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

Genotyping Report

Report Date for this Batch: 11 August 2014

FMDV type O
Country: Algeria
Period: 2014
No. of sequences: 2 (VP1)
Originator: [redacted] National Reference Centre for Vesicular Diseases, Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia Romagna (IZSLER), Brescia, Italy.

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: 1628-1468/Algeria/2014
Batch No: WRLMEG/2014/00030
Sender Ref: 1628-1468_Algeria_2014
Location: not known, Algeria
Date collected: 2014
Date received by WRLFMD: 11/08/2014
Date received for sequencing: n/a
Species: Not Known
Material used: Epithelium susp.
Region sequenced: VP1
RT-PCR primers: not known

Report date: 11/08/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: ME-SA
Genotype/strain: Ind-2001d
Sequence filename: ALG14-AA.SEQ
Date sequence last updated: 11/08/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 3939
Min. no. of nt for comparison: 600
Total turn-around time: 0 days

Comments:

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/1631-FA001/Algeria/2014 (IZSLER)	ALG14-AB	639	637	0	99.69	0.31	ME-SA	Ind-2001d
2	O/TUN/1031/2014* (IZSLER)	TUN14-AA	639	637	0	99.69	0.31	ME-SA	Ind-2001d
3	O/TUN/1054/2014* (IZSLER)	TUN14-AB	639	635	0	99.37	0.63	ME-SA	Ind-2001d
4	O/LIB/1/2013	LIB13-01	639	630	0	98.59	1.41	ME-SA	Ind-2001d
5	O/LIB/11/2013	LIB13-11	639	630	0	98.59	1.41	ME-SA	Ind-2001d
6	O/LIB/12/2013	LIB13-12	639	630	0	98.59	1.41	ME-SA	Ind-2001d
7	O/LIB/4/2013	LIB13-04	639	630	0	98.59	1.41	ME-SA	Ind-2001d
8	O/LIB/5/2013	LIB13-05	639	630	0	98.59	1.41	ME-SA	Ind-2001d
9	O/LIB/7/2013	LIB13-07	639	630	0	98.59	1.41	ME-SA	Ind-2001d
10	O/LIB/13/2013	LIB13-13	639	629	0	98.44	1.56	ME-SA	Ind-2001d

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	O/BHU/3/2009	BHU09-03	639	606	0	94.84	5.16	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	580	0	90.77	9.23	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	577	0	90.30	9.70	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	568	0	89.31	10.69	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	568	0	88.89	11.11	ME-SA	PanAsia-2$^{\text{FAR-09}}$
6	O/UKG/35/2001 (AJ539141)	UKG01-35	639	565	0	88.42	11.58	ME-SA	PanAsia
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	563	0	88.11	11.89	ME-SA	PanAsia-2$^{\text{TER-08}}$
8	O/IRN/8/2005	IRN05-08	639	562	0	87.95	12.05	ME-SA	PanAsia-2
9	O/PAK/16/2010	PAK10-16	639	561	0	87.79	12.21	ME-SA	PanAsia-2$^{\text{PUN-10}}$
10	O/IRN/18/2010	IRN10-18	639	560	0	87.64	12.36	ME-SA	PanAsia-2$^{\text{BAL-09}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O	Report date: 11/08/2014
WRLFMD Ref No: 1631-FA001/Algeria/2014	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00030	Checked by: K. Bachanek-Bankowska
Sender Ref: 1631-FA001_Algeria_2014	
Location: not known, Algeria	Topotype: ME-SA
Date collected: 2014	Genotype/strain: Ind-2001d
Date received by WRLFMD: 11/08/2014	Sequence filename: ALG14-AB.SEQ
Date received for sequencing: n/a	Date sequence last updated: 11/08/2014
Species: Not Known	No. of Nt determined: 639
Material used: Epithelium susp.	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: not known	Total no. of comparisons: 3939
	Min. no. of nt for comparison: 600
	Total turn-around time: 0 days
Comments:	

Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TUN/1031/2014* (IZSLER)	TUN14-AA	639	639	0	100.00	0.00	ME-SA	Ind-2001d
2	O/1628-1468/Algeria/2014 (IZSLER)	ALG14-AA	639	637	0	99.69	0.31	ME-SA	Ind-2001d
3	O/TUN/1054/2014* (IZSLER)	TUN14-AB	639	637	0	99.69	0.31	ME-SA	Ind-2001d
4	O/LIB/1/2013	LIB13-01	639	632	0	98.90	1.10	ME-SA	Ind-2001d
5	O/LIB/11/2013	LIB13-11	639	632	0	98.90	1.10	ME-SA	Ind-2001d
6	O/LIB/12/2013	LIB13-12	639	632	0	98.90	1.10	ME-SA	Ind-2001d
7	O/LIB/4/2013	LIB13-04	639	632	0	98.90	1.10	ME-SA	Ind-2001d
8	O/LIB/5/2013	LIB13-05	639	632	0	98.90	1.10	ME-SA	Ind-2001d
9	O/LIB/7/2013	LIB13-07	639	632	0	98.90	1.10	ME-SA	Ind-2001d
10	O/LIB/13/2013	LIB13-13	639	631	0	98.75	1.25	ME-SA	Ind-2001d

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	O/BHU/3/2009	BHU09-03	639	608	0	95.15	4.85	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	582	0	91.08	8.92	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	579	0	90.61	9.39	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	570	0	89.62	10.38	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	570	0	89.20	10.80	ME-SA	PanAsia-2$^{\text{FAR-09}}$
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	565	0	88.42	11.58	ME-SA	PanAsia-2$^{\text{TER-08}}$
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	565	0	88.42	11.58	ME-SA	PanAsia
8	O/IRN/8/2005	IRN05-08	639	564	0	88.26	11.74	ME-SA	PanAsia-2
9	O/PAK/16/2010	PAK10-16	639	563	0	88.11	11.89	ME-SA	PanAsia-2$^{\text{PUN-10}}$
10	O/IRN/18/2010	IRN10-18	639	562	0	87.95	12.05	ME-SA	PanAsia-2$^{\text{BAL-09}}$

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in Algeria in 2014

Batch: WRLMEG/2014/00030

◆ 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 : 642
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,
11 Auguts 2014