

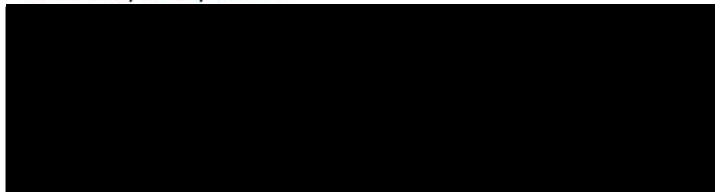


INSTITUTE FOR ANIMAL HEALTH
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath
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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00034

Sender Details:



Date Received: 16th November 2012
Country of Origin: VIETNAM, SOCIALIST REPUBLIC OF
Date Reported: 18th December 2012

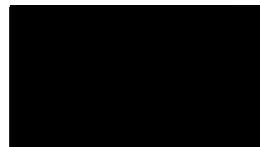
Dear Dr Nguyen Xuan Binh,

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/>

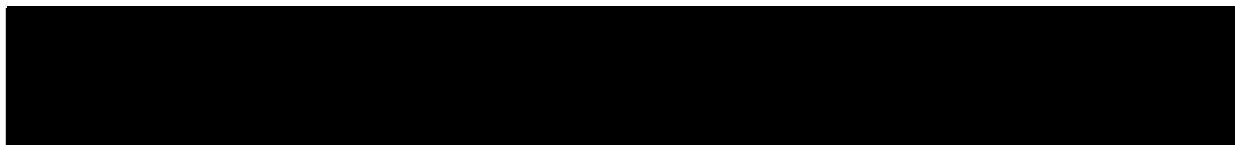
Results Approved By:



Official Stamp:



Date:



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: trish.ryder@p.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: 10 December 2012

FMDV type O

Country: Vietnam

Period: 2012

No. of samples: 3

BATCH: WRLFMD/2012/00034



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 07/12/2012
WRLFMD Ref No: VIT/14/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00034	Checked by: D.P. King
Sender Ref: 1/12-3910	
Location: Dong Nai, Vietnam	Topotype: ME-SA
Date collected: 16/04/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 16/11/2012	Sequence filename: VIT12-14.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 07/12/2012
Species: Pig	No. of Nt determined: 639
Material used: BHK1 BTy1 20/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3415
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 21 days
	Sequencing time: 4 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/VIT/7/2010	VIT10-07	639	635	0	99.37	0.63	ME-SA	PanAsia
2	O/VIT/8/2010	VIT10-08	639	635	0	99.37	0.63	ME-SA	PanAsia
3	O/CAM/2/2010	CAM10-02	639	634	0	99.22	0.78	ME-SA	PanAsia
4	O/CAM/4/2010	CAM10-04	639	634	0	99.22	0.78	ME-SA	PanAsia
5	O/CAM/5/2010	CAM10-05	639	634	0	99.22	0.78	ME-SA	PanAsia
6	O/CAM/8/2010	CAM10-08	639	634	0	99.22	0.78	ME-SA	PanAsia
7	O/VIT/10/2010	VIT10-10	639	634	0	99.22	0.78	ME-SA	PanAsia
8	O/VIT/11/2010	VIT10-11	639	634	0	99.22	0.78	ME-SA	PanAsia
9	O/VIT/13/2010	VIT10-13	639	634	0	99.22	0.78	ME-SA	PanAsia
10	O/VIT/14/2010	VIT10-14	639	634	0	99.22	0.78	ME-SA	PanAsia
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/UKG/35/2001 (AJ539141)	UKG01-35	639	597	0	93.43	6.57	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	584	0	91.39	8.61	ME-SA	Ind-2001a
3	O/IRN/8/2005	IRN05-08	639	583	0	91.24	8.76	ME-SA	PanAsia-2
4	O/IRN/31/2009	IRN09-31	639	582	0	91.08	8.92	ME-SA	PanAsia-2 ^{FAR-09}
5	O/OMN/7/2001 (DQ164941)	OMN01-07	639	580	0	90.77	9.23	ME-SA	Ind-2001b
6	O/IRN/18/2010	IRN10-18	639	579	0	90.61	9.39	ME-SA	PanAsia-2 ^{BAL-09}
7	O/BHU/3/2009	BHU09-03	639	577	0	90.30	9.70	ME-SA	Ind-2001d
8	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
9	O/IRN/88/2009	IRN09-88	639	574	0	89.83	10.17	ME-SA	PanAsia-2 ^{ANT-10}
10	O/PAK/16/2010	PAK10-16	639	574	0	89.83	10.17	ME-SA	PanAsia-2 ^{PUN-10}

