



# Institute for Animal Health

Registered Office: Compton, Newbury, Berkshire RG20 7NN

Telephone: +44 (0) 1635-578411 Facsimile: +44 (0) 1635-577237

e-mail: iah@bbsrc.ac.uk Website: <http://www.iah.bbsrc.ac.uk>

Director: Professor Martin Shirley PhD

Reply to Pirbright Laboratory

Fax: 01483 232621

Direct Dial: 01483 231014

E-mail: [Elizabeth.byrom@bbsrc.ac.uk](mailto:Elizabeth.byrom@bbsrc.ac.uk)

Page 1 of 5

To:

Email:

To:

Email:

From:

Date:

14<sup>th</sup> April 2009

Subject:

Sequencing Report

No. Of Pages:

5

FAX

This message is intended for the use of the person named above and may contain confidential information. Any other distribution, copying or disclosure is strictly prohibited. If you have received this telefax in error, please notify us immediately by telephone or E-mail and then return the original transmission to us by mail.

Thank you.

Dear [REDACTED]

**Virus isolates: A LIB/1/2009 and A LIB/2/2009 plus a phylogenetic tree for a further 35 sequences as they are all very closely related.**

Sequencing work has now been completed in respect of the above virus isolates received at IAH Pirbright on 12<sup>th</sup> of March 2009 and the details are as attached. Please note all of our phylogenetic trees can be accessed via the internet at:

[http://www.iah.bbsrc.ac.uk/primary\\_index/current\\_research/virus/Picornaviridae/Aphthovirus/index.html](http://www.iah.bbsrc.ac.uk/primary_index/current_research/virus/Picornaviridae/Aphthovirus/index.html)

Yours sincerely

[REDACTED]  
Head: World Reference Laboratory for FMD

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Pirbright Laboratory  
Ash Road, Pirbright, Woking  
Surrey GU24 0NF  
Tel: 01483-232441  
Fax: 01483-232448

Compton Laboratory  
Compton, Newbury,  
Berkshire RG20 7NN  
Tel: 01635-578411  
Fax: 01635-577237

# Molecular Epidemiology Report Form

IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: A WRL RefNo: LIB/1/2009 Sender Ref: Batch D F1 Date collected: 20/02/2009 Date received by WRLFMD: 12/03/2009 Date received for sequencing: 16/03/2009 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 18/03/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ASIA Genotype/strain: Iran-05 Sequence filename: LIB09-01.SEQ Date sequence last updated: 17/03/2009 Total no. of comparisons: 1033 Min. no. of nt for comparison: 300 Total turn-around time: 6 days Sequencing time: 2 days
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Comments:

### Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/LIB/2/2009	LIB09-02	639	639	0	100	0
2	A/IRQ/10/2009	IRQ09-10	639	638	0	99.84	0.16
3	A/IRQ/11/2009	IRQ09-11	639	638	0	99.84	0.16
4	A/IRQ/12/2009	IRQ09-12	639	638	0	99.84	0.16
5	A/IRQ/15/2009	IRQ09-15	639	638	0	99.84	0.16
6	A/IRQ/17/2009	IRQ09-17	639	638	0	99.84	0.16
7	A/IRQ/19/2009	IRQ09-19	639	638	0	99.84	0.16
8	A/IRQ/21/2009	IRQ09-21	639	638	0	99.84	0.16
9	A/IRQ/9/2009	IRQ09-09	639	638	0	99.84	0.16
10	A/KUW/4/2009	KUW09-04	639	638	0	99.84	0.16

### Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/IRN/1/2005 (EF208769)	IRN05-01	639	611	0	95.62	4.38
2	A/SAU/41/91	SAU91-41	636	542	0	85.22	14.78
3	A/TAI/118/87* (EF208777)	TAI87-AD	636	538	0	84.59	15.41
4	A/IRN/2/87 (EF208770)	IRN87-02	636	536	0	84.28	15.72
5	A/IRN/22/99 (EF208772)	IRN99-22	636	531	0	83.49	16.51
6	A/SAU/23/86 (EU414536)	SAU86-23	639	532	0	83.26	16.74
7	A/IRN/1/96 (EF208771)	IRN96-01	638	531	1	83.23	16.77
8	A/TAI/2/97 (EF208778)	TAI97-02	636	527	0	82.86	17.14
9	A22/IRQ/24/64 (AJ251474)	IRQ64-24	639	526	0	82.32	17.68
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55-C	639	515	0	80.59	19.41

