WRLFMD

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FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2011/00035
Sender Details: [redacted]

Date Received: 28th July 2011
Country of Origin: Cambodia
Date Reported: 30th August 2011

Dear Wilai Linchongsubongkoch,

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: [redacted]

Official Stamp: [redacted]

Date: 30/8/11

[redacted]

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: elizabeth.wilson@bbsrc.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: 25 August 2011

FMDV type O
Country: Cambodia
Period: 2010
No. of samples: 2

BATCH: WRLFMD/2011/00035

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: CAM/6/2010
Batch No: WRLFMD/2011/00035
Sender Ref: CAM 7/10 R1 B1
Location: Siem Reap, Siem Reap, Cambodia
Date collected: 17/09/2010
Date received by WRLFMD: 28/07/2011
Date received for sequencing: 05/08/2011
Species: Cattle
Material used: LK1 BHK1 BTy1
Region sequenced: VP1
RT-PCR primers: O-1C244F/EUR-2B52R
O-1C272F/EUR-2B52R

Report date: 25/08/2011
Reported by: N.J. Knowles
Checked by: D.P. King

Topotype: ME-SA
Genotype/strain: PanAsia
Sequence filename: CAM10-06.SEQ
Date sequence last updated: 09/08/2011
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3088
Min. no. of nt for comparison: 600
Total turn-around time: 28 days
Sequencing time: 20 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/CAM/1/2010	CAM10-01	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/CAM/3/2010	CAM10-03	639	639	0	100.00	0.00	ME-SA	PanAsia
3	O/CAM/2/2010	CAM10-02	639	638	0	99.84	0.16	ME-SA	PanAsia
4	O/VIT/13/2010	VIT10-13	639	638	0	99.84	0.16	ME-SA	PanAsia
5	O/VIT/7/2010	VIT10-07	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/VIT/8/2010	VIT10-08	639	637	0	99.69	0.31	ME-SA	PanAsia
7	O/CAM/4/2010	CAM10-04	639	636	0	99.53	0.47	ME-SA	PanAsia
8	O/CAM/5/2010	CAM10-05	639	636	0	99.53	0.47	ME-SA	PanAsia
9	O/CAM/8/2010	CAM10-08	639	636	0	99.53	0.47	ME-SA	PanAsia
10	O/VIT/10/2010	VIT10-10	639	636	0	99.53	0.47	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	601	0	94.05	5.95	ME-SA	PanAsia
2	O/IRN/31/2009	IRN09-31	639	586	0	91.71	8.29	ME-SA	PanAsia-2$^{\text{FAR-09}}$
3	O/IRN/8/2005	IRN05-08	639	586	0	91.71	8.29	ME-SA	PanAsia-2
4	O/KUW/3/97 (DQ164904)	KUW97-03	639	585	0	91.55	8.45	ME-SA	Ind-2001a
5	O/IRN/18/2010	IRN10-18	639	583	0	91.24	8.76	ME-SA	PanAsia-2$^{\text{BAL-09}}$
6	O/OMN/7/2001 (DQ164941)	OMN01-07	639	579	0	90.61	9.39	ME-SA	Ind-2001b
7	O/BHU/3/2009	BHU09-03	639	577	0	90.30	9.70	ME-SA	Ind-2001d
8	O/IRN/88/2009	IRN09-88	639	577	0	90.30	9.70	ME-SA	PanAsia-2$^{\text{ANT-10}}$
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	577	0	90.30	9.70	ME-SA	PanAsia-2$^{\text{TER-08}}$
10	O/UAE/4/2008	UAE08-04	636	573	0	90.09	9.91	ME-SA	Ind-2001c

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: 25/08/2011
WRLFMD Ref No: CAM/8/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00035	Checked by: D.P. King
Sender Ref: CAM 18/10 R1 B1	
Location: Mukh Kampol, Kandal, Cambodia	Topotype: ME-SA
Date collected: 22/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 28/07/2011	Sequence filename: CAM10-08.SEQ
Date received for sequencing: 05/08/2011	Date sequence last updated: 09/08/2011
Species: Cattle	No. of Nt determined: 639
Material used: LK1 BHK1 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3088
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 28 days
	Sequencing time: 20 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/CAM/5/2010	CAM10-05	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/VIT/7/2010	VIT10-07	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/VIT/8/2010	VIT10-08	639	638	0	99.84	0.16	ME-SA	PanAsia
4	O/CAM/2/2010	CAM10-02	639	637	0	99.69	0.31	ME-SA	PanAsia
5	O/CAM/4/2010	CAM10-04	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/VIT/10/2010	VIT10-10	639	637	0	99.69	0.31	ME-SA	PanAsia
7	O/VIT/11/2010	VIT10-11	639	637	0	99.69	0.31	ME-SA	PanAsia
8	O/VIT/13/2010	VIT10-13	639	637	0	99.69	0.31	ME-SA	PanAsia
9	O/VIT/14/2010	VIT10-14	639	637	0	99.69	0.31	ME-SA	PanAsia
10	O/VIT/3/2010	VIT10-03	639	637	0	99.69	0.31	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	600	0	93.90	6.10	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	586	0	91.71	8.29	ME-SA	Ind-2001a
3	O/IRN/31/2009	IRN09-31	639	585	0	91.55	8.45	ME-SA	PanAsia-2$^{\text{FAR-09}}$
4	O/IRN/8/2005	IRN05-08	639	585	0	91.55	8.45	ME-SA	PanAsia-2
5	O/IRN/18/2010	IRN10-18	639	582	0	91.08	8.92	ME-SA	PanAsia-2$^{\text{BAL-09}}$
6	O/OMN/7/2001 (DQ164941)	OMN01-07	639	580	0	90.77	9.23	ME-SA	Ind-2001b
7	O/BHU/3/2009	BHU09-03	639	578	0	90.45	9.55	ME-SA	Ind-2001d
8	O/UAE/4/2008	UAE08-04	636	574	0	90.25	9.75	ME-SA	Ind-2001c
9	O/IRN/88/2009	IRN09-88	639	576	0	90.14	9.86	ME-SA	PanAsia-2$^{\text{ANT-10}}$
10	O/PAK/16/2010	PAK10-16	639	576	0	90.14	9.86	ME-SA	PanAsia-2$^{\text{PUN-10}}$

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

Report on FMDV O in Cambodia in 2010

Batch: WRLFMD/2011/00035

◆ 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, 25 August 2011