

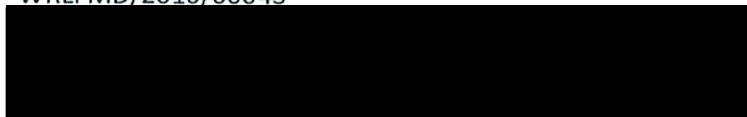


INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00043

Sender Details:



Date Received: 25th November 2010

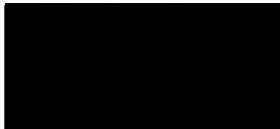
Country of Origin: Cambodia

Date Reported: 5th January 2011

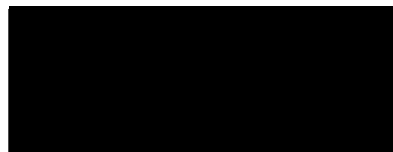
Dear Dr. Linchongsubongkoch,

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:



Official Stamp:



Date: 6/1/11



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)

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

Genotyping Report

Report Date for this Batch: 21 December 2010

FMDV type O

Country: Cambodia

Period: 2010

No. of isolates: 5

BATCH: WRLFMD/2010/00043



The contents of this report are copyright and should not be reproduced without permission

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 21/12/2010
WRLFMD Ref No: CAM/1/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00043	Checked by: D.P. King
Sender Ref: CAM 7/10 R1 B1	
Location: Siem Reap, Siem Reap, Cambodia	Topotype: ME-SA
Date collected: 17/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 25/11/2010	Sequence filename: CAM10-01.SEQ
Date received for sequencing: 19/12/2010	Date sequence last updated: 21/12/2010
Species: Cattle	No. of Nt determined: 639
Material used: LK2 BHK1 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2544
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 2 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/3/2010	CAM10-03	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/CAM/2/2010	CAM10-02	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/VIT/13/2010	VIT10-13	639	638	0	99.84	0.16	ME-SA	PanAsia
4	O/VIT/7/2010	VIT10-07	639	637	0	99.69	0.31	ME-SA	PanAsia
5	O/VIT/8/2010	VIT10-08	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/CAM/4/2010	CAM10-04	639	636	0	99.53	0.47	ME-SA	PanAsia
7	O/CAM/5/2010	CAM10-05	639	636	0	99.53	0.47	ME-SA	PanAsia
8	O/VIT/10/2010	VIT10-10	639	636	0	99.53	0.47	ME-SA	PanAsia
9	O/VIT/11/2010	VIT10-11	639	636	0	99.53	0.47	ME-SA	PanAsia
10	O/VIT/3/2010	VIT10-03	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 ^{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 ^{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 ^{ANT-10}
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{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 v3.11

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 21/12/2010
WRLFMD Ref No: CAM/2/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00043	Checked by: D.P. King
Sender Ref: Cam 8/10 R1 B1	
Location: Siem Reap, Siem Reap, Cambodia	Topotype: ME-SA
Date collected: 17/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 25/11/2010	Sequence filename: CAM10-02.SEQ
Date received for sequencing: 19/12/2010	Date sequence last updated: 21/12/2010
Species: Cattle	No. of Nt determined: 639
Material used: LK2 BHK1 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2544
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 2 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/13/2010	VIT10-13	639	639	0	100.00	0.00	ME-SA	PanAsia
2	O/CAM/1/2010	CAM10-01	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/CAM/3/2010	CAM10-03	639	638	0	99.84	0.16	ME-SA	PanAsia
4	O/VIT/7/2010	VIT10-07	639	638	0	99.84	0.16	ME-SA	PanAsia
5	O/VIT/8/2010	VIT10-08	639	638	0	99.84	0.16	ME-SA	PanAsia
6	O/CAM/4/2010	CAM10-04	639	637	0	99.69	0.31	ME-SA	PanAsia
7	O/CAM/5/2010	CAM10-05	639	637	0	99.69	0.31	ME-SA	PanAsia
8	O/VIT/10/2010	VIT10-10	639	637	0	99.69	0.31	ME-SA	PanAsia
9	O/VIT/11/2010	VIT10-11	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	602	0	94.21	5.79	ME-SA	PanAsia
2	O/IRN/31/2009	IRN09-31	639	587	0	91.86	8.14	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	587	0	91.86	8.14	ME-SA	PanAsia-2
4	O/KUW/3/97 (DQ164904)	KUW97-03	639	586	0	91.71	8.29	ME-SA	Ind-2001a
5	O/IRN/18/2010	IRN10-18	639	584	0	91.39	8.61	ME-SA	PanAsia-2 ^{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/IRN/88/2009	IRN09-88	639	578	0	90.45	9.55	ME-SA	PanAsia-2 ^{ANT-10}
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	578	0	90.45	9.55	ME-SA	PanAsia-2 ^{TER-08}
10	O/UAE/4/2008	UAE08-04	636	574	0	90.25	9.75	ME-SA	Ind-2001c

