

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

## Genotyping Report

Report Date for this Batch: 8 November 2013

FMDV type O

Country: Libya

Period: 2013

No. of samples: 7

BATCH: WRLFMD/2013/00021



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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 WRLFMD Ref No: LIB/1/2013 Batch No: WRLFMD/2013/00021 Sender Ref: O LIB 1/13 (BHK 3) B1 Epi swab Location: Zliten, Libya Date collected: 01/09/2013 Date received by WRLFMD: 29/10/2013 Date received for sequencing: 05/11/2013 Species: Cattle Material used: BTy1 31/10/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 07/11/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001d Sequence filename: LIB13-01.SEQ Date sequence last updated: 07/11/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3703 Min. no. of nt for comparison: 600 Total turn-around time: 9 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/LIB/4/2013	LIB13-04	639	639	0	100.00	0.00	ME-SA	Ind-2001d
2	O/LIB/5/2013	LIB13-05	639	639	0	100.00	0.00	ME-SA	Ind-2001d
3	O/LIB/7/2013	LIB13-07	639	639	0	100.00	0.00	ME-SA	Ind-2001d
4	O/LIB/2/2013	LIB13-02	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/3/2013	LIB13-03	639	638	0	99.84	0.16	ME-SA	Ind-2001d
6	O/LIB/6/2013	LIB13-06	639	638	0	99.84	0.16	ME-SA	Ind-2001d
7	O/BHU/1/2013	BHU13-01	639	620	0	97.03	2.97	ME-SA	Ind-2001d
8	O/BHU/18/2009	BHU09-18	639	615	0	96.24	3.76	ME-SA	Ind-2001d
9	O/BHU/2/2009	BHU09-02	639	615	0	96.24	3.76	ME-SA	Ind-2001d
10	O/BHU/26/2009	BHU09-26	639	615	0	96.24	3.76	ME-SA	Ind-2001d
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/3/2009	BHU09-03	639	615	0	96.24	3.76	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	586	0	91.71	8.29	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	583	0	91.24	8.76	ME-SA	Ind-2001a
4	O/IRN/31/2009	IRN09-31	639	576	0	90.14	9.86	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	573	0	90.09	9.91	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	571	0	89.36	10.64	ME-SA	PanAsia-2 <sup>TER-08</sup>
7	O/IRN/8/2005	IRN05-08	639	570	0	89.20	10.80	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	569	0	89.05	10.95	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	569	0	89.05	10.95	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>BAL-09</sup>

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 WRLFMD Ref No: LIB/2/2013 Batch No: WRLFMD/2013/00021 Sender Ref: O LIB 1/13 (BHK 3) B3 Epi swab Location: Zliten, Libya Date collected: 01/09/2013 Date received by WRLFMD: 29/10/2013 Date received for sequencing: 05/11/2013 Species: Cattle Material used: BTy1 31/10/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 07/11/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001d Sequence filename: LIB13-02.SEQ Date sequence last updated: 07/11/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3703 Min. no. of nt for comparison: 600 Total turn-around time: 9 days Sequencing time: 2 days
Comments:	

Most Closely Related Viruses									
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2	O/LIB/6/2013	LIB13-06	639	639	0	100.00	0.00	ME-SA	Ind-2001d
3	O/LIB/1/2013	LIB13-01	639	638	0	99.84	0.16	ME-SA	Ind-2001d
4	O/LIB/4/2013	LIB13-04	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/5/2013	LIB13-05	639	638	0	99.84	0.16	ME-SA	Ind-2001d
6	O/LIB/7/2013	LIB13-07	639	638	0	99.84	0.16	ME-SA	Ind-2001d
7	O/BHU/1/2013	BHU13-01	639	619	0	96.87	3.13	ME-SA	Ind-2001d
8	O/BHU/18/2009	BHU09-18	639	614	0	96.09	3.91	ME-SA	Ind-2001d
9	O/BHU/2/2009	BHU09-02	639	614	0	96.09	3.91	ME-SA	Ind-2001d
10	O/BHU/26/2009	BHU09-26	639	614	0	96.09	3.91	ME-SA	Ind-2001d
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2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	585	0	91.55	8.45	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	582	0	91.08	8.92	ME-SA	Ind-2001a
4	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 <sup>TER-08</sup>
7	O/IRN/8/2005	IRN05-08	639	569	0	89.05	10.95	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	568	0	88.89	11.11	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	567	0	88.73	11.27	ME-SA	PanAsia-2 <sup>BAL-09</sup>

nt, nucleotides

\* , not a WRLFMD reference number

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Serotype: O	Report date: 07/11/2013
WRLFMD Ref No: LIB/3/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00021	Checked by: K. Bachanek-Bankowska
Sender Ref: O LIB 1/13 (BHK 4) B3 Blood	
Location: Zliten, Libya	Topotype: ME-SA
Date collected: 01/09/2013	Genotype/strain: Ind-2001d
Date received by WRLFMD: 29/10/2013	Sequence filename: LIB13-03.SEQ
Date received for sequencing: 05/11/2013	Date sequence last updated: 07/11/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 31/10/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3703
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 9 days
	Sequencing time: 2 days
Comments:	

