



INSTITUTE FOR ANIMAL HEALTH

Acting Director: Professor David Paton MA, VetMB, PhD, MRCVS

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Pirbright,

Surrey,

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FMD Genotyping Report

Lab Reference WRL Ref Number: VIT/NCVD-8/2010

Sender Details:

Date Received:

Country of Sample Origin:

Date Reported:

Vietnam

16th February 2011

Dear Sir,

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:

16 / 2 / 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: 16 February 2011

FMDV type O

Country: Vietnam

Period: 2010

No. of sequences: 6

VP1 sequences received from National Veterinary Research and Quarantine Service (NVRQS), Anyang, Gyeonggi 430-824, Republic of Korea, 15/02/2011



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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: 16/02/2011
WRLFMD Ref No: VIT/NCVD-8/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-8	
Location: Yen Bai province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AA.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not given	Total no. of comparisons: 2632
	Min. no. of nt for comparison: 600
	Total turn-around time: 1 days
	Sequencing time: 1 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/NCVD-9/2010 (NVRQS)	VIT10-AB	639	638	0	99.84	0.16	SEA	Mya-98
2	O/Ganghwa/SKR/2010 (NVRQS)	SKR10-AB	639	633	0	99.06	0.94	SEA	Mya-98
3	O/HKN/13/2010	HKN10-13	639	633	0	99.06	0.94	SEA	Mya-98
4	O/HKN/14/2010	HKN10-14	639	633	0	99.06	0.94	SEA	Mya-98
5	O/HKN/15/2010	HKN10-15	639	633	0	99.06	0.94	SEA	Mya-98
6	O/HKN/7/2010	HKN10-07	639	633	0	99.06	0.94	SEA	Mya-98
7	O/HKN/8/2010	HKN10-08	639	633	0	99.06	0.94	SEA	Mya-98
8	O/HKN/10/2010	HKN10-10	639	632	0	98.90	1.10	SEA	Mya-98
9	O/HKN/11/2010	HKN10-11	639	632	0	98.90	1.10	SEA	Mya-98
10	O/HKN/12/2010	HKN10-12	639	632	0	98.90	1.10	SEA	Mya-98
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/MYA/7/98 (DQ164925)	MYA98-07	639	599	0	93.74	6.26	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	574	0	89.83	10.17	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	546	0	85.45	14.55	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	543	0	84.98	15.02	SEA	Cam-94
5	O/IRN/8/2005	IRN05-08	639	543	0	84.98	15.02	ME-SA	PanAsia-2
6	O/PAK/16/2010	PAK10-16	639	542	0	84.82	15.18	ME-SA	PanAsia-2 ^{PUN-10}
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	540	0	84.51	15.49	EA-3	unnamed
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	540	0	84.51	15.49	ME-SA	PanAsia
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	539	0	84.35	15.65	ME-SA	PanAsia-2 ^{TER-08}
10	O/IRN/88/2009	IRN09-88	639	538	0	84.19	15.81	ME-SA	PanAsia-2 ^{ANT-10}

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O	Report date: 16/02/2011
WRLFMD Ref No: VIT/NCVD-9/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-9	
Location: Yen Bai province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AB.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not given	Total no. of comparisons: 2632
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Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/VIT/NCVD-8/2010 (NVRQS)	VIT10-AA	639	638	0	99.84	0.16	SEA	Mya-98
2	O/Ganghwa/SKR/2010 (NVRQS)	SKR10-AB	639	632	0	98.90	1.10	SEA	Mya-98
3	O/HKN/13/2010	HKN10-13	639	632	0	98.90	1.10	SEA	Mya-98
4	O/HKN/14/2010	HKN10-14	639	632	0	98.90	1.10	SEA	Mya-98
5	O/HKN/15/2010	HKN10-15	639	632	0	98.90	1.10	SEA	Mya-98
6	O/HKN/7/2010	HKN10-07	639	632	0	98.90	1.10	SEA	Mya-98
7	O/HKN/8/2010	HKN10-08	639	632	0	98.90	1.10	SEA	Mya-98
8	O/HKN/10/2010	HKN10-10	639	631	0	98.75	1.25	SEA	Mya-98
9	O/HKN/11/2010	HKN10-11	639	631	0	98.75	1.25	SEA	Mya-98
10	O/HKN/12/2010	HKN10-12	639	631	0	98.75	1.25	SEA	Mya-98
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/MYA/7/98 (DQ164925)	MYA98-07	639	600	0	93.90	6.10	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	575	0	89.98	10.02	SEA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	547	0	85.60	14.40	ME-SA	unnamed
4	O/CAM/3/98 (AJ294910)	CAM98-03	639	544	0	85.13	14.87	SEA	Cam-94
5	O/PAK/16/2010	PAK10-16	639	543	0	84.98	15.02	ME-SA	PanAsia-2 ^{PUN-10}
6	O/IRN/8/2005	IRN05-08	639	542	0	84.82	15.18	ME-SA	PanAsia-2
7	O/ETH/3/2004 (FJ798109)	ETH04-03	639	541	0	84.66	15.34	EA-3	unnamed
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	541	0	84.66	15.34	ME-SA	PanAsia
9	O/TUR/257/2008* (FMDI)	TUR08-AD	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{TER-08}
10	O/IRN/88/2009	IRN09-88	639	539	0	84.35	15.65	ME-SA	PanAsia-2 ^{ANT-10}

