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

Genotyping Report

Report Date for this Batch: 4 April 2014

FMDV type Asia 1
Country: Iran
Period: 2013
No. of samples: 1

BATCH: WRLFMD/2014/000006

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: ASIA1	Report date: 04/04/2014
WRLFMD Ref No: IRN/15/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2014/00006	Checked by: K. Bachanek-Bankowska
Sender Ref: IR-92 A-23	
Location: Tehran, Iran	Topotype: ASIA
Date collected: 21/09/2013	Genotype/strain: Sindh-08
Date received by WRLFMD: 05/02/2014	Sequence filename: IRN13-15.SEQ
Date received for sequencing: 11/03/2014	Date sequence last updated: 18/03/2014
Species: Cattle	No. of Nt determined: 633
Material used: BTy1 25/02/2014	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: As1-1C530F/EUR-2B52R	Total no. of comparisons: 523
As1-1C613F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 58 days
	Sequencing time: 24 days

Comments:

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/23/2013	PAK13-23	633	625	0	98.74	1.26	ASIA	Sindh-08
2	Asia1/PAK/10/2012	PAK12-10	633	614	0	97.00	3.00	ASIA	Sindh-08
3	Asia1/IRN/49/2011	IRN11-49	633	613	0	96.84	3.16	ASIA	Sindh-08
4	Asia1/PAK/106/2010	PAK10106	633	613	0	96.84	3.16	ASIA	Sindh-08
5	Asia1/PAK/108/2010	PAK10108	633	613	0	96.84	3.16	ASIA	Sindh-08
6	Asia1/PAK/11/2011	PAK11-11	633	613	0	96.84	3.16	ASIA	Sindh-08
7	Asia1/PAK/110/2010	PAK10110	633	613	0	96.84	3.16	ASIA	Sindh-08
8	Asia1/PAK/111/2010	PAK10111	633	613	0	96.84	3.16	ASIA	Sindh-08
9	Asia1/PAK/12/2011	PAK11-12	633	613	0	96.84	3.16	ASIA	Sindh-08
10	Asia1/PAK/13/2011	PAK11-13	633	613	0	96.84	3.16	ASIA	Sindh-08

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	Asia1/PAK/8/2008	PAK08-08	633	600	0	94.79	5.21	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	577	0	91.15	8.85	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	536	0	84.68	15.32	ASIA	Group III
4	Asia1/IND/63/72* (AY304994)	IND72C63	630	530	0	84.13	15.87	ASIA	Unnamed
5	Asia1/IND/18/80 (DQ121116)	IND80-18	633	528	0	83.41	16.59	ASIA	Group V
6	Asia1/HKN/19/74	HKN74-19	633	526	0	83.10	16.90	ASIA	Unnamed
7	Asia1/Shamir/ISR/89	ISR89--A	633	525	0	82.94	17.06	ASIA	Unnamed
8	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	525	0	82.94	17.06	ASIA	Unnamed
9	Asia1/IND/14/95* (AF390678)	IND95-AA	633	524	0	82.78	17.22	ASIA	Unnamed
10	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	519	0	81.99	18.01	ASIA	Group VIb

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.1

Report on FMDV Asia 1 in Iran in 2013

Batch: WRLFMD/2014/00006

◆ indicates viruses in this batch

Software: MEGA 6.06
Analysis
  Analysis ---------------------------- Phylogeny Reconstruction
  Scope ------------------------------ All Selected Taxa
  Statistical Method ------------------ Minimum Evolution method
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
Tree Inference Options
  ME Heuristic Method ----------------- Close-Neighbor-Interchange (CNI)
  Initial Tree for ME ----------------- Obtain initial tree by Neighbor-Joining
  Codons Included --------------------- 1st+2nd+3rd+Non-Coding
No. of Sites : 633
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,
04 April 2014