Most Closely Related Viruses									
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2	O/LIB/6/2013	LIB13-06	639	639	0	100.00	0.00	ME-SA	Ind-2001d
3	O/LIB/1/2013	LIB13-01	639	638	0	99.84	0.16	ME-SA	Ind-2001d
4	O/LIB/4/2013	LIB13-04	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/5/2013	LIB13-05	639	638	0	99.84	0.16	ME-SA	Ind-2001d
6	O/LIB/7/2013	LIB13-07	639	638	0	99.84	0.16	ME-SA	Ind-2001d
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9	O/BHU/2/2009	BHU09-02	639	614	0	96.09	3.91	ME-SA	Ind-2001d
10	O/BHU/26/2009	BHU09-26	639	614	0	96.09	3.91	ME-SA	Ind-2001d
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4	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 <sup>TER-08</sup>
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9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	568	0	88.89	11.11	ME-SA	PanAsia
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Serotype: O	Report date: 07/11/2013
WRLFMD Ref No: LIB/4/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00021	Checked by: K. Bachanek-Bankowska
Sender Ref: O LIB 1/13 (BHK 3) B4 Epi swab	
Location: Zliten, Libya	Topotype: ME-SA
Date collected: 01/09/2013	Genotype/strain: Ind-2001d
Date received by WRLFMD: 29/10/2013	Sequence filename: LIB13-04.SEQ
Date received for sequencing: 05/11/2013	Date sequence last updated: 07/11/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 31/10/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3703
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 9 days
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1	O/LIB/1/2013	LIB13-01	639	639	0	100.00	0.00	ME-SA	Ind-2001d
2	O/LIB/5/2013	LIB13-05	639	639	0	100.00	0.00	ME-SA	Ind-2001d
3	O/LIB/7/2013	LIB13-07	639	639	0	100.00	0.00	ME-SA	Ind-2001d
4	O/LIB/2/2013	LIB13-02	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/3/2013	LIB13-03	639	638	0	99.84	0.16	ME-SA	Ind-2001d
6	O/LIB/6/2013	LIB13-06	639	638	0	99.84	0.16	ME-SA	Ind-2001d
7	O/BHU/1/2013	BHU13-01	639	620	0	97.03	2.97	ME-SA	Ind-2001d
8	O/BHU/18/2009	BHU09-18	639	615	0	96.24	3.76	ME-SA	Ind-2001d
9	O/BHU/2/2009	BHU09-02	639	615	0	96.24	3.76	ME-SA	Ind-2001d
10	O/BHU/26/2009	BHU09-26	639	615	0	96.24	3.76	ME-SA	Ind-2001d

## Most Closely Related Reference Viruses

(see [http://www.wrlfmd.org/fmd\\_genotyping/prototypes.htm](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/OMN/7/2001 (DQ164941)	OMN01-07	639	586	0	91.71	8.29	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	583	0	91.24	8.76	ME-SA	Ind-2001a
4	O/IRN/31/2009	IRN09-31	639	576	0	90.14	9.86	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	573	0	90.09	9.91	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	571	0	89.36	10.64	ME-SA	PanAsia-2 <sup>TER-08</sup>
7	O/IRN/8/2005	IRN05-08	639	570	0	89.20	10.80	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	569	0	89.05	10.95	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	569	0	89.05	10.95	ME-SA	PanAsia
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Serotype: O WRLFMD Ref No: LIB/5/2013 Batch No: WRLFMD/2013/00021 Sender Ref: O LIB 1/13 (BHK 2) B5 Epi tissue Location: Zliten, Libya Date collected: 01/09/2013 Date received by WRLFMD: 29/10/2013 Date received for sequencing: 05/11/2013 Species: Cattle Material used: BTy1 31/10/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 07/11/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: ME-SA Genotype/strain: Ind-2001d Sequence filename: LIB13-05.SEQ Date sequence last updated: 07/11/2013 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3703 Min. no. of nt for comparison: 600 Total turn-around time: 9 days Sequencing time: 2 days
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3	O/KUW/3/97 (DQ164904)	KUW97-03	639	583	0	91.24	8.76	ME-SA	Ind-2001a
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10	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>BAL-09</sup>

