

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

Genotyping Report

Report Date for this Batch: 7 August 2014

FMDV type O

Country: Cambodia

Period: 2013

No. of samples: 3

BATCH: WRLFMD/2014/000024



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O WRLFMD Ref No: CAM/1/2013 Batch No: WRLFMD/2014/00024 Sender Ref: CAM 7/13 R1B3 Location: Kampong Speu Province, Cambodia Date collected: 19/09/2013 Date received by WRLFMD: 19/06/2014 Date received for sequencing: 01/08/2014 Species: Cattle Material used: BTy1 29/07/2014 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 07/08/2014 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: PanAsia Sequence filename: CAM13-01.SEQ Date sequence last updated: 05/08/2014 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3936 Min. no. of nt for comparison: 600 Total turn-around time: 49 days Sequencing time: 6 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/20/2013	VIT13-20	639	638	0	99.84	0.16	ME-SA	PanAsia
2	O/VIT/45/2013	VIT13-45	639	637	0	99.69	0.31	ME-SA	PanAsia
3	O/LAO/1/2011	LAO11-01	639	621	0	97.18	2.82	ME-SA	PanAsia
4	O/LAO/2/2011	LAO11-02	639	621	0	97.18	2.82	ME-SA	PanAsia
5	O/VIT/19/2010	VIT10-19	639	621	0	97.18	2.82	ME-SA	PanAsia
6	O/VIT/22/2010	VIT10-22	639	621	0	97.18	2.82	ME-SA	PanAsia
7	O/VIT/7/2010	VIT10-07	639	621	0	97.18	2.82	ME-SA	PanAsia
8	O/VIT/8/2010	VIT10-08	639	621	0	97.18	2.82	ME-SA	PanAsia
9	O/VIT/9/2010	VIT10-09	639	621	0	97.18	2.82	ME-SA	PanAsia
10	O/CAM/2/2010	CAM10-02	639	620	0	97.03	2.97	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	591	0	92.49	7.51	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
3	O/BHU/3/2009	BHU09-03	639	578	0	90.45	9.55	ME-SA	Ind-2001d
4	O/IRN/8/2005	IRN05-08	639	578	0	90.45	9.55	ME-SA	PanAsia-2
5	O/OMN/7/2001 (DQ164941)	OMN01-07	639	578	0	90.45	9.55	ME-SA	Ind-2001b
6	O/IRN/31/2009	IRN09-31	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{FAR-09}
7	O/IRN/18/2010	IRN10-18	639	576	0	90.14	9.86	ME-SA	PanAsia-2 ^{BAL-09}
8	O/UAE/4/2008	UAE08-04	636	569	0	89.47	10.53	ME-SA	Ind-2001c
9	O/PAK/16/2003 (DQ165068)	PAK03-16	639	571	0	89.36	10.64	ME-SA	Pak-98
10	O/IRN/88/2009	IRN09-88	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O	Report date: 07/08/2014
WRLFMD Ref No: CAM/2/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00024	Checked by: K. Bachanek-Bankowska
Sender Ref: CAM 12/13 R1B3	
Location: Svay Rieng Province, Cambodia	Topotype: ME-SA
Date collected: 19/09/2013	Genotype/strain: PanAsia
Date received by WRLFMD: 19/06/2014	Sequence filename: CAM13-02.SEQ
Date received for sequencing: 01/08/2014	Date sequence last updated: 05/08/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 29/07/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3936
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 49 days
	Sequencing time: 6 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/3/2013	CAM13-03	639	637	0	99.69	0.31	ME-SA	PanAsia
2	O/VIT/40/2013	VIT13-40	639	634	0	99.22	0.78	ME-SA	PanAsia
3	O/VIT/13/2013	VIT13-13	639	633	0	99.06	0.94	ME-SA	PanAsia
4	O/VIT/15/2013	VIT13-15	639	633	0	99.06	0.94	ME-SA	PanAsia
5	O/MOG/1/2014	MOG14-01	639	632	0	98.90	1.10	ME-SA	PanAsia
6	O/VIT/32/2013	VIT13-32	639	632	0	98.90	1.10	ME-SA	PanAsia
7	O/VIT/33/2013	VIT13-33	639	632	0	98.90	1.10	ME-SA	PanAsia
8	O/VIT/46/2013	VIT13-46	639	632	0	98.90	1.10	ME-SA	PanAsia
9	O/VIT/47/2013	VIT13-47	639	632	0	98.90	1.10	ME-SA	PanAsia
10	O/VIT/51/2013	VIT13-51	639	632	0	98.90	1.10	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	584	0	91.39	8.61	ME-SA	Ind-2001a
3	O/UAE/4/2008	UAE08-04	636	578	0	90.88	9.12	ME-SA	Ind-2001c
4	O/OMN/7/2001 (DQ164941)	OMN01-07	639	580	0	90.77	9.23	ME-SA	Ind-2001b
5	O/IRN/8/2005	IRN05-08	639	579	0	90.61	9.39	ME-SA	PanAsia-2
6	O/BHU/3/2009	BHU09-03	639	576	0	90.14	9.86	ME-SA	Ind-2001d
7	O/IRN/61/2001 (DQ164896)	IRN01-61	638	573	1	89.81	10.19	ME-SA	Irn-2001
8	O/IRN/31/2009	IRN09-31	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{FAR-09}
9	O/IRN/18/2010	IRN10-18	639	571	0	89.36	10.64	ME-SA	PanAsia-2 ^{BAL-09}
10	O/PAK/16/2003 (DQ165068)	PAK03-16	639	570	0	89.20	10.80	ME-SA	Pak-98

