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

Genotyping Report

Report Date for this Batch: 10 June 2014

FMDV type Asia 1
Country: People's Republic of China
Period: 2013
No. of sequences: 3 (VP1)
Originator: Sequences deposited on GenBank by the College of Animal Science, Guizhou University, Xueshi Road, Guiyang, Guizhou 550025, P.R. China.

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: ASIA1	Report date: 09/06/2014
WRLFMD Ref No: GZ-ZJ/CHA/2013	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00012	Checked by: K. Bachanek-Bankowska
Sender Ref: GZ-ZJ	
Location: GuiZhou Province, China	Topotype: ASIA
Date collected: 04/05/2013	Genotype/strain: unnamed
Date received by WRLFMD: 07/06/2014	Sequence filename: CHA13-AM.SEQ
Date received for sequencing: n/a	Date sequence last updated: 09/06/2014
Species: Cow	No. of Nt determined: 633
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: Not known	Total no. of comparisons: 530
	Min. no. of nt for comparison: 600
	Total turn-around time: 2 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/GZ-QZ/CHA/2013 (KJ646654)	CHA13-AO	633	626	0	98.89	1.11	ASIA	unnamed
2	Asia1/GZ-KY/CHA/2013 (KJ646653)	CHA13-AN	633	606	0	95.73	4.27	ASIA	unnamed
3	Asia1/HKN/1/2005 (DQ121114)	HKN05-01	633	604	0	95.42	4.58	ASIA	unnamed
4	Asia1/HKN/3/2005	HKN05-03	633	604	0	95.42	4.58	ASIA	unnamed
5	Asia1/HKN/5/2005	HKN05-05	633	604	0	95.42	4.58	ASIA	unnamed
6	Asia1/HKN/7/2005	HKN05-07	633	604	0	95.42	4.58	ASIA	unnamed
7	Asia1/HKN/2/2005 (DQ121115)	HKN05-02	633	603	0	95.26	4.74	ASIA	unnamed
8	Asia1/HKN/4/2005	HKN05-04	633	603	0	95.26	4.74	ASIA	unnamed
9	Asia1/HKN/6/2005	HKN05-06	633	603	0	95.26	4.74	ASIA	unnamed
10	Asia1/HKN/8/2005	HKN05-08	633	603	0	95.26	4.74	ASIA	unnamed

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/IRN/10/2004 (DQ121119)	IRN04-10	633	568	0	89.73	10.27	ASIA	Group VIb
2	Asia1/IND/14/95* (AF390678)	IND95-AA	633	567	0	89.57	10.43	ASIA	Unnamed
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	556	0	87.84	12.16	ASIA	Group III
4	Asia1/Shamir/ISR/89	ISR89--A	633	554	0	87.52	12.48	ASIA	Unnamed
5	Asia1/IND/18/80 (DQ121116)	IND80-18	633	542	0	85.62	14.38	ASIA	Group V
6	Asia1/IND/63/72* (AY304994)	IND72C63	630	535	0	84.92	15.08	ASIA	Unnamed
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	535	0	84.52	15.48	ASIA	Unnamed
8	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	525	0	82.94	17.06	ASIA	Group I
9	Asia1/HKN/19/74	HKN74-19	633	525	0	82.94	17.06	ASIA	Unnamed
10	Asia1/PAK/8/2008	PAK08-08	633	523	0	82.62	17.38	ASIA	Sindh-08

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: ASIA1	Report date: 09/06/2014
WRLFMD Ref No: GZ-KY/CHA/2013	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00012	Checked by: K. Bachanek-Bankowska
Sender Ref: GZ-KY	
Location: GuiZhou Province, China	Topotype: ASIA
Date collected: 04/05/2013	Genotype/strain: unnamed
Date received by WRLFMD: 07/06/2014	Sequence filename: CHA13-AN.SEQ
Date received for sequencing: n/a	Date sequence last updated: 09/06/2014
Species: Cow	No. of Nt determined: 633
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: Not known	Total no. of comparisons: 530
	Min. no. of nt for comparison: 600
	Total turn-around time: 2 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/GZ-QZ/CHA/2013 (KJ646654)	CHA13-AO	633	613	0	96.84	3.16	ASIA	unnamed
2	Asia1/GZ-ZJ/CHA/2013 (KJ646652)	CHA13-AM	633	606	0	95.73	4.27	ASIA	unnamed
3	Asia1/HKN/1/2005 (DQ121114)	HKN05-01	633	598	0	94.47	5.53	ASIA	unnamed
4	Asia1/HKN/3/2005	HKN05-03	633	598	0	94.47	5.53	ASIA	unnamed
5	Asia1/HKN/5/2005	HKN05-05	633	598	0	94.47	5.53	ASIA	unnamed
6	Asia1/HKN/7/2005	HKN05-07	633	598	0	94.47	5.53	ASIA	unnamed
7	Asia1/HKN/2/2005 (DQ121115)	HKN05-02	633	597	0	94.31	5.69	ASIA	unnamed
8	Asia1/HKN/4/2005	HKN05-04	633	597	0	94.31	5.69	ASIA	unnamed
9	Asia1/HKN/6/2005	HKN05-06	633	597	0	94.31	5.69	ASIA	unnamed
10	Asia1/HKN/8/2005	HKN05-08	633	597	0	94.31	5.69	ASIA	unnamed

