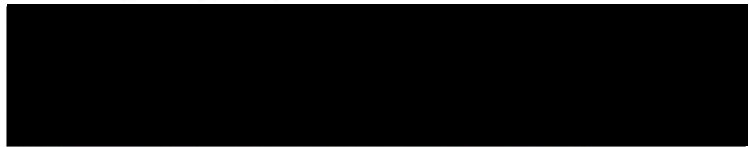




INSTITUTE FOR ANIMAL HEALTH
Director: Professor Martin W. Shirley, PhD
PIRBRIGHT LABORATORY
Ash Road,
Pirbright,
Surrey,
GU24 0NF
Intn Tel: 00 44 1483 232441
Tel: 01483 232441 Fax: 01483 232621

FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2010/00029
Sender Details:



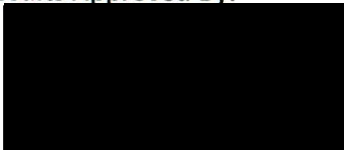
Date Received: 31st August 2010
Country of Origin: Pakistan
Date Reported: 8th October 2010

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:

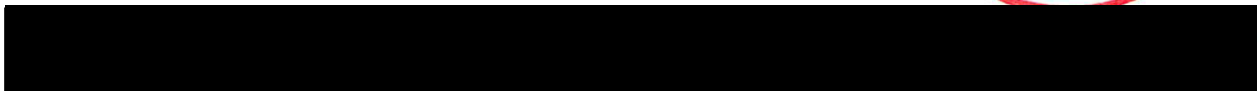


Official Stamp:



Date:

8/10/10



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: 7 October 2010

FMDV type A

Country: Pakistan

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00029



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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: 03/10/2010 |
| WRLFMD Ref No: PAK/37/2010 | Reported by: N.J. Knowles |
| Batch No: WRLFMD/2010/00029 | Checked by: D.P. King |
| Sender Ref: PSW 1 | |
| Location: Sahiwal, Pakistan | Topotype: ASIA |
| Date collected: 30/07/2010 | Genotype/strain: Iran-05 ^{AFG-07} |
| Date received by WRLFMD: 31/08/2010 | Sequence filename: PAK10-37.SEQ |
| Date received for sequencing: 17/09/2010 | Date sequence last updated: 03/10/2010 |
| Species: Buffalo | 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: 1171 |
| A-1C612F/EUR-2B52R | Min. no. of nt for comparison: 600 |
| | Total turn-around time: 33 days |
| | Sequencing time: 16 days |
| Comments: FMDV type O also isolated from this sample. | |

| Most Closely Related Viruses | | | | | | | | | |
|--|-------------------------------|----------|--------------|---------------|---------------|-------|---------|----------|---------------------------|
| Pos. | Virus name | Filename | No. nt comp. | No. nt match. | No. of ambig. | % Id. | % Diff. | Topotype | Strain |
| 1 | A/IRN/125/2010 | IRN10125 | 639 | 637 | 0 | 99.69 | 0.31 | ASIA | Iran-05 ^{AFG-07} |
| 2 | A/IRN/151/2010 | IRN10151 | 639 | 635 | 0 | 99.37 | 0.63 | ASIA | Iran-05 ^{AFG-07} |
| 3 | A/IRN/4/2008 (FJ755067) | IRN08-04 | 639 | 611 | 0 | 95.62 | 4.38 | ASIA | Iran-05 ^{AFG-07} |
| 4 | A/AFG/44/2007 | AFG07-44 | 639 | 608 | 0 | 95.15 | 4.85 | ASIA | Iran-05 ^{AFG-07} |
| 5 | A/AFG/6/2007 | AFG07-06 | 639 | 607 | 0 | 94.99 | 5.01 | ASIA | Iran-05 ^{AFG-07} |
| 6 | A/PAK/5/2006 | PAK06-05 | 639 | 606 | 0 | 94.84 | 5.16 | ASIA | Iran-05 ^{AFG-07} |
| 7 | A/PAK/5/2006 (EF494488) | PAK06-AC | 639 | 606 | 0 | 94.84 | 5.16 | ASIA | Iran-05 ^{AFG-07} |
| 8 | A/BAR/2/2009 | BAR09-02 | 639 | 604 | 0 | 94.52 | 5.48 | ASIA | Iran-05 ^{AFG-07} |
| 9 | A/BAR/4/2009 | BAR09-04 | 639 | 604 | 0 | 94.52 | 5.48 | ASIA | Iran-05 ^{AFG-07} |
| 10 | A/IRN/9/2009 | IRN09-09 | 639 | 604 | 0 | 94.52 | 5.48 | 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 | 607 | 0 | 94.99 | 5.01 | ASIA | Iran-05 ^{AFG-07} |
| 2 | A/BAR/6/2008 | BAR08-06 | 639 | 599 | 0 | 93.74 | 6.26 | ASIA | Iran-05 ^{BAR-08} |
| 3 | A/TUR/33/2008 | TUR08-33 | 639 | 598 | 0 | 93.58 | 6.42 | ASIA | Iran-05 ^{EZM-07} |
| 4 | A/IRN/1/2005 (EF208769) | IRN05-01 | 639 | 597 | 0 | 93.43 | 6.57 | ASIA | Iran-05 |
| 5 | A/TUR/1/2008 | TUR08-01 | 639 | 595 | 0 | 93.11 | 6.89 | ASIA | Iran-05 ^{ARD-07} |
| 6 | A/IRN/22/99 (EF208772) | IRN99-22 | 636 | 538 | 0 | 84.59 | 15.41 | ASIA | Iran-99 |
| 7 | A/IRN/2/87 (EF208770) | IRN87-02 | 636 | 535 | 0 | 84.12 | 15.88 | ASIA | Iran-87 |
| 8 | A/TAI/118/87* (EF208777) | TAI87-AD | 636 | 528 | 0 | 83.02 | 16.98 | ASIA | Thai-87 |
| 9 | A15/Bangkok/TAI/60 (AY593755) | TAI60--D | 639 | 526 | 0 | 82.32 | 17.68 | ASIA | A ₁₅ |
| 10 | A/IRN/1/96 (EF208771) | IRN96-01 | 638 | 525 | 1 | 82.29 | 17.71 | ASIA | Iran-96 |