nt, nucleotides

*, not a WRLFMD reference number

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Batch No: WRLFMD/2014/00024	Checked by: K. Bachanek-Bankowska
Sender Ref: CAM 13/13 R1B3	
Location: Svay Rieng Province, Cambodia	Topotype: ME-SA
Date collected: 19/09/2013	Genotype/strain: PanAsia
Date received by WRLFMD: 19/06/2014	Sequence filename: CAM13-03.SEQ
Date received for sequencing: 01/08/2014	Date sequence last updated: 05/08/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 29/07/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3936
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
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1	O/CAM/2/2013	CAM13-02	639	637	0	99.69	0.31	ME-SA	PanAsia
2	O/VIT/40/2013	VIT13-40	639	636	0	99.53	0.47	ME-SA	PanAsia
3	O/VIT/13/2013	VIT13-13	639	635	0	99.37	0.63	ME-SA	PanAsia
4	O/VIT/15/2013	VIT13-15	639	635	0	99.37	0.63	ME-SA	PanAsia
5	O/VIT/46/2013	VIT13-46	639	634	0	99.22	0.78	ME-SA	PanAsia
6	O/VIT/47/2013	VIT13-47	639	634	0	99.22	0.78	ME-SA	PanAsia
7	O/VIT/51/2013	VIT13-51	639	634	0	99.22	0.78	ME-SA	PanAsia
8	O/VIT/11/2013	VIT13-11	639	633	0	99.06	0.94	ME-SA	PanAsia
9	O/VIT/12/2013	VIT13-12	639	633	0	99.06	0.94	ME-SA	PanAsia
10	O/VIT/36/2013	VIT13-36	639	633	0	99.06	0.94	ME-SA	PanAsia
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
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2	O/KUW/3/97 (DQ164904)	KUW97-03	639	586	0	91.71	8.29	ME-SA	Ind-2001a
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	582	0	91.08	8.92	ME-SA	Ind-2001b
4	O/IRN/8/2005	IRN05-08	639	581	0	90.92	9.08	ME-SA	PanAsia-2
5	O/UAE/4/2008	UAE08-04	636	576	0	90.57	9.43	ME-SA	Ind-2001c
6	O/BHU/3/2009	BHU09-03	639	578	0	90.45	9.55	ME-SA	Ind-2001d
7	O/IRN/61/2001 (DQ164896)	IRN01-61	638	575	1	90.13	9.87	ME-SA	Irn-2001
8	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 ^{FAR-09}
9	O/IRN/18/2010	IRN10-18	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{BAL-09}
10	O/PAK/16/2010	PAK10-16	639	572	0	89.51	10.49	ME-SA	PanAsia-2 ^{PUN-10}

nt, nucleotides

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Assembled with Report Generator v4.3