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 21/12/2010
WRLFMD Ref No: CAM/3/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00043	Checked by: D.P. King
Sender Ref: CAM 9/10 R1 B1	
Location: Siem Reap, Siem Reap, Cambodia	Topotype: ME-SA
Date collected: 17/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 25/11/2010	Sequence filename: CAM10-03.SEQ
Date received for sequencing: 19/12/2010	Date sequence last updated: 21/12/2010
Species: Not Known	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: 2544
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 2 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/2/2010	CAM10-02	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/VIT/13/2010	VIT10-13	639	638	0	99.84	0.16	ME-SA	PanAsia
4	O/VIT/7/2010	VIT10-07	639	637	0	99.69	0.31	ME-SA	PanAsia
5	O/VIT/8/2010	VIT10-08	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/CAM/4/2010	CAM10-04	639	636	0	99.53	0.47	ME-SA	PanAsia
7	O/CAM/5/2010	CAM10-05	639	636	0	99.53	0.47	ME-SA	PanAsia
8	O/VIT/10/2010	VIT10-10	639	636	0	99.53	0.47	ME-SA	PanAsia
9	O/VIT/11/2010	VIT10-11	639	636	0	99.53	0.47	ME-SA	PanAsia
10	O/VIT/3/2010	VIT10-03	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 ^{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 ^{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 ^{ANT-10}
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{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 v3.11

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 21/12/2010
WRLFMD Ref No: CAM/4/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00043	Checked by: D.P. King
Sender Ref: CAM 17/10 R1	
Location: Mokom Pol, Kandal, Cambodia	Topotype: ME-SA
Date collected: 22/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 25/11/2010	Sequence filename: CAM10-04.SEQ
Date received for sequencing: 19/12/2010	Date sequence last updated: 21/12/2010
Species: Not Known	No. of Nt determined: 639
Material used: LK1 BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2544
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 2 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	638	0	99.84	0.16	ME-SA	PanAsia
2	O/VIT/8/2010	VIT10-08	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/CAM/2/2010	CAM10-02	639	637	0	99.69	0.31	ME-SA	PanAsia
4	O/CAM/5/2010	CAM10-05	639	637	0	99.69	0.31	ME-SA	PanAsia
5	O/VIT/10/2010	VIT10-10	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/VIT/11/2010	VIT10-11	639	637	0	99.69	0.31	ME-SA	PanAsia
7	O/VIT/13/2010	VIT10-13	639	637	0	99.69	0.31	ME-SA	PanAsia
8	O/VIT/3/2010	VIT10-03	639	637	0	99.69	0.31	ME-SA	PanAsia
9	O/CAM/1/2010	CAM10-01	639	636	0	99.53	0.47	ME-SA	PanAsia
10	O/CAM/3/2010	CAM10-03	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 ^{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	586	0	91.71	8.29	ME-SA	Ind-2001a
5	O/IRN/18/2010	IRN10-18	639	583	0	91.24	8.76	ME-SA	PanAsia-2 ^{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/IRN/88/2009	IRN09-88	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{ANT-10}
9	O/PAK/16/2010	PAK10-16	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{PUN-10}
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	577	0	90.30	9.70	ME-SA	PanAsia-2 ^{TER-08}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