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Serotype: O	Report date: 16/02/2011
WRLFMD Ref No: VIT/NCVD-17/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-17	
Location: Son La province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AC.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not given	Total no. of comparisons: 2632
	Min. no. of nt for comparison: 600
	Total turn-around time: 1 days
	Sequencing time: 1 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/MIT/NCVD-18/2010 (NVRQS)	VIT10-AD	639	639	0	100.00	0.00	SEA	Mya-98
2	O/MIT/NCVD-19/2010 (NVRQS)	VIT10-AE	639	638	0	99.84	0.16	SEA	Mya-98
3	O/MIT/NCVD-20/2010 (NVRQS)	VIT10-AF	639	638	0	99.84	0.16	SEA	Mya-98
4	O/LAO/101/2009*	LAO09-AF	639	634	0	99.22	0.78	SEA	Mya-98
5	O/TAI/22/2009 (HQ116269)	TAI09-22	639	631	0	98.75	1.25	SEA	Mya-98
6	O/HKN/13/2010	HKN10-13	639	628	0	98.28	1.72	SEA	Mya-98
7	O/HKN/14/2010	HKN10-14	639	628	0	98.28	1.72	SEA	Mya-98
8	O/HKN/15/2010	HKN10-15	639	628	0	98.28	1.72	SEA	Mya-98
9	O/HKN/7/2010	HKN10-07	639	628	0	98.28	1.72	SEA	Mya-98
10	O/HKN/8/2010	HKN10-08	639	628	0	98.28	1.72	SEA	Mya-98
Most Closely Related Reference Viruses									
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Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/MYA/7/98 (DQ164925)	MYA98-07	639	596	0	93.27	6.73	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	573	0	89.67	10.33	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	546	0	85.45	14.55	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	543	0	84.98	15.02	ME-SA	PanAsia-2 ^{PUN-10}
6	O/IRN/8/2005	IRN05-08	639	541	0	84.66	15.34	ME-SA	PanAsia-2
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	541	0	84.66	15.34	ME-SA	PanAsia-2 ^{TER-08}
8	O/TUR/264/2009* (FMDI)	TUR09-AK	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{SAN-09}
9	O/ETH/3/2004 (FJ798109)	ETH04-03	639	539	0	84.35	15.65	EA-3	unnamed
10	O/UKG/35/2001 (AJ539141)	UKG01-35	639	538	0	84.19	15.81	ME-SA	PanAsia

