



INSTITUTE FOR ANIMAL HEALTH

Director: Professor John Fazakerley BSc, MBA, PhD, FRCPath

PIRBRIGHT LABORATORY

Ash Road,

Pirbright,

Surrey,

GU24 0NF

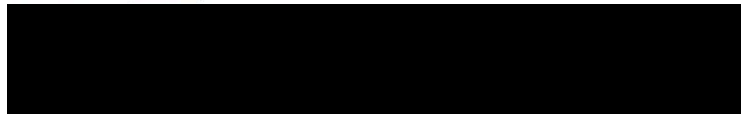
Intn Tel: 00 44 1483 232441

Tel: 01483 232441, Fax: 01483 232621

FMD Genotyping Report

Lab Reference WRL Batch Number: WRLFMD/2012/00033

Sender Details:



Date Received: 25th October 2012


Country of Origin: SRI LANKA

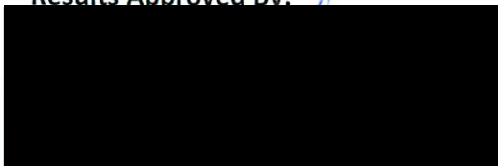
Date Reported: 18th December 2012

Dear Dr Ranjani Hettiarachchi,

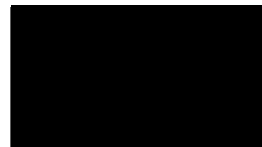
Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at:

<http://www.wrlfmd.org/>

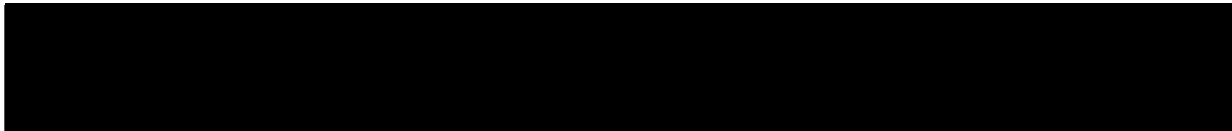
Results Approved By: 



Official Stamp:



Date:



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: trish.ryder@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: 10 December 2012

FMDV type O

Country: Sri Lanka

Period: 2009, 2010 & 2012

No. of samples: 5

BATCH: WRLFMD/2012/00033



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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: 07/12/2012
WRLFMD Ref No: SRL/3/2009	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00033	Checked by: D.P. King
Sender Ref: FMD/SL/WRL/09/03	
Location: Ampara, Akkaraipattu, Sri Lanka	Topotype: ME-SA
Date collected: 09/09/2009	Genotype/strain: unnamed
Date received by WRLFMD: 25/10/2012	Sequence filename: SRL09-03.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 06/12/2012
Species: Bovine	No. of Nt determined: 639
Material used: BTY1 07/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3420
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 4 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/SRL/1/2009	SRL09-01	639	630	0	98.59	1.41	ME-SA	unnamed
2	O/SRL/1/2010	SRL10-01	639	630	0	98.59	1.41	ME-SA	unnamed
3	O/SRL/9/2010	SRL10-09	639	629	0	98.44	1.56	ME-SA	unnamed
4	O/SRL/13/2010	SRL10-13	639	624	0	97.65	2.35	ME-SA	unnamed
5	O/SRL/3/2010	SRL10-03	639	622	0	97.34	2.66	ME-SA	unnamed
6	O/SRL/2/2012	SRL12-02	639	614	0	96.09	3.91	ME-SA	unnamed
7	O/SRL/7/99	SRL99-07	639	593	0	92.80	7.20	ME-SA	unnamed
8	O/SRL/1/2000	SRL00-01	639	592	0	92.64	7.36	ME-SA	unnamed
9	O/SRL/5/99	SRL99-05	639	588	0	92.02	7.98	ME-SA	unnamed
10	O/TAI/7/2011	TAI11-07	639	586	0	91.71	8.29	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	574	0	89.83	10.17	ME-SA	PanAsia
2	O/PAK/16/2010	PAK10-16	639	572	0	89.51	10.49	ME-SA	PanAsia-2 ^{PUN-10}
3	O/IRN/31/2009	IRN09-31	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{FAR-09}
4	O/IRN/88/2009	IRN09-88	639	569	0	89.05	10.95	ME-SA	PanAsia-2 ^{ANT-10}
5	O/IRN/8/2005	IRN05-08	639	568	0	88.89	11.11	ME-SA	PanAsia-2
6	O/IRN/18/2010	IRN10-18	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{BAL-09}
7	O/KUW/3/97 (DQ164904)	KUW97-03	639	567	0	88.73	11.27	ME-SA	Ind-2001a
8	O/UAE/4/2008	UAE08-04	636	563	0	88.52	11.48	ME-SA	Ind-2001c
9	O/OMN/7/2001 (DQ164941)	OMN01-07	639	565	0	88.42	11.58	ME-SA	Ind-2001b
10	O/TUR/257/2008* (FMDI)	TUR08-AD	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{TER-08}