nt, nucleotides

*, not a WRLFMD reference number

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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 07/12/2012
WRLFMD Ref No: VIT/21/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00034	Checked by: D.P. King
Sender Ref: 2/12-11771	
Location: Ben Tre, Vietnam	Topotype: ME-SA
Date collected: 05/11/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 16/11/2012	Sequence filename: VIT12-21.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 07/12/2012
Species: Pig	No. of Nt determined: 639
Material used: ZZ-TRI BTy1 20/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3415
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 21 days
	Sequencing time: 4 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/VIT/22/2012	VIT12-22	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/VIT/32/2011	VIT11-32	639	631	0	98.75	1.25	ME-SA	PanAsia
3	O/VIT/3/2011	VIT11-03	639	629	0	98.44	1.56	ME-SA	PanAsia
4	O/VIT/16/2011	VIT11-16	639	628	0	98.28	1.72	ME-SA	PanAsia
5	O/VIT/3/2010	VIT10-03	639	628	0	98.28	1.72	ME-SA	PanAsia
6	O/VIT/5/2011	VIT11-05	639	628	0	98.28	1.72	ME-SA	PanAsia
7	O/VIT/6/2011	VIT11-06	639	628	0	98.28	1.72	ME-SA	PanAsia
8	O/VIT/7/2010	VIT10-07	639	628	0	98.28	1.72	ME-SA	PanAsia
9	O/VIT/8/2010	VIT10-08	639	628	0	98.28	1.72	ME-SA	PanAsia
10	O/CAM/2/2010	CAM10-02	639	627	0	98.12	1.88	ME-SA	PanAsia
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/UKG/35/2001 (AJ539141)	UKG01-35	639	592	0	92.64	7.36	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	580	0	90.77	9.23	ME-SA	Ind-2001a
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	578	0	90.45	9.55	ME-SA	Ind-2001b
4	O/IRN/8/2005	IRN05-08	639	577	0	90.30	9.70	ME-SA	PanAsia-2
5	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 ^{FAR-09}
6	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
7	O/IRN/18/2010	IRN10-18	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{BAL-09}
8	O/BHU/3/2009	BHU09-03	639	572	0	89.51	10.49	ME-SA	Ind-2001d
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	571	0	89.36	10.64	ME-SA	Pak-98
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{TER-08}

nt, nucleotides

*, not a WRLFMD reference number

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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 07/12/2012
WRLFMD Ref No: VIT/22/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00034	Checked by: D.P. King
Sender Ref: 3/12-11771	
Location: Ben Tre, Vietnam	Topotype: ME-SA
Date collected: 05/11/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 16/11/2012	Sequence filename: VIT12-22.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 07/12/2012
Species: Pig	No. of Nt determined: 639
Material used: BTy1 20/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3415
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 21 days
	Sequencing time: 4 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/VIT/21/2012	VIT12-21	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/VIT/32/2011	VIT11-32	639	631	0	98.75	1.25	ME-SA	PanAsia
3	O/VIT/3/2011	VIT11-03	639	629	0	98.44	1.56	ME-SA	PanAsia
4	O/VIT/16/2011	VIT11-16	639	628	0	98.28	1.72	ME-SA	PanAsia
5	O/VIT/3/2010	VIT10-03	639	628	0	98.28	1.72	ME-SA	PanAsia
6	O/VIT/5/2011	VIT11-05	639	628	0	98.28	1.72	ME-SA	PanAsia
7	O/VIT/6/2011	VIT11-06	639	628	0	98.28	1.72	ME-SA	PanAsia
8	O/VIT/7/2010	VIT10-07	639	628	0	98.28	1.72	ME-SA	PanAsia
9	O/VIT/8/2010	VIT10-08	639	628	0	98.28	1.72	ME-SA	PanAsia
10	O/CAM/2/2010	CAM10-02	639	627	0	98.12	1.88	ME-SA	PanAsia
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/UKG/35/2001 (AJ539141)	UKG01-35	639	592	0	92.64	7.36	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	580	0	90.77	9.23	ME-SA	Ind-2001a
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	578	0	90.45	9.55	ME-SA	Ind-2001b
4	O/IRN/8/2005	IRN05-08	639	577	0	90.30	9.70	ME-SA	PanAsia-2
5	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 ^{FAR-09}
6	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
7	O/IRN/18/2010	IRN10-18	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{BAL-09}
8	O/BHU/3/2009	BHU09-03	639	572	0	89.51	10.49	ME-SA	Ind-2001d
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	571	0	89.36	10.64	ME-SA	Pak-98
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{TER-08}

nt, nucleotides

*, not a WRLFMD reference number

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Report on FMDV O in Vietnam in 2012

Batch: WRLFMD/2012/00034

◆ indicates viruses in this batch

Software: MEGA 5.1

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, 10 December 2012

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