nt, nucleotides

\*, not a WRLFMD reference number

# Molecular Epidemiology Report Form

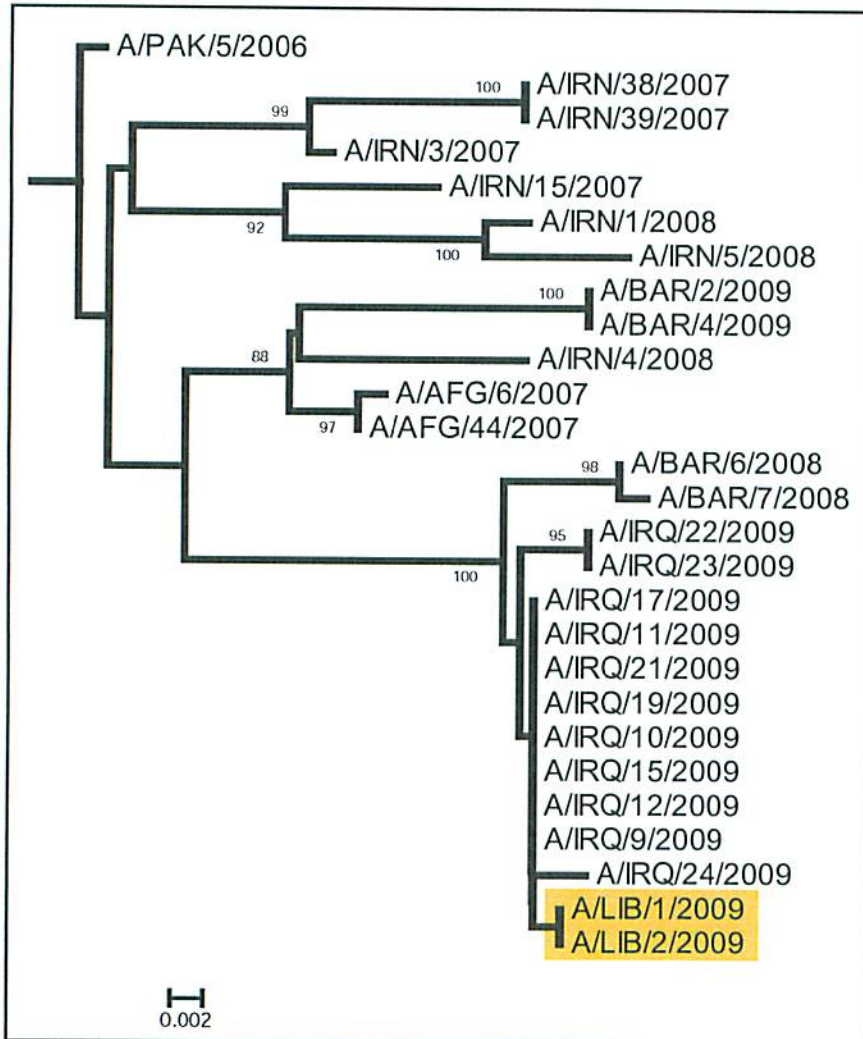
IAH-P-EP-MEG-FOR-005-1

Page 1 of 1

Serotype: A WRL RefNo: LIB/2/2009 Sender Ref: Batch D F2 Date collected: 20/02/2009 Date received by WRLFMD: 12/03/2009 Date received for sequencing: 16/03/2009 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639	Report date: 18/03/2009 Reported by: N.J. Knowles Checked by: D.P. King  Topotype: ASIA Genotype/strain: Iran-05 Sequence filename: LIB09-02.SEQ Date sequence last updated: 17/03/2009 Total no. of comparisons: 1033 Min. no. of nt for comparison: 300 Total turn-around time: 6 days Sequencing time: 2 days																																																																																								
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nt, nucleotides *, not a WRLFMD reference number																																																																																									

# Report on FMDV A from Libya in 2009

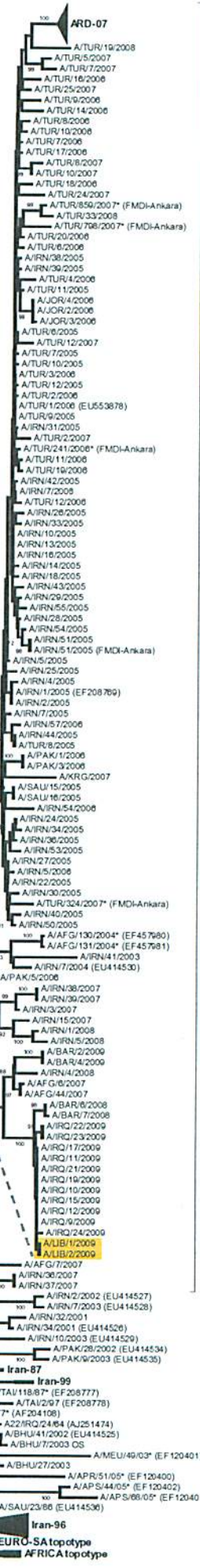
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 ->Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)  
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 ->Gaps/Missing Data : Pairwise Deletion  
 ->Codon Positions : 1st+2nd+3rd+Noncoding  
 Substitution Model : =====  
 ->Model : Nucleotide: Kimura 2-parameter  
 ->Substitutions to Include : d: Transitions + Transversions  
 ->Pattern among Lineages : Same (Homogeneous)  
 ->Rates among sites : Uniform rates  
 No. of Sites : 645  
 No Of Bootstrap Reps = 1000  
 Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

