



**INSTITUTE FOR ANIMAL HEALTH**

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## FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2011/00019

Sender Details:

Date Received: 6<sup>th</sup> April 2011

Country of Origin: Iraq

Date Reported: 24<sup>th</sup> May 2011

Dear Dr. Basem Adhadh,

**Re.: Serotype A**

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: 24/05/2011

Testing carried out by WRLFMD is UKAS ISO/IEC 17025 accredited. Please see link for scope of accreditation:

[http://www.ukas.org/testing/lab\\_detail.asp?lab\\_id=2811&location\\_id=&vMenuOption=3](http://www.ukas.org/testing/lab_detail.asp?lab_id=2811&location_id=&vMenuOption=3) . 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](mailto:elizabeth.wilson@bbsrc.ac.uk))

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

## Genotyping Report

Report Date for this Batch: 24 May 2011

FMDV type A

Country: Iraq

Period: 2010

No. of samples: 1

BATCH: WRLFMD/2011/000019



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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: A	Report date: 24/05/2011
WRLFMD Ref No: IRQ/5/2010	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00019	Checked by: D.P. King
Sender Ref: 6	
Location: Baghdad, Iraq	Topotype: ASIA
Date collected: 12/09/2010	Genotype/strain: Iran-05 <sup>AFG-07</sup>
Date received by WRLFMD: 06/04/2011	Sequence filename: IRQ10-05.SEQ
Date received for sequencing: 18/04/2011	Date sequence last updated: 21/04/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1298
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 48 days
	Sequencing time: 36 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/PAK/37/2010	PAK10-37	639	634	0	99.22	0.78	ASIA	Iran-05 <sup>AFG-07</sup>
2	A/IRN/4/2011	IRN11-04	639	633	0	99.06	0.94	ASIA	Iran-05 <sup>AFG-07</sup>
3	A/TUR/1538/2010* (FMDI)	TUR10-AN	639	633	0	99.06	0.94	ASIA	Iran-05 <sup>AFG-07</sup>
4	A/TUR/40/2010	TUR10-40	639	633	0	99.06	0.94	ASIA	Iran-05 <sup>AFG-07</sup>
5	A/TUR/5/2011	TUR11-05	639	633	0	99.06	0.94	ASIA	Iran-05 <sup>AFG-07</sup>
6	A/IRN/125/2010	IRN10125	639	632	0	98.90	1.10	ASIA	Iran-05 <sup>AFG-07</sup>
7	A/IRN/24/2011	IRN11-24	639	632	0	98.90	1.10	ASIA	Iran-05 <sup>AFG-07</sup>
8	A/IRN/5/2011	IRN11-05	639	632	0	98.90	1.10	ASIA	Iran-05 <sup>AFG-07</sup>
9	A/TUR/10/2011	TUR11-10	639	632	0	98.90	1.10	ASIA	Iran-05 <sup>AFG-07</sup>
10	A/TUR/13/2011	TUR11-13	639	632	0	98.90	1.10	ASIA	Iran-05 <sup>AFG-07</sup>
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	A/AFG/6/2007	AFG07-06	639	604	0	94.52	5.48	ASIA	Iran-05 <sup>AFG-07</sup>
2	A/BAR/6/2008	BAR08-06	639	598	0	93.58	6.42	ASIA	Iran-05 <sup>BAR-08</sup>
3	A/TUR/33/2008	TUR08-33	639	595	0	93.11	6.89	ASIA	Iran-05 <sup>EZM-07</sup>
4	A/IRN/1/2005 (EF208769)	IRN05-01	639	594	0	92.96	7.04	ASIA	Iran-05
5	A/TUR/1/2008	TUR08-01	639	592	0	92.64	7.36	ASIA	Iran-05 <sup>ARD-07</sup>
6	A/IRN/22/99 (EF208772)	IRN99-22	636	537	0	84.43	15.57	ASIA	Iran-99
7	A/IRN/2/87 (EF208770)	IRN87-02	636	532	0	83.65	16.35	ASIA	Iran-87
8	A/TAI/118/87* (EF208777)	TAI87-AD	636	527	0	82.86	17.14	ASIA	Thai-87
9	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	525	0	82.16	17.84	ASIA	A <sub>15</sub>
10	A/IRN/1/96 (EF208771)	IRN96-01	638	524	1	82.13	17.87	ASIA	Iran-96