nt, nucleotides

*, not a WRLFMD reference number

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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: 07/12/2012
WRLFMD Ref No: SRL/3/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00033	Checked by: D.P. King
Sender Ref: FMD/SL/WRL/10/02	
Location: Polonnaruwa, Minneriya, Sri Lanka	Topotype: ME-SA
Date collected: 13/01/2010	Genotype/strain: unnamed
Date received by WRLFMD: 25/10/2012	Sequence filename: SRL10-03.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 06/12/2012
Species: Bovine	No. of Nt determined: 639
Material used: BTY1 08/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3420
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 4 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/SRL/1/2009	SRL09-01	639	627	0	98.12	1.88	ME-SA	unnamed
2	O/SRL/1/2010	SRL10-01	639	627	0	98.12	1.88	ME-SA	unnamed
3	O/SRL/3/2009	SRL09-03	639	622	0	97.34	2.66	ME-SA	unnamed
4	O/SRL/9/2010	SRL10-09	639	622	0	97.34	2.66	ME-SA	unnamed
5	O/SRL/13/2010	SRL10-13	639	617	0	96.56	3.44	ME-SA	unnamed
6	O/SRL/2/2012	SRL12-02	639	609	0	95.31	4.69	ME-SA	unnamed
7	O/SRL/7/99	SRL99-07	639	591	0	92.49	7.51	ME-SA	unnamed
8	O/SRL/1/2000	SRL00-01	639	590	0	92.33	7.67	ME-SA	unnamed
9	O/SRL/5/99	SRL99-05	639	588	0	92.02	7.98	ME-SA	unnamed
10	O/SRL/2/97	SRL97-02	639	581	0	90.92	9.08	ME-SA	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/IRN/31/2009	IRN09-31	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{FAR-09}
2	O/PAK/16/2010	PAK10-16	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{PUN-10}
3	O/UKG/35/2001 (AJ539141)	UKG01-35	639	566	0	88.58	11.42	ME-SA	PanAsia
4	O/IRN/88/2009	IRN09-88	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{ANT-10}
5	O/UAE/4/2008	UAE08-04	636	561	0	88.21	11.79	ME-SA	Ind-2001c
6	O/KUW/3/97 (DQ164904)	KUW97-03	639	563	0	88.11	11.89	ME-SA	Ind-2001a
7	O/OMN/7/2001 (DQ164941)	OMN01-07	639	563	0	88.11	11.89	ME-SA	Ind-2001b
8	O/IRN/61/2001 (DQ164896)	IRN01-61	638	560	1	87.77	12.23	ME-SA	Irn-2001
9	O/IRN/18/2010	IRN10-18	639	560	0	87.64	12.36	ME-SA	PanAsia-2 ^{BAL-09}
10	O/IRN/8/2005	IRN05-08	639	560	0	87.64	12.36	ME-SA	PanAsia-2

