

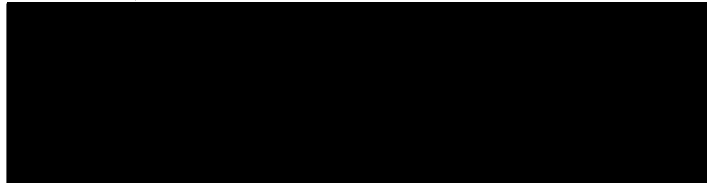


INSTITUTE FOR ANIMAL HEALTH
Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00001

Sender Details:



Date Received: 3rd January 2012
Country of Origin: Vietnam, Socialist Republic of
Date Reported: 13th January 2012

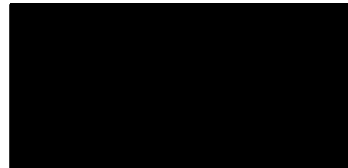
Dear Dr Ngo Thanh Long

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:

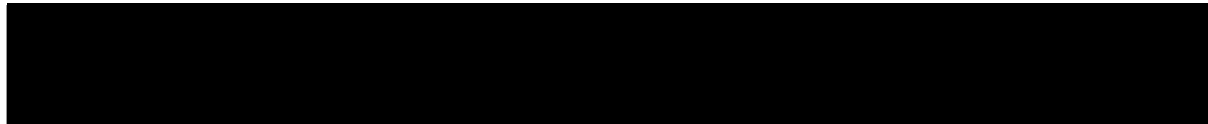


Official Stamp:



Date:

13/1/12



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: gareth.shimmon@iah.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: 11 January 2012

FMDV type O

Country: Vietnam

Period: 2008 & 2011

No. of samples: 4

BATCH: WRLFMD/2012/00001



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O	Report date: 11/01/2012
WRLFMD Ref No: VIT/9/2008	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00001	Checked by: D.P. King
Sender Ref: 08-1045 3/11/11	
Location: Ho Chi Minh City, Vietnam	Topotype: CATHAY
Date collected: 04/02/2008	Genotype/strain: unnamed
Date received by WRLFMD: 03/01/2012	Sequence filename: VIT08-09.SEQ
Date received for sequencing: 09/01/2012	Date sequence last updated: 11/01/2012
Species: Pig	No. of Nt determined: 639
Material used: BHK2 RS1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3204
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/1/2006 (HQ116284)	VIT06-01	639	622	0	97.34	2.66	CATHAY	unnamed
2	O/VIT/1/2008 (HQ116291)	VIT08-01	639	622	0	97.34	2.66	CATHAY	unnamed
3	O/VIT/2/2006 (HQ116285)	VIT06-02	639	622	0	97.34	2.66	CATHAY	unnamed
4	O/VIT/3/2006 (HQ116286)	VIT06-03	639	620	0	97.03	2.97	CATHAY	unnamed
5	O/VIT/3/2008* (TRRL)	VIT08-AB	639	618	0	96.71	3.29	CATHAY	unnamed
6	O/MAY/8/2005 (HQ116202)	MAY05-08	639	614	0	96.09	3.91	CATHAY	unnamed
7	O/VIT/2/2008* (TRRL)	VIT08-AA	639	613	0	95.93	4.07	CATHAY	unnamed
8	O/VIT/2/05* (TRRL)	VIT05-AB	639	608	0	95.15	4.85	CATHAY	unnamed
9	O/VIT/9/2005 (HQ116281)	VIT05-09	639	600	0	93.90	6.10	CATHAY	unnamed
10	O/VIT/1/2005 (HQ116276)	VIT05-01	639	599	0	93.74	6.26	CATHAY	unnamed
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/Yunlin/TAW/97 (AF308157)	TAW97--B	639	564	0	88.26	11.74	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926)	PHI96-07	639	559	0	87.48	12.52	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	637	540	2	84.77	15.23	CATHAY	unnamed
4	O/IRN/31/2009	IRN09-31	639	516	0	80.75	19.25	ME-SA	PanAsia-2 ^{FAR-09}
5	O/HKN/21/70 (AJ294911)	HKN70A21	637	514	2	80.69	19.31	CATHAY	unnamed
6	O/BHU/3/2009	BHU09-03	639	512	0	80.13	19.87	ME-SA	Ind-2001d
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	512	0	80.13	19.87	ME-SA	Ind-2001a
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	512	0	80.13	19.87	ME-SA	PanAsia
9	O/IRN/8/2005	IRN05-08	639	511	0	79.97	20.03	ME-SA	PanAsia-2
10	O/IRN/18/2010	IRN10-18	639	510	0	79.81	20.19	ME-SA	PanAsia-2 ^{BAL-09}