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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# Report on FMDV A in Iraq in 2010

Batch: WRLFMD/2011/00019

◆ 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 : 639

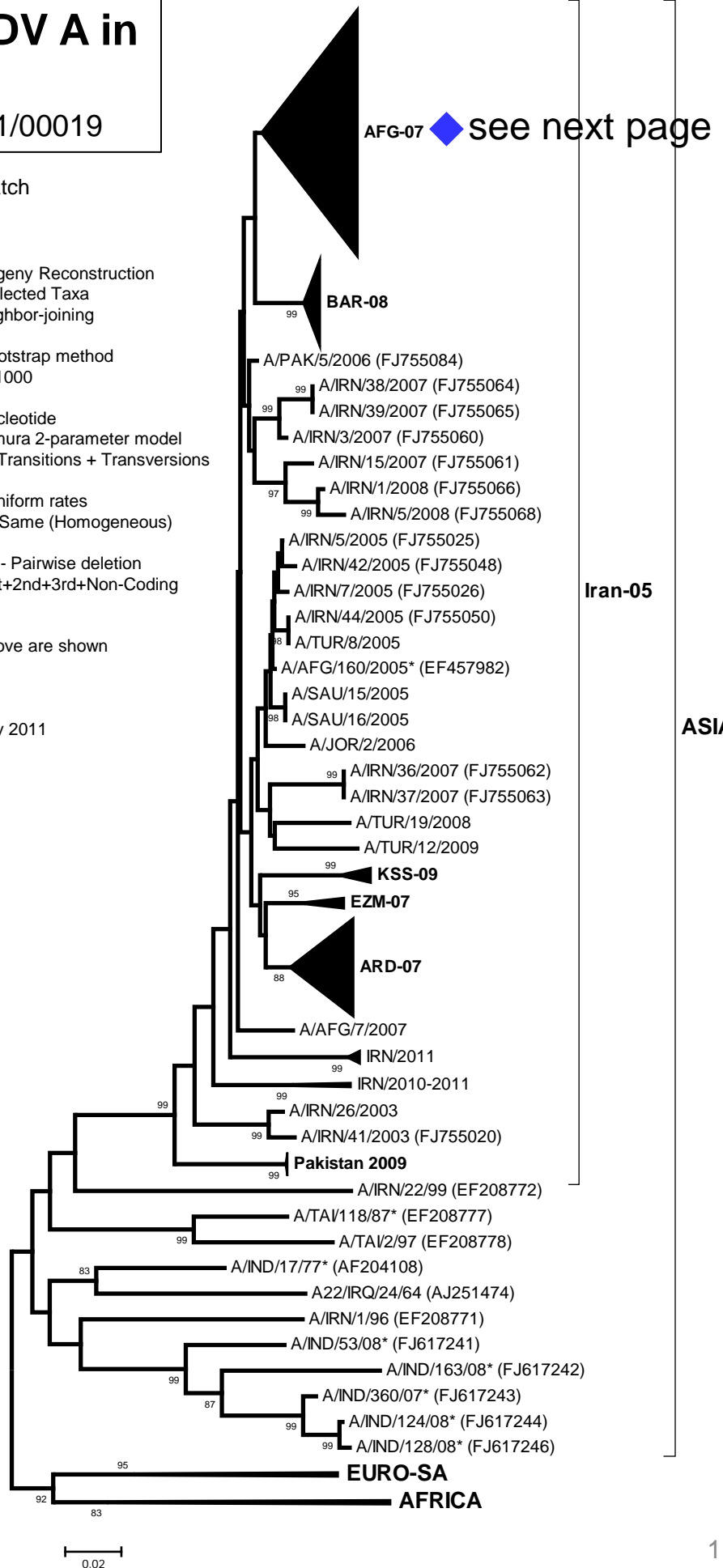
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 24 May 2011

