

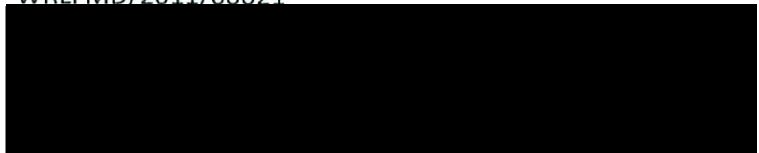


INSTITUTE FOR ANIMAL HEALTH
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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2011/00021

Sender Details:



Date Received: 31st March 2011

Country of Origin: Pakistan

Date Reported: 26th May 2011

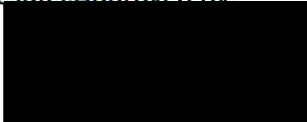
Dear Dr. Ehtisham Khan,

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/>

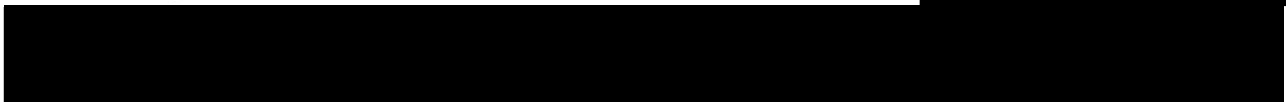
Results Approved By:



Official Stamp:



Date: 26/5/11



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: 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: Pakistan

Period: 2011

No. of samples: 1

BATCH: WRLFMD/2011/00021



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FAO World Reference Laboratory for FMD Genotyping Report

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

Page 1 of 1

Serotype: A	Report date: 24/05/2011
WRLFMD Ref No: PAK/86/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00021	Checked by: D.P. King
Sender Ref: PSG 41	
Location: Sargodha, Punjab, Pakistan	Topotype: ASIA
Date collected: 21/02/2011	Genotype/strain: Iran-05 ^{AFG-07}
Date received by WRLFMD: 31/03/2011	Sequence filename: PAK11-86.SEQ
Date received for sequencing: 03/05/2011	Date sequence last updated: 04/05/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy2	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: A-1C562F/EUR-2B52R	Total no. of comparisons: 1299
A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 54 days
	Sequencing time: 21 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/AFG/47/2010	AFG10-47	639	635	0	99.37	0.63	ASIA	Iran-05 ^{AFG-07}
2	A/IRN/134/2010	IRN10134	639	635	0	99.37	0.63	ASIA	Iran-05 ^{AFG-07}
3	A/IRN/32/2011	IRN11-32	639	635	0	99.37	0.63	ASIA	Iran-05 ^{AFG-07}
4	A/AFG/10/2010	AFG10-10	639	633	0	99.06	0.94	ASIA	Iran-05 ^{AFG-07}
5	A/IRN/37/2011	IRN11-37	639	633	0	99.06	0.94	ASIA	Iran-05 ^{AFG-07}
6	A/IRN/7/2011	IRN11-07	639	633	0	99.06	0.94	ASIA	Iran-05 ^{AFG-07}
7	A/IRN/12/2011	IRN11-12	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
8	A/IRN/215/2010	IRN10215	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
9	A/IRN/41/2011	IRN11-41	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
10	A/IRN/53/2011	IRN11-53	639	632	0	98.90	1.10	ASIA	Iran-05 ^{AFG-07}
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	A/AFG/6/2007	AFG07-06	639	612	0	95.77	4.23	ASIA	Iran-05 ^{AFG-07}
2	A/IRN/1/2005 (EF208769)	IRN05-01	639	605	0	94.68	5.32	ASIA	Iran-05
3	A/BAR/6/2008	BAR08-06	639	602	0	94.21	5.79	ASIA	Iran-05 ^{BAR-08}
4	A/TUR/1/2008	TUR08-01	639	598	0	93.58	6.42	ASIA	Iran-05 ^{ARD-07}
5	A/TUR/33/2008	TUR08-33	639	595	0	93.11	6.89	ASIA	Iran-05 ^{EZM-07}
6	A/IRN/9/2011	IRN11-09	639	586	0	91.71	8.29	ASIA	Iran-05 ^{QAZ-11}
7	A/IRN/9/2010	IRN10-09	639	584	0	91.39	8.61	ASIA	Iran-05 ^{ESF-10}
8	A/TAI/118/87* (EF208777)	TAI87-AD	636	532	0	83.65	16.35	ASIA	Thai-87
9	A/IRN/2/87 (EF208770)	IRN87-02	636	530	0	83.33	16.67	ASIA	Iran-87
10	A/TAI/2/97 (EF208778)	TAI97-02	636	527	0	82.86	17.14	ASIA	Thai-97