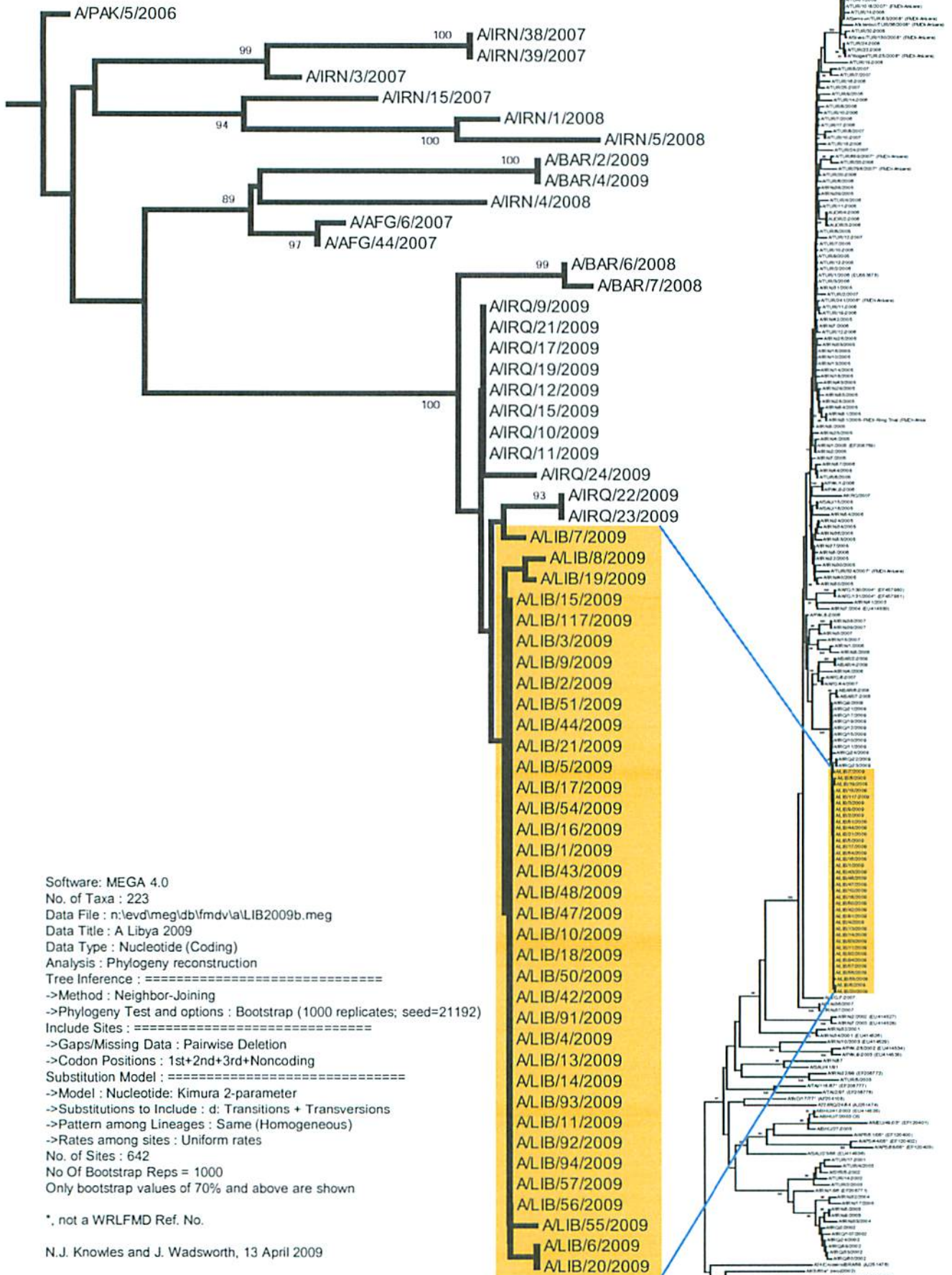
N.J. Knowles and J. Wadsworth, 17 March 2009





# Report on FMDV A from Libya in 2009

Batch: WRLFMD/2009/00011



Software: MEGA 4.0  
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 Data File : n:\evd\meg\lb\fmv\al\LIB2009b.meg  
 Data Title : A Libya 2009  
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 Only bootstrap values of 70% and above are shown

\*. not a WRLFMD Ref. No.

N.J. Knowles and J. Wadsworth, 13 April 2009

0.002