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: 07/12/2012
WRLFMD Ref No: SRL/9/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00033	Checked by: D.P. King
Sender Ref: FMD/SL/WRL/10/06b	
Location: Kandy, Kundasale, Sri Lanka	Topotype: ME-SA
Date collected: 21/04/2010	Genotype/strain: unnamed
Date received by WRLFMD: 25/10/2012	Sequence filename: SRL10-09.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 06/12/2012
Species: Water Buffalo	No. of Nt determined: 639
Material used: BTY1 09/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3420
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 4 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/SRL/13/2010	SRL10-13	639	634	0	99.22	0.78	ME-SA	unnamed
2	O/SRL/3/2009	SRL09-03	639	629	0	98.44	1.56	ME-SA	unnamed
3	O/SRL/1/2009	SRL09-01	639	628	0	98.28	1.72	ME-SA	unnamed
4	O/SRL/1/2010	SRL10-01	639	628	0	98.28	1.72	ME-SA	unnamed
5	O/SRL/2/2012	SRL12-02	639	624	0	97.65	2.35	ME-SA	unnamed
6	O/SRL/3/2010	SRL10-03	639	622	0	97.34	2.66	ME-SA	unnamed
7	O/SRL/7/99	SRL99-07	639	592	0	92.64	7.36	ME-SA	unnamed
8	O/SRL/1/2000	SRL00-01	639	591	0	92.49	7.51	ME-SA	unnamed
9	O/SRL/5/99	SRL99-05	639	587	0	91.86	8.14	ME-SA	unnamed
10	O/SRL/2/97	SRL97-02	639	584	0	91.39	8.61	ME-SA	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/UKG/35/2001 (AJ539141)	UKG01-35	639	573	0	89.67	10.33	ME-SA	PanAsia
2	O/IRN/31/2009	IRN09-31	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{FAR-09}
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	569	0	89.05	10.95	ME-SA	Ind-2001a
4	O/IRN/88/2009	IRN09-88	639	568	0	88.89	11.11	ME-SA	PanAsia-2 ^{ANT-10}
5	O/PAK/16/2010	PAK10-16	639	568	0	88.89	11.11	ME-SA	PanAsia-2 ^{PUN-10}
6	O/UAE/4/2008	UAE08-04	636	565	0	88.84	11.16	ME-SA	Ind-2001c
7	O/IRN/18/2010	IRN10-18	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{BAL-09}
8	O/OMN/7/2001 (DQ164941)	OMN01-07	639	567	0	88.73	11.27	ME-SA	Ind-2001b
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	566	1	88.71	11.29	ME-SA	Irn-2001
10	O/IRN/8/2005	IRN05-08	639	565	0	88.42	11.58	ME-SA	PanAsia-2

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: 07/12/2012
WRLFMD Ref No: SRL/13/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00033	Checked by: D.P. King
Sender Ref: FMD/SL/WRL/10/10	
Location: Kandy, Kundasale, Sri Lanka	Topotype: ME-SA
Date collected: 02/12/2010	Genotype/strain: unnamed
Date received by WRLFMD: 25/10/2012	Sequence filename: SRL10-13.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 06/12/2012
Species: Bovine	No. of Nt determined: 639
Material used: BTY1 11/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3420
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 4 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/SRL/9/2010	SRL10-09	639	634	0	99.22	0.78	ME-SA	unnamed
2	O/SRL/3/2009	SRL09-03	639	624	0	97.65	2.35	ME-SA	unnamed
3	O/SRL/1/2009	SRL09-01	639	623	0	97.50	2.50	ME-SA	unnamed
4	O/SRL/1/2010	SRL10-01	639	623	0	97.50	2.50	ME-SA	unnamed
5	O/SRL/2/2012	SRL12-02	639	621	0	97.18	2.82	ME-SA	unnamed
6	O/SRL/3/2010	SRL10-03	639	617	0	96.56	3.44	ME-SA	unnamed
7	O/SRL/7/99	SRL99-07	639	587	0	91.86	8.14	ME-SA	unnamed
8	O/SRL/1/2000	SRL00-01	639	586	0	91.71	8.29	ME-SA	unnamed
9	O/SRL/5/99	SRL99-05	639	582	0	91.08	8.92	ME-SA	unnamed
10	O/SRL/2/97	SRL97-02	639	579	0	90.61	9.39	ME-SA	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/UKG/35/2001 (AJ539141)	UKG01-35	639	568	0	88.89	11.11	ME-SA	PanAsia
2	O/IRN/31/2009	IRN09-31	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/88/2009	IRN09-88	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{ANT-10}
4	O/PAK/16/2010	PAK10-16	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{PUN-10}
5	O/IRN/18/2010	IRN10-18	639	564	0	88.26	11.74	ME-SA	PanAsia-2 ^{BAL-09}
6	O/KUW/3/97 (DQ164904)	KUW97-03	639	564	0	88.26	11.74	ME-SA	Ind-2001a
7	O/IRN/61/2001 (DQ164896)	IRN01-61	638	563	1	88.24	11.76	ME-SA	Irn-2001
8	O/UAE/4/2008	UAE08-04	636	560	0	88.05	11.95	ME-SA	Ind-2001c
9	O/IRN/8/2005	IRN05-08	639	562	0	87.95	12.05	ME-SA	PanAsia-2
10	O/OMN/7/2001 (DQ164941)	OMN01-07	639	562	0	87.95	12.05	ME-SA	Ind-2001b