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: 11/01/2012
WRLFMD Ref No: VIT/10/2008	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00001	Checked by: D.P. King
Sender Ref: 11-6449 10/8/11	
Location: Long An, Vietnam	Topotype: ME-SA
Date collected: 18/07/2008	Genotype/strain: PanAsia
Date received by WRLFMD: 03/01/2012	Sequence filename: VIT08-10.SEQ
Date received for sequencing: 09/01/2012	Date sequence last updated: 11/01/2012
Species: Pig	No. of Nt determined: 639
Material used: BHK1 RS1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3204
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/12/2011	VIT11-12	639	634	0	99.22	0.78	ME-SA	PanAsia
2	O/VIT/4/2011	VIT11-04	639	634	0	99.22	0.78	ME-SA	PanAsia
3	O/VIT/9/2011	VIT11-09	639	634	0	99.22	0.78	ME-SA	PanAsia
4	O/LAO/2/2010	LAO10-02	639	633	0	99.06	0.94	ME-SA	PanAsia
5	O/VIT/16/2011	VIT11-16	639	633	0	99.06	0.94	ME-SA	PanAsia
6	O/VIT/29/2011	VIT11-29	639	633	0	99.06	0.94	ME-SA	PanAsia
7	O/VIT/31/2011	VIT11-31	639	633	0	99.06	0.94	ME-SA	PanAsia
8	O/VIT/5/2011	VIT11-05	639	633	0	99.06	0.94	ME-SA	PanAsia
9	O/VIT/6/2011	VIT11-06	639	633	0	99.06	0.94	ME-SA	PanAsia
10	O/VIT/7/2011	VIT11-07	639	633	0	99.06	0.94	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	599	0	93.74	6.26	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	587	0	91.86	8.14	ME-SA	Ind-2001a
3	O/IRN/31/2009	IRN09-31	639	586	0	91.71	8.29	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/8/2005	IRN05-08	639	586	0	91.71	8.29	ME-SA	PanAsia-2
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/TUR/257/2008* (FMDI)	TUR08-AD	639	579	0	90.61	9.39	ME-SA	PanAsia-2 ^{TER-08}
8	O/PAK/16/2010	PAK10-16	639	578	0	90.45	9.55	ME-SA	PanAsia-2 ^{PUN-10}
9	O/TUR/264/2009* (FMDI)	TUR09-AK	639	578	0	90.45	9.55	ME-SA	PanAsia-2 ^{SAN-09}
10	O/BHU/3/2009	BHU09-03	639	577	0	90.30	9.70	ME-SA	Ind-2001d

