

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

## Genotyping Report

Report Date for this Batch: 2 July 2013

FMDV type O

Country: Cambodia

Period: 2012

No. of samples: 2

BATCH: WRLFMD/2013/00013



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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	Report date: 02/07/2013
WRLFMD Ref No: CAM/1/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00013	Checked by: D.P. King
Sender Ref: CAM 2/12R1B3	
Location: Kratie province, Cambodia	Topotype: ME-SA
Date collected: 24/09/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 17/06/2013	Sequence filename: CAM12-01.SEQ
Date received for sequencing: 21/06/2013	Date sequence last updated: 02/07/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 19/06/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3665
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 15 days
	Sequencing time: 11 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/2/2012	CAM12-02	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/CAM/1/2010	CAM10-01	639	626	0	97.97	2.03	ME-SA	PanAsia
3	O/CAM/3/2010	CAM10-03	639	626	0	97.97	2.03	ME-SA	PanAsia
4	O/CAM/6/2010	CAM10-06	639	626	0	97.97	2.03	ME-SA	PanAsia
5	O/CAM/2/2010	CAM10-02	639	625	0	97.81	2.19	ME-SA	PanAsia
6	O/VIT/13/2010	VIT10-13	639	625	0	97.81	2.19	ME-SA	PanAsia
7	O/VIT/7/2010	VIT10-07	639	624	0	97.65	2.35	ME-SA	PanAsia
8	O/VIT/8/2010	VIT10-08	639	624	0	97.65	2.35	ME-SA	PanAsia
9	O/CAM/4/2010	CAM10-04	639	623	0	97.50	2.50	ME-SA	PanAsia
10	O/CAM/5/2010	CAM10-05	639	623	0	97.50	2.50	ME-SA	PanAsia
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/UKG/35/2001 (AJ539141)	UKG01-35	639	594	0	92.96	7.04	ME-SA	PanAsia
2	O/IRN/8/2005	IRN05-08	639	582	0	91.08	8.92	ME-SA	PanAsia-2
3	O/IRN/31/2009	IRN09-31	639	581	0	90.92	9.08	ME-SA	PanAsia-2 <sup>FAR-09</sup>
4	O/IRN/18/2010	IRN10-18	639	578	0	90.45	9.55	ME-SA	PanAsia-2 <sup>BAL-09</sup>
5	O/KUW/3/97 (DQ164904)	KUW97-03	639	578	0	90.45	9.55	ME-SA	Ind-2001a
6	O/IRN/88/2009	IRN09-88	639	576	0	90.14	9.86	ME-SA	PanAsia-2 <sup>ANT-10</sup>
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	576	0	90.14	9.86	ME-SA	PanAsia-2 <sup>TER-08</sup>
8	O/BHU/3/2009	BHU09-03	639	575	0	89.98	10.02	ME-SA	Ind-2001d
9	O/PAK/16/2010	PAK10-16	639	574	0	89.83	10.17	ME-SA	PanAsia-2 <sup>PUN-10</sup>
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	573	0	89.67	10.33	ME-SA	Ind-2001b

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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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	Report date: 02/07/2013
WRLFMD Ref No: CAM/2/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00013	Checked by: D.P. King
Sender Ref: CAM 4/12R1B3	
Location: Kratie province, Cambodia	Topotype: ME-SA
Date collected: 24/09/2012	Genotype/strain: PanAsia
Date received by WRLFMD: 17/06/2013	Sequence filename: CAM12-02.SEQ
Date received for sequencing: 21/06/2013	Date sequence last updated: 02/07/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 19/06/2013	No. of ambiguities: 0
Region sequenced: VPI	Gene length: 639
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3	O/CAM/3/2010	CAM10-03	639	626	0	97.97	2.03	ME-SA	PanAsia
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# Report on FMDV O in Cambodia in 2012

Batch: WRLFMD/2013/00013

◆ indicates viruses in this batch

Software: MEGA 5.2

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 : 645

No Of Bootstrap Reps = 1000

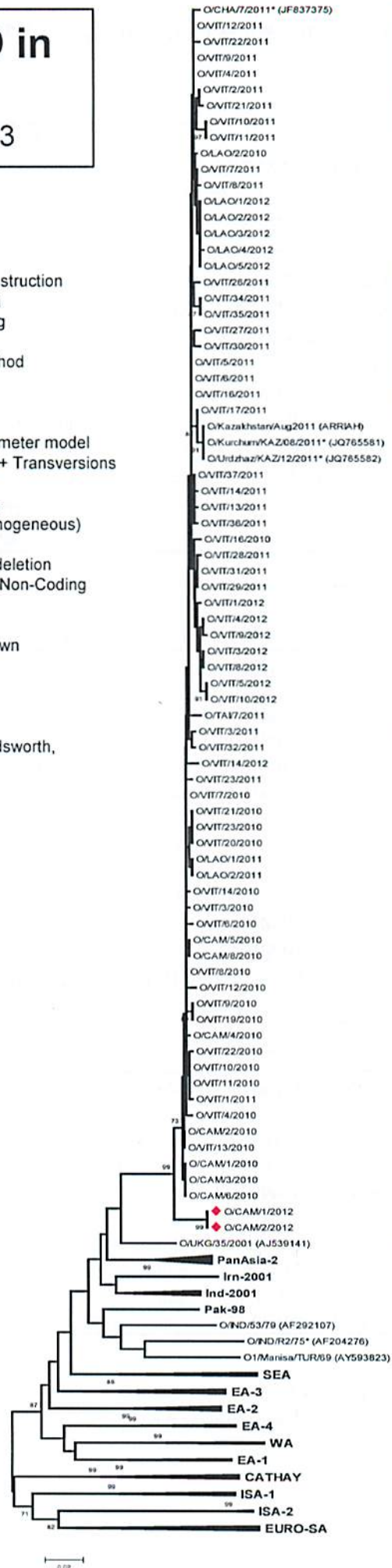
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles, K. Bachanek-Bankowska & J. Wadsworth,  
02 July 2013

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PanAsia

ME-SA

0.02