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: 07/12/2012
WRLFMD Ref No: SRL/2/2012	Reported by: N.J. Knowles
Batch No: WRLFMD/2012/00033	Checked by: D.P. King
Sender Ref: FMD/SL/WRL/12/02	
Location: Ampara, Sammanthurai, Sri Lanka	Topotype: ME-SA
Date collected: 15/06/2012	Genotype/strain: unnamed
Date received by WRLFMD: 25/10/2012	Sequence filename: SRL12-02.SEQ
Date received for sequencing: 03/12/2012	Date sequence last updated: 06/12/2012
Species: Bovine	No. of Nt determined: 639
Material used: BTY1 20/11/2012	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3420
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 43 days
	Sequencing time: 4 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/SRL/9/2010	SRL10-09	639	624	0	97.65	2.35	ME-SA	unnamed
2	O/SRL/13/2010	SRL10-13	639	621	0	97.18	2.82	ME-SA	unnamed
3	O/SRL/1/2009	SRL09-01	639	615	0	96.24	3.76	ME-SA	unnamed
4	O/SRL/1/2010	SRL10-01	639	615	0	96.24	3.76	ME-SA	unnamed
5	O/SRL/3/2009	SRL09-03	639	614	0	96.09	3.91	ME-SA	unnamed
6	O/SRL/3/2010	SRL10-03	639	609	0	95.31	4.69	ME-SA	unnamed
7	O/SRL/7/99	SRL99-07	639	587	0	91.86	8.14	ME-SA	unnamed
8	O/SRL/1/2000	SRL00-01	639	586	0	91.71	8.29	ME-SA	unnamed
9	O/SRL/5/99	SRL99-05	639	582	0	91.08	8.92	ME-SA	unnamed
10	O/BHU/2/2002 (DQ165037)	BHU02-02	638	581	1	91.07	8.93	ME-SA	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/IRN/31/2009	IRN09-31	639	573	0	89.67	10.33	ME-SA	PanAsia-2 ^{FAR-09}
2	O/KUW/3/97 (DQ164904)	KUW97-03	639	569	0	89.05	10.95	ME-SA	Ind-2001a
3	O/PAK/16/2010	PAK10-16	639	569	0	89.05	10.95	ME-SA	PanAsia-2 ^{PUN-10}
4	O/UKG/35/2001 (AJ539141)	UKG01-35	639	569	0	89.05	10.95	ME-SA	PanAsia
5	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2 ^{BAL-09}
6	O/IRN/8/2005	IRN05-08	639	568	0	88.89	11.11	ME-SA	PanAsia-2
7	O/IRN/88/2009	IRN09-88	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{ANT-10}
8	O/OMN/7/2001 (DQ164941)	OMN01-07	639	567	0	88.73	11.27	ME-SA	Ind-2001b
9	O/UAE/4/2008	UAE08-04	636	563	0	88.52	11.48	ME-SA	Ind-2001c
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	564	1	88.40	11.60	ME-SA	Irn-2001

nt, nucleotides

*, not a WRLFMD reference number

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Report on FMDV O in Sri Lanka in 2009, 2010 & 2012