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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Report on FMDV A in Pakistan in 2010

Batch: WRLFMD/2010/00029

Software: MEGA 4.0

No. of Taxa : 199

Data File : n:\evd\meg\db\fmdv\A\tUR2010c.meg

Data Title : A Turkey and Pakistan 2010

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=24054)

Include Sites : =====

->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 : 639

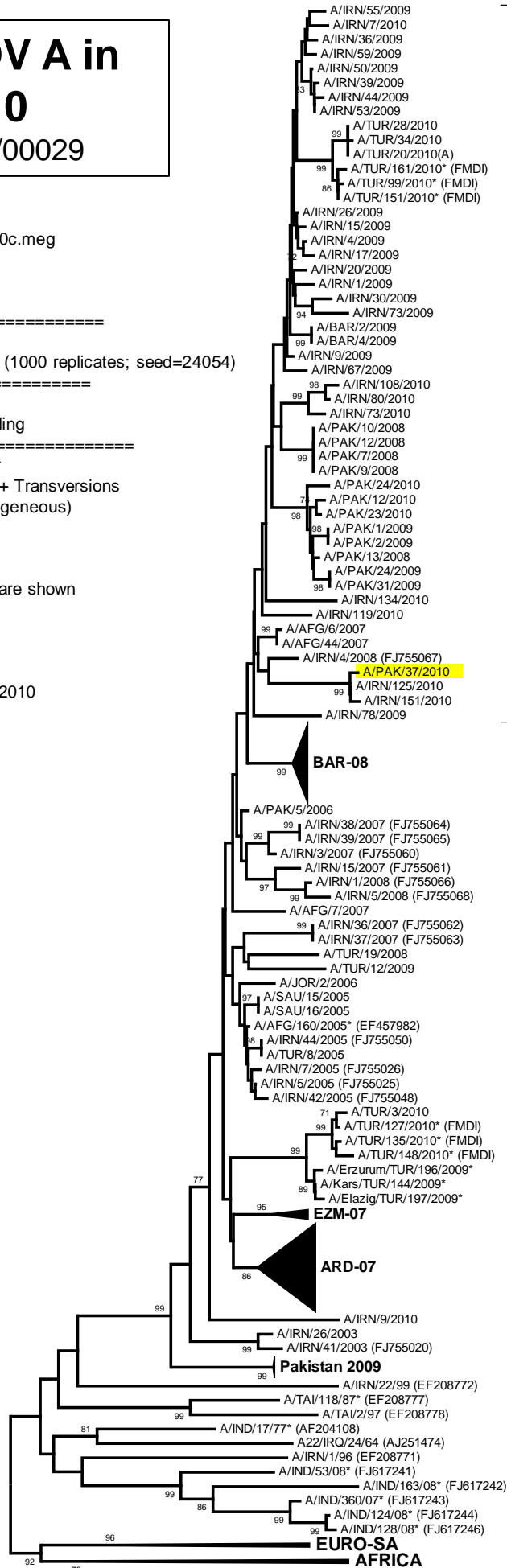
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 7 October 2010

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AFG-07

Iran-05

ASIA

0.02