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: 11/01/2012
WRLFMD Ref No: VIT/41/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00001	Checked by: D.P. King
Sender Ref: 11-9260 28/9/11	
Location: Dong Nai, Vietnam	Topotype: ME-SA
Date collected: 28/09/2011	Genotype/strain: PanAsia
Date received by WRLFMD: 03/01/2012	Sequence filename: VIT11-41.SEQ
Date received for sequencing: 09/01/2012	Date sequence last updated: 11/01/2012
Species: Pig	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3204
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/42/2011	VIT11-42	639	638	0	99.84	0.16	ME-SA	PanAsia
2	O/VIT/16/2011	VIT11-16	639	634	0	99.22	0.78	ME-SA	PanAsia
3	O/VIT/29/2011	VIT11-29	639	634	0	99.22	0.78	ME-SA	PanAsia
4	O/VIT/31/2011	VIT11-31	639	634	0	99.22	0.78	ME-SA	PanAsia
5	O/VIT/5/2011	VIT11-05	639	634	0	99.22	0.78	ME-SA	PanAsia
6	O/VIT/6/2011	VIT11-06	639	634	0	99.22	0.78	ME-SA	PanAsia
7	O/TAI/7/2011	TAI11-07	639	633	0	99.06	0.94	ME-SA	PanAsia
8	O/VIT/12/2011	VIT11-12	639	633	0	99.06	0.94	ME-SA	PanAsia
9	O/VIT/16/2010	VIT10-16	639	633	0	99.06	0.94	ME-SA	PanAsia
10	O/VIT/28/2011	VIT11-28	639	633	0	99.06	0.94	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	596	0	93.27	6.73	ME-SA	PanAsia
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	588	0	92.02	7.98	ME-SA	Ind-2001a
3	O/IRN/31/2009	IRN09-31	639	581	0	90.92	9.08	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/8/2005	IRN05-08	639	581	0	90.92	9.08	ME-SA	PanAsia-2
5	O/OMN/7/2001 (DQ164941)	OMN01-07	639	580	0	90.77	9.23	ME-SA	Ind-2001b
6	O/BHU/3/2009	BHU09-03	639	578	0	90.45	9.55	ME-SA	Ind-2001d
7	O/IRN/18/2010	IRN10-18	639	578	0	90.45	9.55	ME-SA	PanAsia-2 ^{BAL-09}
8	O/UAE/4/2008	UAE08-04	636	573	0	90.09	9.91	ME-SA	Ind-2001c
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	574	0	89.83	10.17	ME-SA	PanAsia-2 ^{TER-08}
10	O/PAK/16/2010	PAK10-16	639	573	0	89.67	10.33	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: 11/01/2012
WRLFMD Ref No: VIT/42/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00001	Checked by: D.P. King
Sender Ref: 11-9213	
Location: Dong Nai, Vietnam	Topotype: ME-SA
Date collected: 28/09/2011	Genotype/strain: PanAsia
Date received by WRLFMD: 03/01/2012	Sequence filename: VIT11-42.SEQ
Date received for sequencing: 09/01/2012	Date sequence last updated: 11/01/2012
Species: Pig	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3204
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/41/2011	VIT11-41	639	638	0	99.84	0.16	ME-SA	PanAsia
2	O/VIT/16/2011	VIT11-16	639	635	0	99.37	0.63	ME-SA	PanAsia
3	O/VIT/29/2011	VIT11-29	639	635	0	99.37	0.63	ME-SA	PanAsia
4	O/VIT/31/2011	VIT11-31	639	635	0	99.37	0.63	ME-SA	PanAsia
5	O/VIT/5/2011	VIT11-05	639	635	0	99.37	0.63	ME-SA	PanAsia
6	O/VIT/6/2011	VIT11-06	639	635	0	99.37	0.63	ME-SA	PanAsia
7	O/VIT/12/2011	VIT11-12	639	634	0	99.22	0.78	ME-SA	PanAsia
8	O/VIT/16/2010	VIT10-16	639	634	0	99.22	0.78	ME-SA	PanAsia
9	O/VIT/28/2011	VIT11-28	639	634	0	99.22	0.78	ME-SA	PanAsia
10	O/VIT/34/2011	VIT11-34	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	587	0	91.86	8.14	ME-SA	Ind-2001a
3	O/IRN/31/2009	IRN09-31	639	582	0	91.08	8.92	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/8/2005	IRN05-08	639	582	0	91.08	8.92	ME-SA	PanAsia-2
5	O/BHU/3/2009	BHU09-03	639	579	0	90.61	9.39	ME-SA	Ind-2001d
6	O/IRN/18/2010	IRN10-18	639	579	0	90.61	9.39	ME-SA	PanAsia-2 ^{BAL-09}
7	O/OMN/7/2001 (DQ164941)	OMN01-07	639	579	0	90.61	9.39	ME-SA	Ind-2001b
8	O/UAE/4/2008	UAE08-04	636	574	0	90.25	9.75	ME-SA	Ind-2001c
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	575	0	89.98	10.02	ME-SA	PanAsia-2 ^{TER-08}
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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Report on FMDV O in Vietnam in 2008 & 2011