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Serotype: O	Report date: 16/02/2011
WRLFMD Ref No: VIT/NCVD-18/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-18	
Location: Son La province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AD.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not given	Total no. of comparisons: 2632
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Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/MIT/NCVD-17/2010 (NVRQS)	VIT10-AC	639	639	0	100.00	0.00	SEA	Mya-98
2	O/MIT/NCVD-19/2010 (NVRQS)	VIT10-AE	639	638	0	99.84	0.16	SEA	Mya-98
3	O/MIT/NCVD-20/2010 (NVRQS)	VIT10-AF	639	638	0	99.84	0.16	SEA	Mya-98
4	O/LAO/101/2009*	LAO09-AF	639	634	0	99.22	0.78	SEA	Mya-98
5	O/TAI/22/2009 (HQ116269)	TAI09-22	639	631	0	98.75	1.25	SEA	Mya-98
6	O/HKN/13/2010	HKN10-13	639	628	0	98.28	1.72	SEA	Mya-98
7	O/HKN/14/2010	HKN10-14	639	628	0	98.28	1.72	SEA	Mya-98
8	O/HKN/15/2010	HKN10-15	639	628	0	98.28	1.72	SEA	Mya-98
9	O/HKN/7/2010	HKN10-07	639	628	0	98.28	1.72	SEA	Mya-98
10	O/HKN/8/2010	HKN10-08	639	628	0	98.28	1.72	SEA	Mya-98
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
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1	O/MYA/7/98 (DQ164925)	MYA98-07	639	596	0	93.27	6.73	SEA	Mya-98
2	O/TAI/189/87* (TRRL)	TAI87-AC	639	573	0	89.67	10.33	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	546	0	85.45	14.55	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	543	0	84.98	15.02	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	543	0	84.98	15.02	ME-SA	PanAsia-2 ^{PUN-10}
6	O/IRN/8/2005	IRN05-08	639	541	0	84.66	15.34	ME-SA	PanAsia-2
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	541	0	84.66	15.34	ME-SA	PanAsia-2 ^{TER-08}
8	O/TUR/264/2009* (FMDI)	TUR09-AK	639	540	0	84.51	15.49	ME-SA	PanAsia-2 ^{SAN-09}
9	O/ETH/3/2004 (FJ798109)	ETH04-03	639	539	0	84.35	15.65	EA-3	unnamed
10	O/UKG/35/2001 (AJ539141)	UKG01-35	639	538	0	84.19	15.81	ME-SA	PanAsia

nt, nucleotides

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Serotype: O	Report date: 16/02/2011
WRLFMD Ref No: VIT/NCVD-19/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-19	
Location: Son La province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AE.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not given	Total no. of comparisons: 2632
	Min. no. of nt for comparison: 600
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Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/MIT/NCVD-20/2010 (NVRQS)	VIT10-AF	639	639	0	100.00	0.00	SEA	Mya-98
2	O/MIT/NCVD-17/2010 (NVRQS)	VIT10-AC	639	638	0	99.84	0.16	SEA	Mya-98
3	O/MIT/NCVD-18/2010 (NVRQS)	VIT10-AD	639	638	0	99.84	0.16	SEA	Mya-98
4	O/LAO/101/2009*	LAO09-AF	639	635	0	99.37	0.63	SEA	Mya-98
5	O/TAI/22/2009 (HQ116269)	TAI09-22	639	632	0	98.90	1.10	SEA	Mya-98
6	O/HKN/13/2010	HKN10-13	639	629	0	98.44	1.56	SEA	Mya-98
7	O/HKN/14/2010	HKN10-14	639	629	0	98.44	1.56	SEA	Mya-98
8	O/HKN/15/2010	HKN10-15	639	629	0	98.44	1.56	SEA	Mya-98
9	O/HKN/7/2010	HKN10-07	639	629	0	98.44	1.56	SEA	Mya-98
10	O/HKN/8/2010	HKN10-08	639	629	0	98.44	1.56	SEA	Mya-98
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3	O/CAM/3/98 (AJ294910)	CAM98-03	639	547	0	85.60	14.40	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	544	0	85.13	14.87	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	544	0	85.13	14.87	ME-SA	PanAsia-2 ^{PUN-10}
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9	O/ETH/3/2004 (FJ798109)	ETH04-03	639	540	0	84.51	15.49	EA-3	unnamed
10	O/UKG/35/2001 (AJ539141)	UKG01-35	639	539	0	84.35	15.65	ME-SA	PanAsia

