 (AJ539141)	UKG01-35	639	583	0	91.24	8.76	ME-SA	PanAsia
3	O/IRN/61/2001 (DQ164896)	IRN01-61	638	570	1	89.34	10.66	ME-SA	Irn-2001
4	O/OMN/7/2001 (DQ164941)	OMN01-07	639	569	0	89.05	10.95	ME-SA	Ind-2001b
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	568	0	88.89	11.11	ME-SA	Pak-98
6	O/UAE/4/2008	UAE08-04	636	565	0	88.84	11.16	ME-SA	Ind-2001c
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	567	0	88.73	11.27	ME-SA	Ind-2001a
8	O/IND/R2/75* (AF204276)	IND75--A	639	566	0	88.58	11.42	ME-SA	unnamed
9	O/IND/53/79 (AF292107)	IND79A53	639	564	0	88.26	11.74	ME-SA	unnamed
10	O/BHU/3/2009	BHU09-03	639	563	0	88.11	11.89	ME-SA	Ind-2001d

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: UAE/3/2010 Batch No: WRLFMD/2010/00016 Sender Ref: D 761/10 Location: Al Ain Wildlife Park, United Arab Emirates Date collected: 29/03/2010 Date received by WRLFMD: 28/04/2010 Date received for sequencing: 10/05/2010 Species: Arabian Gazelle ( <i>Gazella arabica</i> ) Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 20/05/2010 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: UAE10-03.SEQ Date sequence last updated: 19/05/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2408 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 10 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/2/2010	UAE10-02	639	639	0	100.00	0.00	ME-SA	PanAsia-2
2	O/UAE/4/2010	UAE10-04	639	638	0	99.84	0.16	ME-SA	PanAsia-2
3	O/UAE/1/2010	UAE10-01	639	637	0	99.69	0.31	ME-SA	PanAsia-2
4	O/IRN/20/2010	IRN10-20	639	636	0	99.53	0.47	ME-SA	PanAsia-2
5	O/IRN/33/2010	IRN10-33	639	636	0	99.53	0.47	ME-SA	PanAsia-2
6	O/IRN/34/2010	IRN10-34	639	636	0	99.53	0.47	ME-SA	PanAsia-2
7	O/IRN/37/2010	IRN10-37	639	636	0	99.53	0.47	ME-SA	PanAsia-2
8	O/IRN/38/2010	IRN10-38	639	636	0	99.53	0.47	ME-SA	PanAsia-2
9	O/IRN/39/2010	IRN10-39	639	636	0	99.53	0.47	ME-SA	PanAsia-2
10	O/IRN/15/2010	IRN10-15	639	635	0	99.37	0.63	ME-SA	PanAsia-2
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/8/2005	IRN05-08	639	604	0	94.52	5.48	ME-SA	PanAsia-2
2	O/UKG/35/2001 (AJ539141)	UKG01-35	639	583	0	91.24	8.76	ME-SA	PanAsia
3	O/IRN/61/2001 (DQ164896)	IRN01-61	638	570	1	89.34	10.66	ME-SA	Irn-2001
4	O/OMN/7/2001 (DQ164941)	OMN01-07	639	569	0	89.05	10.95	ME-SA	Ind-2001b
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	568	0	88.89	11.11	ME-SA	Pak-98
6	O/UAE/4/2008	UAE08-04	636	565	0	88.84	11.16	ME-SA	Ind-2001c
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	567	0	88.73	11.27	ME-SA	Ind-2001a
8	O/IND/R2/75* (AF204276)	IND75--A	639	566	0	88.58	11.42	ME-SA	unnamed
9	O/IND/53/79 (AF292107)	IND79A53	639	564	0	88.26	11.74	ME-SA	unnamed
10	O/BHU/3/2009	BHU09-03	639	563	0	88.11	11.89	ME-SA	Ind-2001d