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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Report on FMDV A in Pakistan in 2011

Batch: WRLFMD/2011/00021

◆ indicates viruses in this batch

Software: MEGA 5.0

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 639

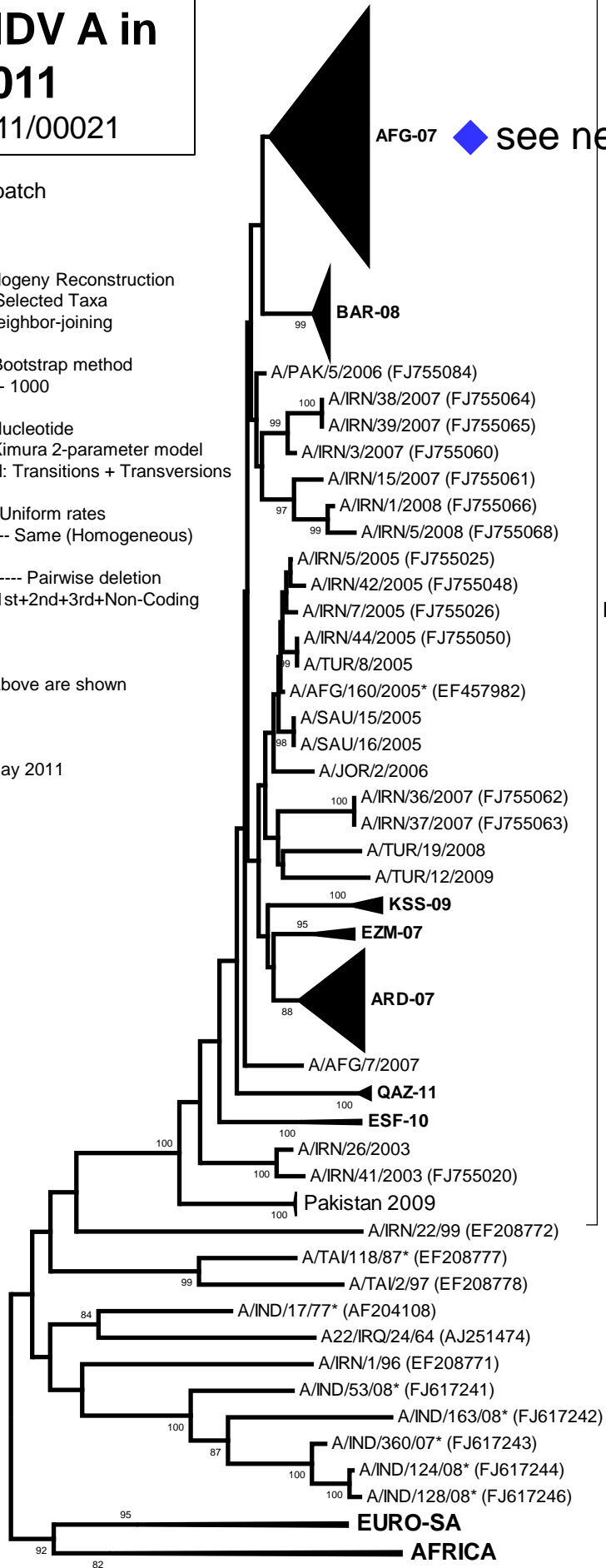
No Of Bootstrap Reps = 1000

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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AFG-07 ◆ see next page