Batch: WRLFMD/2012/00033

◆ indicates viruses in this batch

Software: MEGA 5.1

Analysis

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

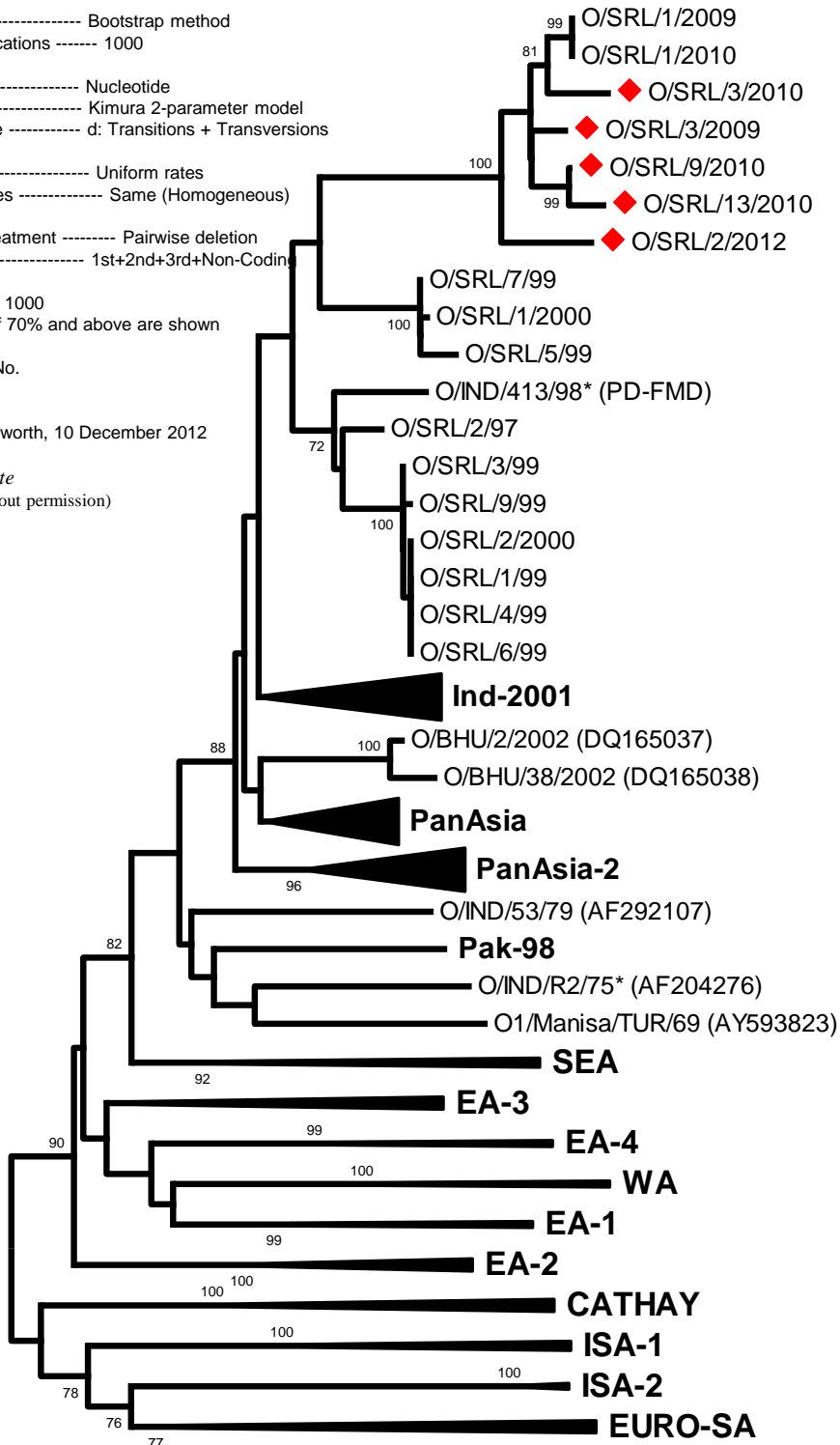
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 10 December 2012

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ME-SA