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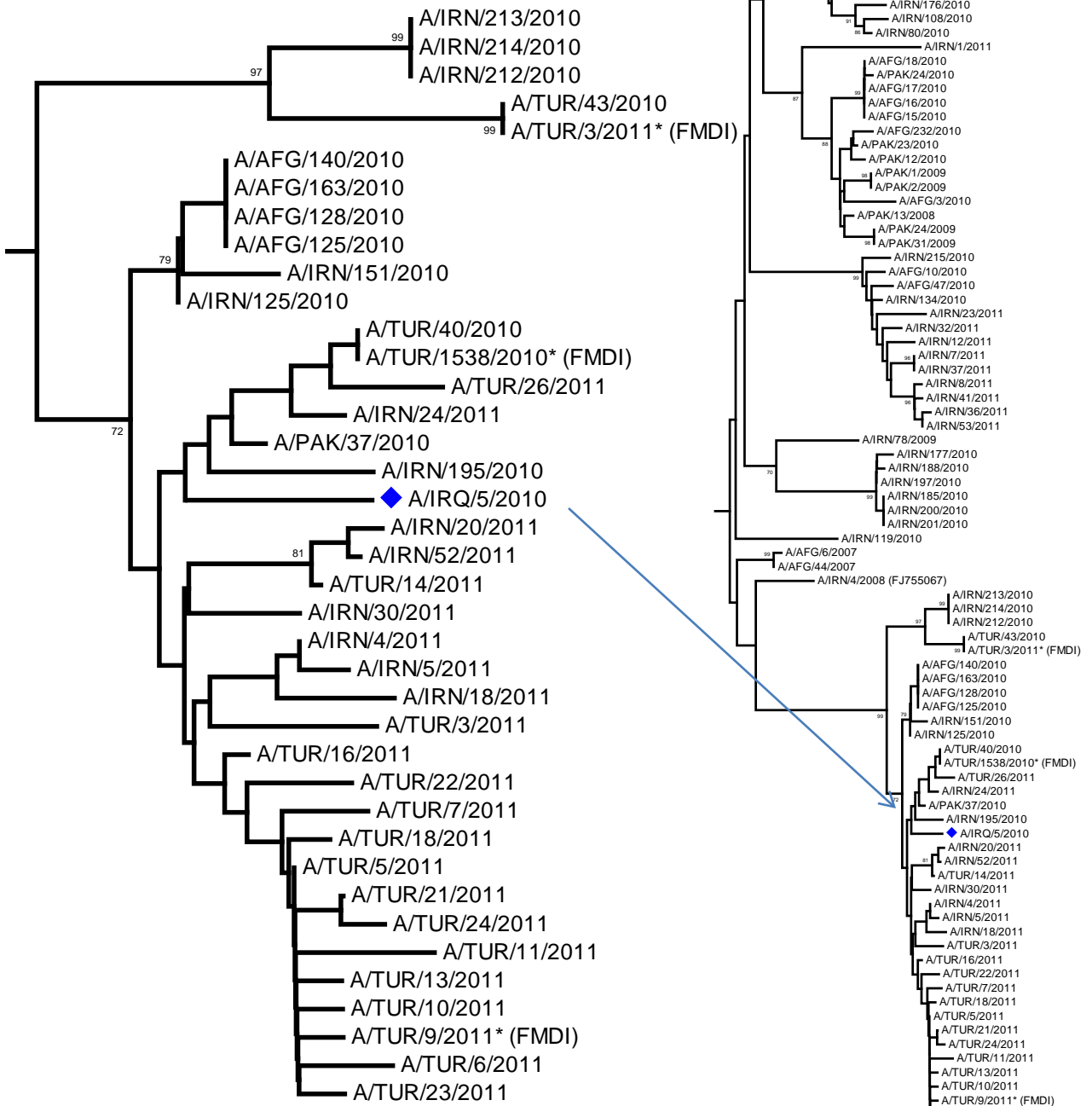


# Report on FMDV A in Iraq in 2010

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◆ indicates viruses in this batch

## A/ASIA/Iran-05<sup>AFG-07</sup>



0.002

0.005