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Report on FMDV O in Cambodia in 2013

Batch: WRLFMD/2014/00024

◆ indicates viruses in this batch

Software: MEGA 6.06

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

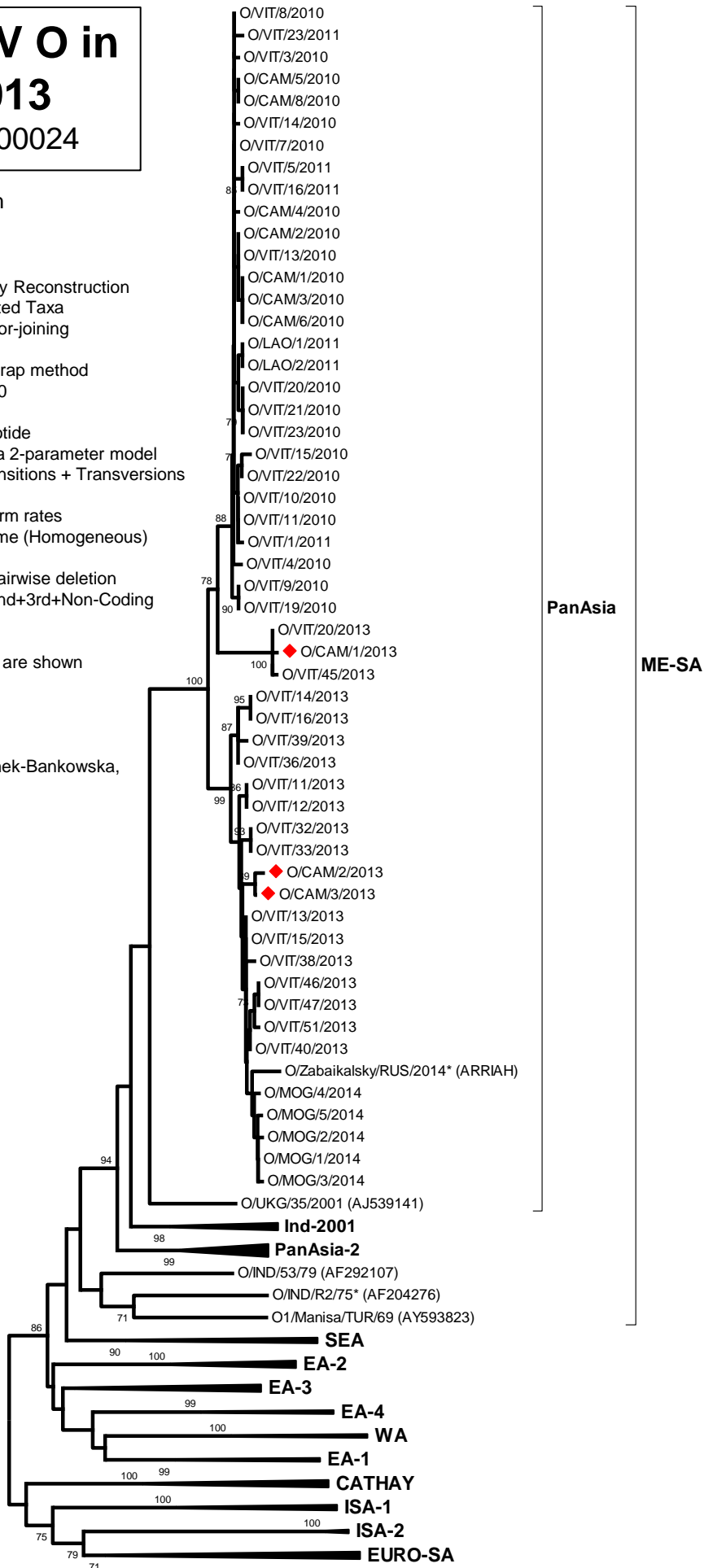
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
07 August 2014

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PanAsia

ME-SA

0.02