Iran-05

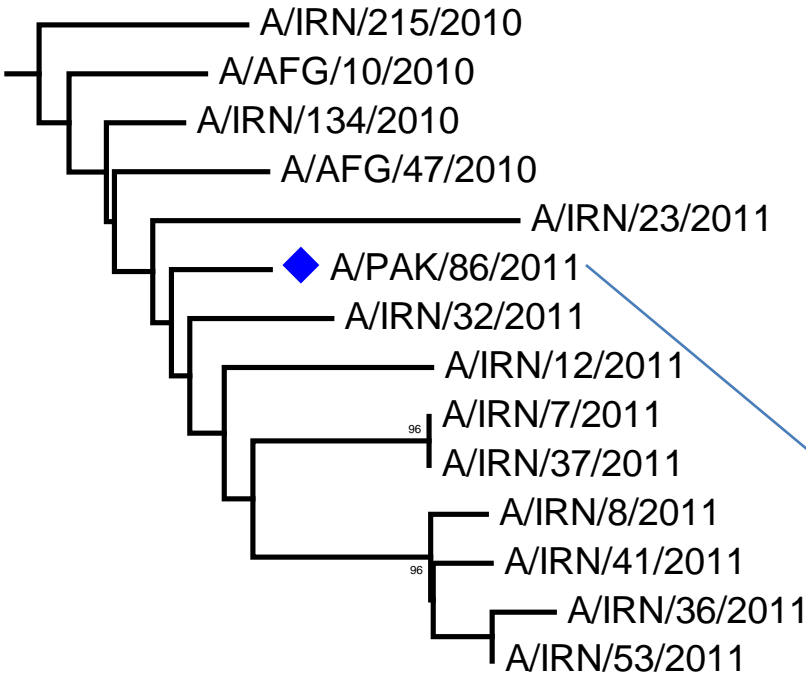
ASIA

0.02

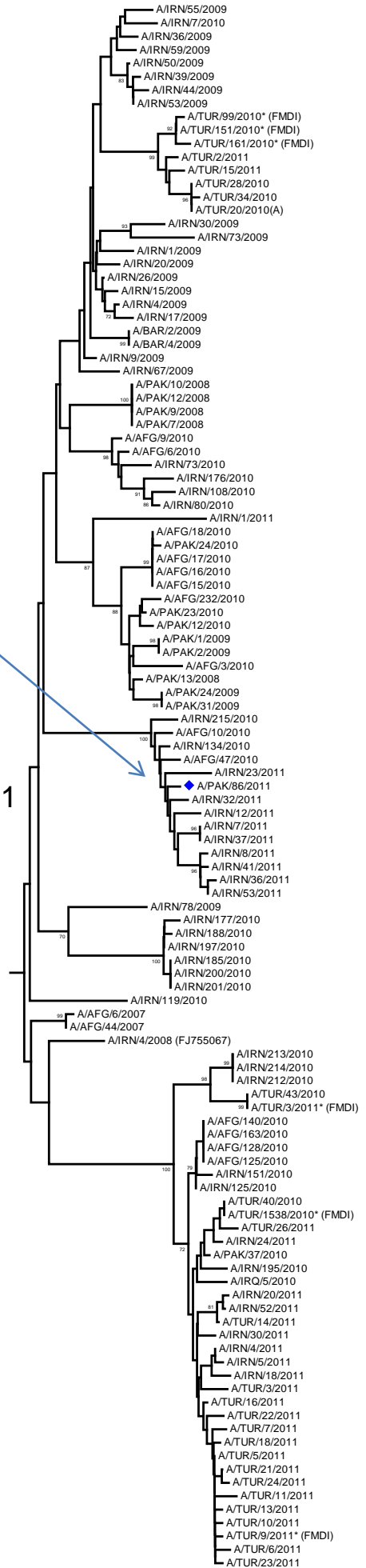
Report on FMDV A in Pakistan in 2011

Batch: WRLFMD/2011/00021

◆ indicates viruses in this batch



0.001



A/ASIA/Iran-05AFG-07

0.005