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Serotype: O	Report date: 16/02/2011
WRLFMD Ref No: VIT/NCVD-20/2010	Reported by: N.J. Knowles
Batch No: n/a	Checked by: D.P. King
Sender Ref: NCVD-20	
Location: Son La province, Vietnam	Topotype: SEA
Date collected: 2010	Genotype/strain: Mya-98
Date received by WRLFMD: 15/02/2011	Sequence filename: VIT10-AF.SEQ
Date received for sequencing: 15/02/2011	Date sequence last updated: 16/02/2011
Species: Cattle	No. of Nt determined: 639
Material used: not given	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
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2	O/MIT/NCVD-17/2010 (NVRQS)	VIT10-AC	639	638	0	99.84	0.16	SEA	Mya-98
3	O/MIT/NCVD-18/2010 (NVRQS)	VIT10-AD	639	638	0	99.84	0.16	SEA	Mya-98
4	O/LAO/101/2009*	LAO09-AF	639	635	0	99.37	0.63	SEA	Mya-98
5	O/TAI/22/2009 (HQ116269)	TAI09-22	639	632	0	98.90	1.10	SEA	Mya-98
6	O/HKN/13/2010	HKN10-13	639	629	0	98.44	1.56	SEA	Mya-98
7	O/HKN/14/2010	HKN10-14	639	629	0	98.44	1.56	SEA	Mya-98
8	O/HKN/15/2010	HKN10-15	639	629	0	98.44	1.56	SEA	Mya-98
9	O/HKN/7/2010	HKN10-07	639	629	0	98.44	1.56	SEA	Mya-98
10	O/HKN/8/2010	HKN10-08	639	629	0	98.44	1.56	SEA	Mya-98
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(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
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2	O/TAI/189/87* (TRRL)	TAI87-AC	639	574	0	89.83	10.17	SEA	unnamed
3	O/CAM/3/98 (AJ294910)	CAM98-03	639	547	0	85.60	14.40	SEA	Cam-94
4	O/IND/R2/75* (AF204276)	IND75--A	639	544	0	85.13	14.87	ME-SA	unnamed
5	O/PAK/16/2010	PAK10-16	639	544	0	85.13	14.87	ME-SA	PanAsia-2 ^{PUN-10}
6	O/IRN/8/2005	IRN05-08	639	542	0	84.82	15.18	ME-SA	PanAsia-2
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	542	0	84.82	15.18	ME-SA	PanAsia-2 ^{TER-08}
8	O/TUR/264/2009* (FMDI)	TUR09-AK	639	541	0	84.66	15.34	ME-SA	PanAsia-2 ^{SAN-09}
9	O/ETH/3/2004 (FJ798109)	ETH04-03	639	540	0	84.51	15.49	EA-3	unnamed
10	O/UKG/35/2001 (AJ539141)	UKG01-35	639	539	0	84.35	15.65	ME-SA	PanAsia

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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Report on FMDV O in Vietnam in 2010

6 x VP1 sequences received from National Veterinary Research and Quarantine Service (NVRQS), Anyang, Gyeonggi 430-824, Republic of Korea, 15/02/2011

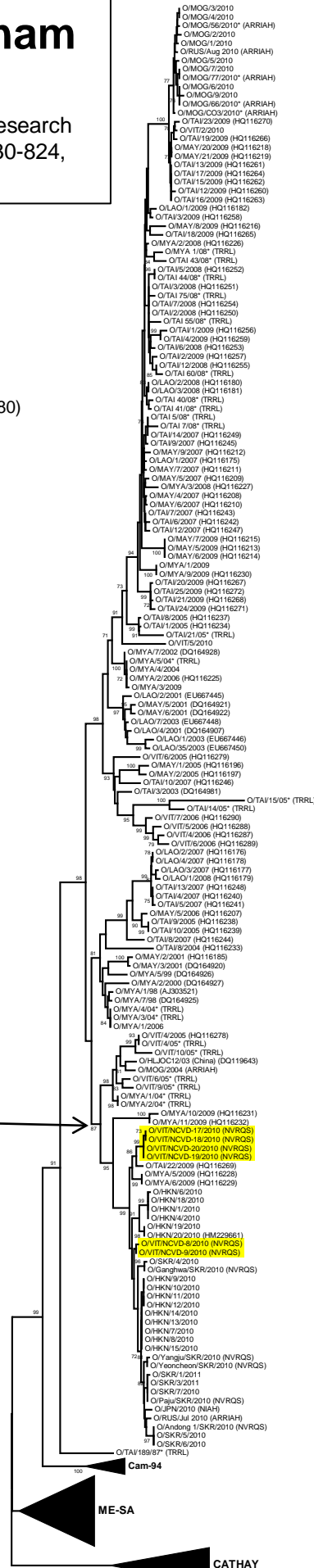
Software: MEGA 4.0
 No. of Taxa : 273
 Data File : n:\evd\meg\db\fmdv\o\SKR2010f.meg
 Data Title : O SKR 2010-2011
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 ->Method : Neighbor-Joining
 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=46980)
 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