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O WRLFMD Ref No: UAE/4/2010 Batch No: WRLFMD/2010/00016 Sender Ref: D 762/10 Location: Al Ain Wildlife Park, United Arab Emirates Date collected: 29/03/2010 Date received by WRLFMD: 28/04/2010 Date received for sequencing: 10/05/2010 Species: Arabian Gazelle ( <i>Gazella arabica</i> ) Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 20/05/2010 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ME-SA Genotype/strain: PanAsia-2 Sequence filename: UAE10-04.SEQ Date sequence last updated: 19/05/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 2408 Min. no. of nt for comparison: 300 Total turn-around time: 22 days Sequencing time: 10 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/1/2010	UAE10-01	639	638	0	99.84	0.16	ME-SA	PanAsia-2
2	O/UAE/2/2010	UAE10-02	639	638	0	99.84	0.16	ME-SA	PanAsia-2
3	O/UAE/3/2010	UAE10-03	639	638	0	99.84	0.16	ME-SA	PanAsia-2
4	O/IRN/20/2010	IRN10-20	639	637	0	99.69	0.31	ME-SA	PanAsia-2
5	O/IRN/33/2010	IRN10-33	639	637	0	99.69	0.31	ME-SA	PanAsia-2
6	O/IRN/34/2010	IRN10-34	639	637	0	99.69	0.31	ME-SA	PanAsia-2
7	O/IRN/37/2010	IRN10-37	639	637	0	99.69	0.31	ME-SA	PanAsia-2
8	O/IRN/38/2010	IRN10-38	639	637	0	99.69	0.31	ME-SA	PanAsia-2
9	O/IRN/39/2010	IRN10-39	639	637	0	99.69	0.31	ME-SA	PanAsia-2
10	O/IRN/15/2010	IRN10-15	639	636	0	99.53	0.47	ME-SA	PanAsia-2
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/IRN/8/2005	IRN05-08	639	605	0	94.68	5.32	ME-SA	PanAsia-2
2	O/UKG/35/2001 (AJ539141)	UKG01-35	639	584	0	91.39	8.61	ME-SA	PanAsia
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	570	0	89.20	10.80	ME-SA	Ind-2001b
4	O/IRN/61/2001 (DQ164896)	IRN01-61	638	569	1	89.18	10.82	ME-SA	Irn-2001
5	O/PAK/16/2003 (DQ165068)	PAK03-16	639	569	0	89.05	10.95	ME-SA	Pak-98
6	O/UAE/4/2008	UAE08-04	636	566	0	88.99	11.01	ME-SA	Ind-2001c
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	568	0	88.89	11.11	ME-SA	Ind-2001a
8	O/IND/53/79 (AF292107)	IND79A53	639	565	0	88.42	11.58	ME-SA	unnamed
9	O/IND/R2/75* (AF204276)	IND75--A	639	565	0	88.42	11.58	ME-SA	unnamed
10	O/BHU/3/2009	BHU09-03	639	564	0	88.26	11.74	ME-SA	Ind-2001d

nt, nucleotides

\*, not a WRLFMD reference number

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# Report on FMDV O in the United Arab Emirates in 2010

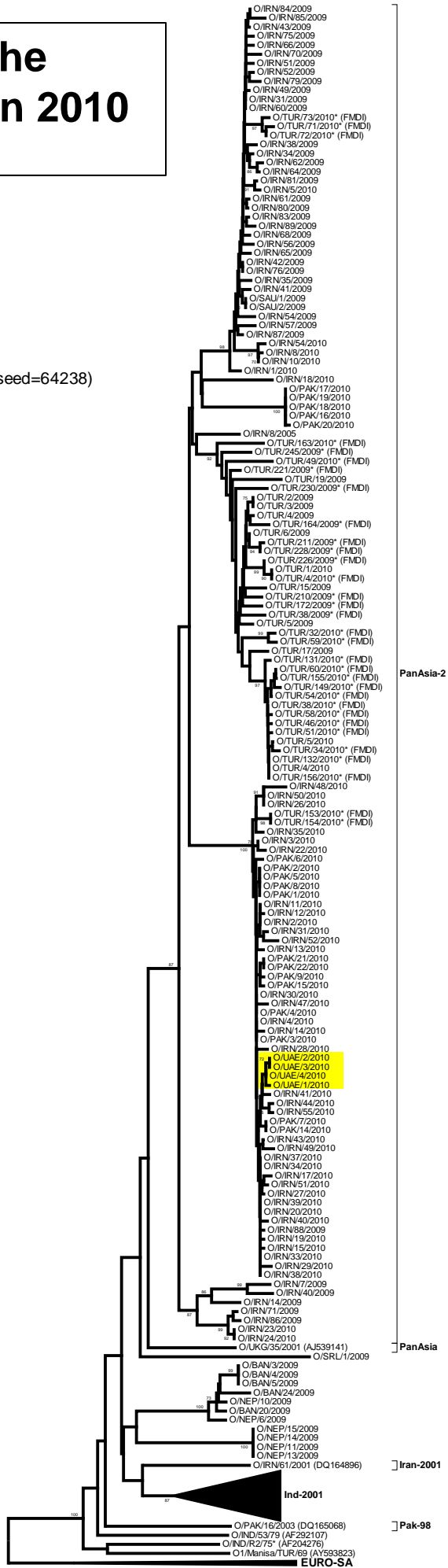
Batch: WRLFMD/2010/00016

Software: MEGA 4.0  
 No. of Taxa : 212  
 Data File : n:\evd\meg\db\fmvd\o\IRN2010b.meg  
 Data Title : O Iran 2010  
 Data Type : Nucleotide (Coding)  
 Analysis : Phylogeny reconstruction  
 Tree Inference : =====  
 ->Method : Neighbor-Joining  
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)  
 Include Sites : =====  
 ->Gaps/Missing Data : Pairwise Deletion  
 ->Codon Positions : 1st+2nd+3rd+Noncoding  
 Substitution Model : =====  
 ->Model : Nucleotide: Kimura 2-parameter  
 ->Substitutions to Include : d: Transitions + Transversions  
 ->Pattern among Lineages : Same (Homogeneous)  
 ->Rates among sites : Uniform rates  
 No. of Sites : 639  
 No Of Bootstrap Reps = 1000  
 Only bootstrap values of 70% and above are shown

\* , not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 20 May 2010

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0.02