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Serotype: O	Report date: 07/11/2013
WRLFMD Ref No: LIB/6/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00021	Checked by: K. Bachanek-Bankowska
Sender Ref: O LIB 1/13 (BHK 4) B6 Blood	
Location: Zliten, Libya	Topotype: ME-SA
Date collected: 01/09/2013	Genotype/strain: Ind-2001d
Date received by WRLFMD: 29/10/2013	Sequence filename: LIB13-06.SEQ
Date received for sequencing: 05/11/2013	Date sequence last updated: 07/11/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 31/10/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3703
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 9 days
	Sequencing time: 2 days
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3	O/LIB/1/2013	LIB13-01	639	638	0	99.84	0.16	ME-SA	Ind-2001d
4	O/LIB/4/2013	LIB13-04	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/5/2013	LIB13-05	639	638	0	99.84	0.16	ME-SA	Ind-2001d
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3	O/KUW/3/97 (DQ164904)	KUW97-03	639	582	0	91.08	8.92	ME-SA	Ind-2001a
4	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 <sup>TER-08</sup>
7	O/IRN/8/2005	IRN05-08	639	569	0	89.05	10.95	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	568	0	88.89	11.11	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	567	0	88.73	11.27	ME-SA	PanAsia-2 <sup>BAL-09</sup>

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: O	Report date: 07/11/2013
WRLFMD Ref No: LIB/7/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00021	Checked by: K. Bachanek-Bankowska
Sender Ref: O LIB 1/13 (BHK 4) E1 Blood	
Location: Zliten, Libya	Topotype: ME-SA
Date collected: 08/09/2013	Genotype/strain: Ind-2001d
Date received by WRLFMD: 29/10/2013	Sequence filename: LIB13-07.SEQ
Date received for sequencing: 05/11/2013	Date sequence last updated: 07/11/2013
Species: Cattle	No. of Nt determined: 639
Material used: BTy1 31/10/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3703
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 9 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/LIB/1/2013	LIB13-01	639	639	0	100.00	0.00	ME-SA	Ind-2001d
2	O/LIB/4/2013	LIB13-04	639	639	0	100.00	0.00	ME-SA	Ind-2001d
3	O/LIB/5/2013	LIB13-05	639	639	0	100.00	0.00	ME-SA	Ind-2001d
4	O/LIB/2/2013	LIB13-02	639	638	0	99.84	0.16	ME-SA	Ind-2001d
5	O/LIB/3/2013	LIB13-03	639	638	0	99.84	0.16	ME-SA	Ind-2001d
6	O/LIB/6/2013	LIB13-06	639	638	0	99.84	0.16	ME-SA	Ind-2001d
7	O/BHU/1/2013	BHU13-01	639	620	0	97.03	2.97	ME-SA	Ind-2001d
8	O/BHU/18/2009	BHU09-18	639	615	0	96.24	3.76	ME-SA	Ind-2001d
9	O/BHU/2/2009	BHU09-02	639	615	0	96.24	3.76	ME-SA	Ind-2001d
10	O/BHU/26/2009	BHU09-26	639	615	0	96.24	3.76	ME-SA	Ind-2001d
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/3/2009	BHU09-03	639	615	0	96.24	3.76	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	586	0	91.71	8.29	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	583	0	91.24	8.76	ME-SA	Ind-2001a
4	O/IRN/31/2009	IRN09-31	639	576	0	90.14	9.86	ME-SA	PanAsia-2 <sup>FAR-09</sup>
5	O/UAE/4/2008	UAE08-04	636	573	0	90.09	9.91	ME-SA	Ind-2001c
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	571	0	89.36	10.64	ME-SA	PanAsia-2 <sup>TER-08</sup>
7	O/IRN/8/2005	IRN05-08	639	570	0	89.20	10.80	ME-SA	PanAsia-2
8	O/PAK/16/2010	PAK10-16	639	569	0	89.05	10.95	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/UKG/35/2001 (AJ539141)	UKG01-35	639	569	0	89.05	10.95	ME-SA	PanAsia
10	O/IRN/18/2010	IRN10-18	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>BAL-09</sup>

nt, nucleotides

\*, not a WRLFMD reference number

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# Report on FMDV O in Libya in 2013

Batch: WRLFMD/2013/00021

◆ indicates viruses in this batch

Software: MEGA 5.2

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

8 November 2013

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