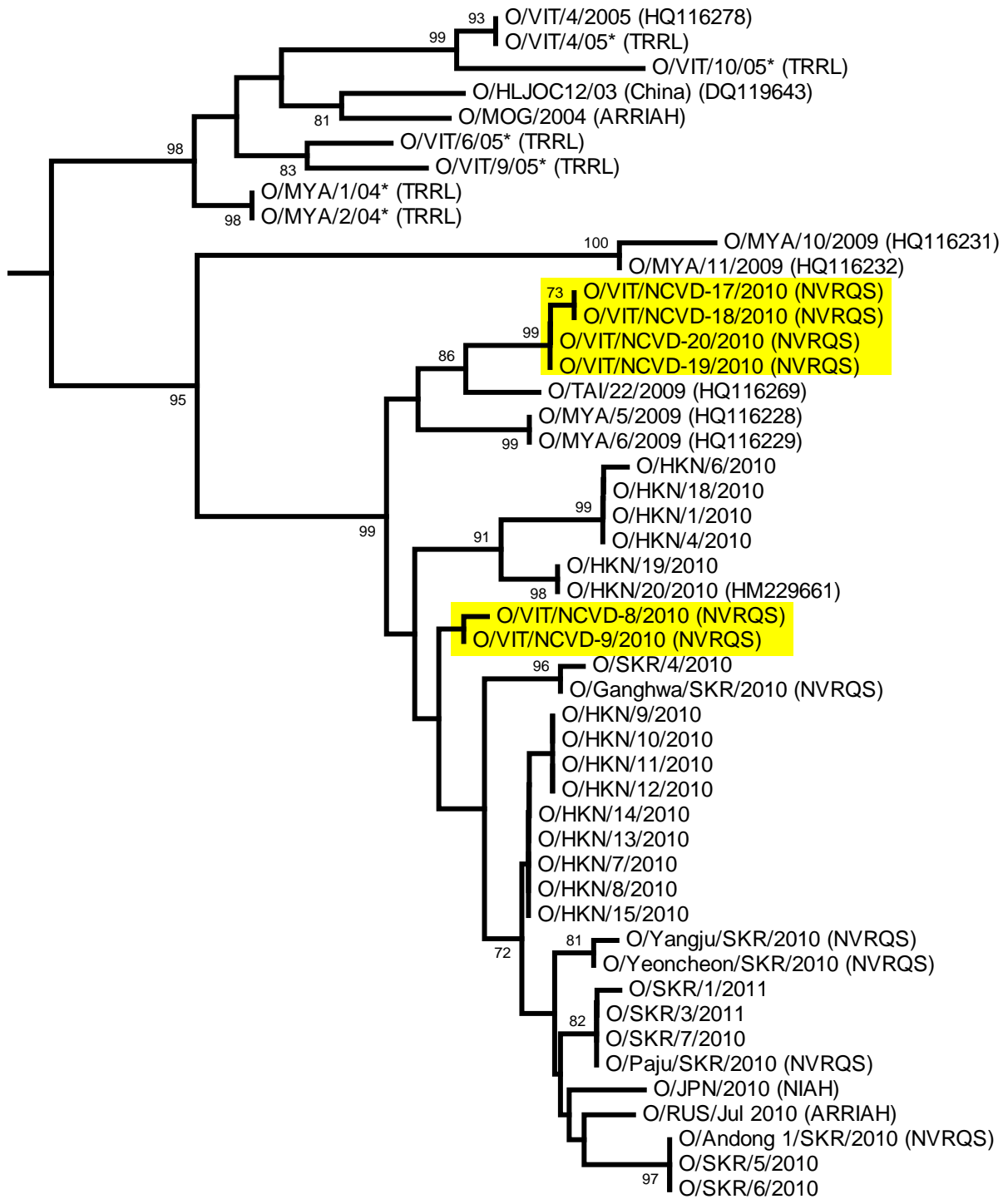
* , not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 16 February 2011

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Sub-tree on next page





0.005