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/IRN/10/2004 (DQ121119)	IRN04-10	633	566	0	89.42	10.58	ASIA	Group VIb
2	Asia1/IND/14/95* (AF390678)	IND95-AA	633	562	0	88.78	11.22	ASIA	Unnamed
3	Asia1/Shamir/ISR/89	ISR89--A	633	554	0	87.52	12.48	ASIA	Unnamed
4	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	553	0	87.36	12.64	ASIA	Group III
5	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	541	0	85.47	14.53	ASIA	Unnamed
6	Asia1/IND/63/72* (AY304994)	IND72C63	630	535	0	84.92	15.08	ASIA	Unnamed
7	Asia1/IND/18/80 (DQ121116)	IND80-18	633	533	0	84.20	15.80	ASIA	Group V
8	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	524	0	82.78	17.22	ASIA	Group I
9	Asia1/HKN/19/74	HKN74-19	633	524	0	82.78	17.22	ASIA	Unnamed
10	Asia1/PAK/8/2008	PAK08-08	633	520	0	82.15	17.85	ASIA	Sindh-08

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: ASIA1	Report date: 09/06/2014
WRLFMD Ref No: GZ-QZ/CHA/2013	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00012	Checked by: K. Bachanek-Bankowska
Sender Ref: GZ-QZ	
Location: GuiZhou Province, China	Topotype: ASIA
Date collected: 04/05/2013	Genotype/strain: unnamed
Date received by WRLFMD: 07/06/2014	Sequence filename: CHA13-AO.SEQ
Date received for sequencing: n/a	Date sequence last updated: 09/06/2014
Species: Cow	No. of Nt determined: 633
Material used: Not known	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: Not known	Total no. of comparisons: 530
	Min. no. of nt for comparison: 600
	Total turn-around time: 2 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/GZ-ZJ/CHA/2013 (KJ646652)	CHA13-AM	633	626	0	98.89	1.11	ASIA	unnamed
2	Asia1/GZ-KY/CHA/2013 (KJ646653)	CHA13-AN	633	613	0	96.84	3.16	ASIA	unnamed
3	Asia1/HKN/1/2005 (DQ121114)	HKN05-01	633	611	0	96.52	3.48	ASIA	unnamed
4	Asia1/HKN/3/2005	HKN05-03	633	611	0	96.52	3.48	ASIA	unnamed
5	Asia1/HKN/5/2005	HKN05-05	633	611	0	96.52	3.48	ASIA	unnamed
6	Asia1/HKN/7/2005	HKN05-07	633	611	0	96.52	3.48	ASIA	unnamed
7	Asia1/HKN/2/2005 (DQ121115)	HKN05-02	633	610	0	96.37	3.63	ASIA	unnamed
8	Asia1/HKN/4/2005	HKN05-04	633	610	0	96.37	3.63	ASIA	unnamed
9	Asia1/HKN/6/2005	HKN05-06	633	610	0	96.37	3.63	ASIA	unnamed
10	Asia1/HKN/8/2005	HKN05-08	633	610	0	96.37	3.63	ASIA	unnamed

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/IRN/10/2004 (DQ121119)	IRN04-10	633	573	0	90.52	9.48	ASIA	Group VIb
2	Asia1/IND/14/95* (AF390678)	IND95-AA	633	570	0	90.05	9.95	ASIA	Unnamed
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	561	0	88.63	11.37	ASIA	Group III
4	Asia1/Shamir/ISR/89	ISR89--A	633	558	0	88.15	11.85	ASIA	Unnamed
5	Asia1/IND/63/72* (AY304994)	IND72C63	630	539	0	85.56	14.44	ASIA	Unnamed
6	Asia1/IND/18/80 (DQ121116)	IND80-18	633	541	0	85.47	14.53	ASIA	Group V
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	537	0	84.83	15.17	ASIA	Unnamed
8	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	529	0	83.57	16.43	ASIA	Group I
9	Asia1/HKN/19/74	HKN74-19	633	529	0	83.57	16.43	ASIA	Unnamed
10	Asia1/PAK/8/2008	PAK08-08	633	526	0	83.10	16.90	ASIA	Sindh-08

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV Asia 1 in P.R. China in 2013

Batch: WRLMEG/2014/00012

◆ indicates viruses in this batch

Software: MEGA 6.06
Analysis
  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 : 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,
10 June 2014