Batch: WRLFMD/2012/00001

◆ indicates viruses in this batch

Software: MEGA 5.0

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

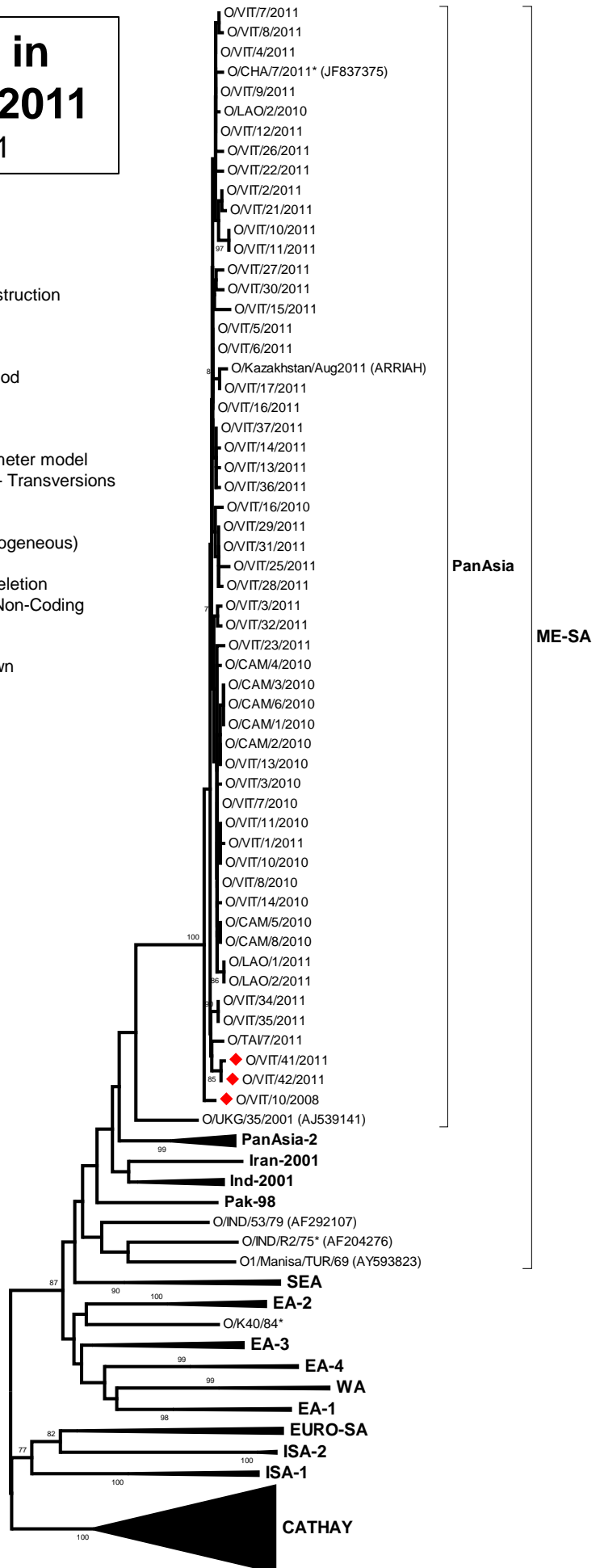
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 11 January 2012

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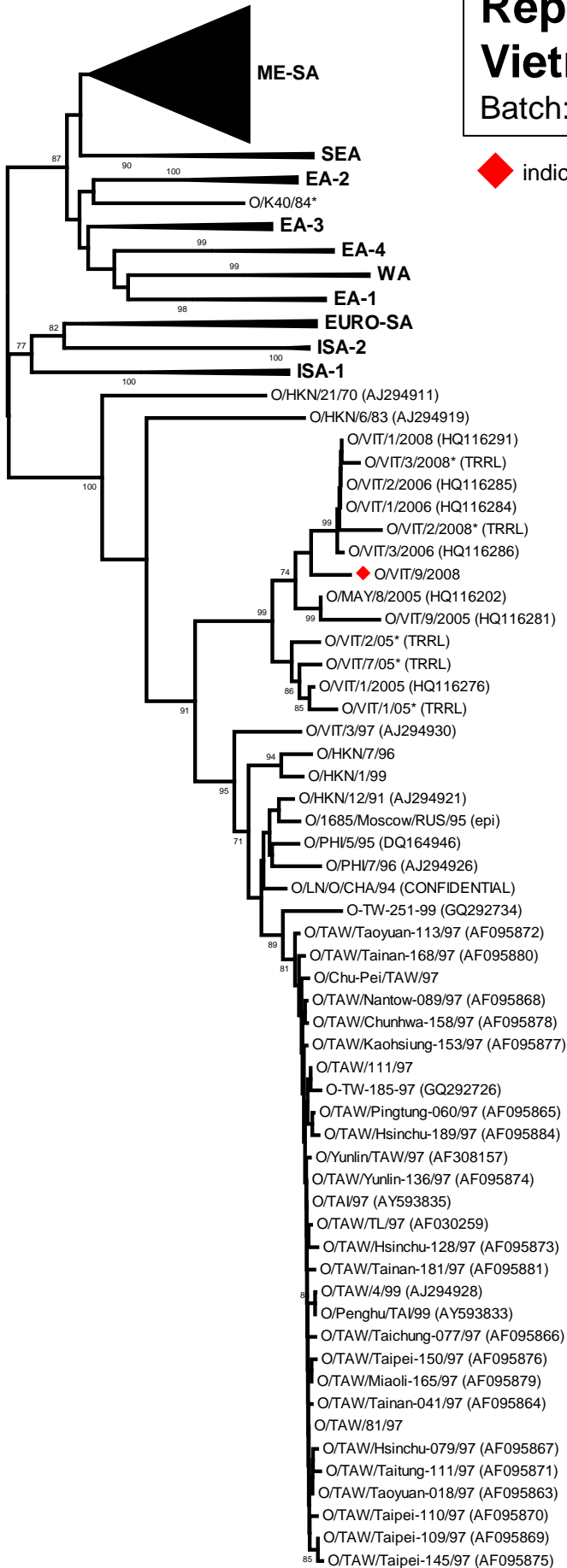
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Report on FMDV O in Vietnam in 2008 & 2011

Batch: WRLFMD/2012/00001

◆ indicates viruses in this batch



0.02