© Institute for Animal Health

FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 21/12/2010
WRLFMD Ref No: CAM/5/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2010/00043	Checked by: D.P. King
Sender Ref: CAM 18/10 R1 B1	
Location: Mokom Pol, Kandal, Cambodia	Topotype: ME-SA
Date collected: 22/09/2010	Genotype/strain: PanAsia
Date received by WRLFMD: 25/11/2010	Sequence filename: CAM10-05.SEQ
Date received for sequencing: 19/12/2010	Date sequence last updated: 21/12/2010
Species: Not Known	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: 2544
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 26 days
	Sequencing time: 2 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	638	0	99.84	0.16	ME-SA	PanAsia
2	O/VIT/8/2010	VIT10-08	639	638	0	99.84	0.16	ME-SA	PanAsia
3	O/CAM/2/2010	CAM10-02	639	637	0	99.69	0.31	ME-SA	PanAsia
4	O/CAM/4/2010	CAM10-04	639	637	0	99.69	0.31	ME-SA	PanAsia
5	O/VIT/10/2010	VIT10-10	639	637	0	99.69	0.31	ME-SA	PanAsia
6	O/VIT/11/2010	VIT10-11	639	637	0	99.69	0.31	ME-SA	PanAsia
7	O/VIT/13/2010	VIT10-13	639	637	0	99.69	0.31	ME-SA	PanAsia
8	O/VIT/3/2010	VIT10-03	639	637	0	99.69	0.31	ME-SA	PanAsia
9	O/CAM/1/2010	CAM10-01	639	636	0	99.53	0.47	ME-SA	PanAsia
10	O/CAM/3/2010	CAM10-03	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	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 ^{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 ^{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 ^{ANT-10}
10	O/PAK/16/2010	PAK10-16	639	576	0	90.14	9.86	ME-SA	PanAsia-2 ^{PUN-10}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

© Institute for Animal Health

Report on FMDV O in Cambodia in 2010

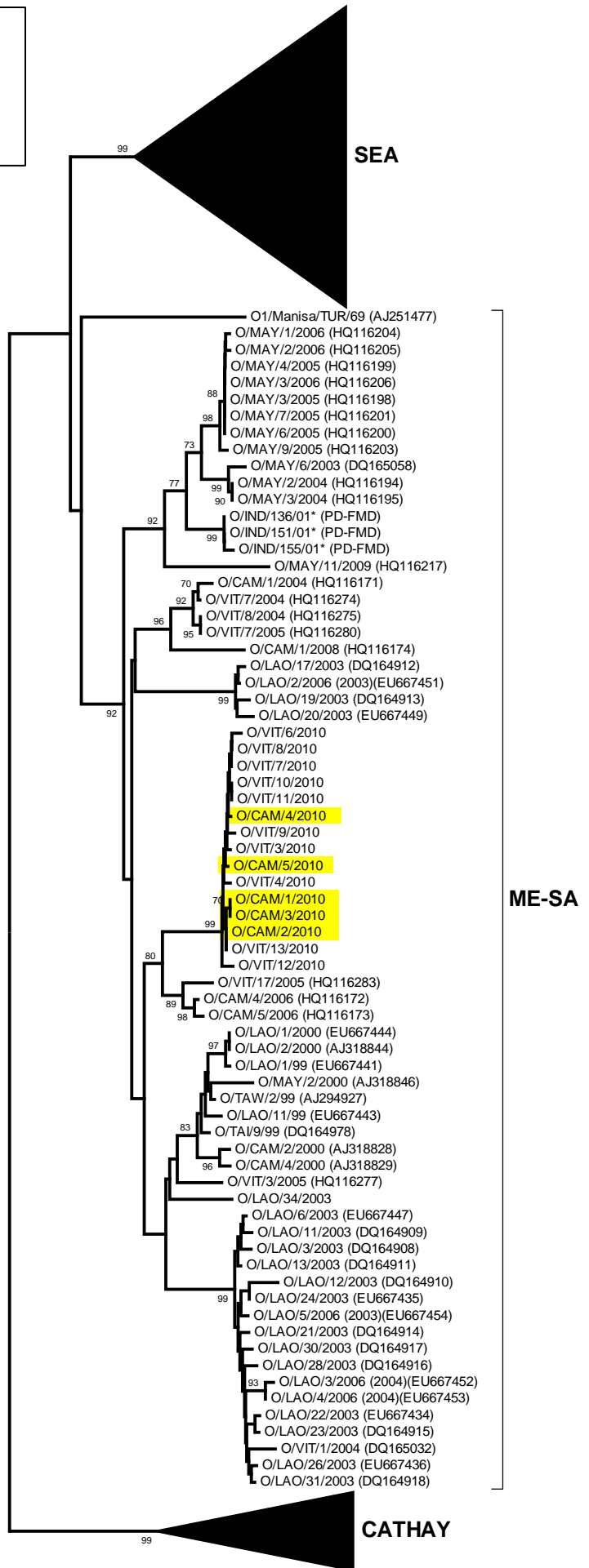
Batch: WRLFMD/2010/00043

Software: MEGA 4.0
 No. of Taxa : 254
 Data File : n:\levd\meg\db\fmv\o\HKN-TAI-CAM-2010a.meg
 Data Title : O HKN-TAI-CAM 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, 21 December 2010

© Institute for Animal Health



0.02