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

Genotyping Report

Report date for this batch: 16-Apr-2015

FMDV type: NVD

Country: ETHIOPIA

Year: 2014

WRL BATCH: WRLFMD/2014/00038

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

Genotyping Report

Report Date for this Batch: 18 December 2014

FMDV type O
Country: Ethiopia
Period: 2014
No. of samples: 1

BATCH: WRLFMD/2014/00038

Results of VP1 RT-PCR

Although no FMD virus could be isolated from the 16 Ethiopian samples in batch WRLFMD/2014/00038, real time RT-PCR revealed the presence of FMDV genome in eight samples. Six of these (with Ct values below 27) were subjected to conventional RT-PCRs using primer sets (for FMDV types O, A, SAT 1 and SAT 2) aimed at amplification of the VP1-coding region of the genome. Only two samples gave amplicons, which when subjected to DNA sequencing, gave positive results. The samples ETH/6/2014 and ETH/10/2014 were thus identified as FMDV type O. Only one of these, ETH/6/2014, produced enough sequence data to be able to produce this genotyping report.

N.J. Knowles, 18 December 2014

FAO World Reference Laboratory for FMD Genotyping Report

Serotype: O
WRLFMD Ref No: ETH/6/2014
Batch No: WRLFMD/2014/00038
Sender Ref: ET-7644/14
Location: Dinsho, Bale, Oromia, Ethiopia
Date collected: 13/02/2014
Date received by WRLFMD: 27/11/2014
Date received for sequencing: 15/11/2014
Species: Bovine
Material used: RNA
Region sequenced: VP1
RT-PCR primers: O-1C272F/EUR-2B52R

Report date: 18/12/2014
Reported by: N.J. Knowles
Checked by: K. Bachanek-Bankowska

Topotype: EA-3
Genotype/strain: unnamed
Sequence filename: ETH14-06.SEQ
Date sequence last updated: 18/12/2014
No. of Nt determined: 639
No. of ambiguities: 0
Gene length: 639
Total no. of comparisons: 4100
Min. no. of nt for comparison: 600
Total turn-around time: 21 days
Sequencing time: 33 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/ETH/45/2009	ETH09-45	639	620	0	97.03	2.97	EA-3	unnamed
2	O/ETH/7/2010	ETH10-07	639	617	0	96.56	3.44	EA-3	unnamed
3	O/ETH/8/2010	ETH10-08	639	616	0	96.40	3.60	EA-3	unnamed
4	O/ETH/38/2011	ETH11-38	639	615	0	96.24	3.76	EA-3	unnamed
5	O/ETH/13/2011	ETH11-13	639	614	0	96.09	3.91	EA-3	unnamed
6	O/ETH/3/2011	ETH11-03	639	614	0	96.09	3.91	EA-3	unnamed
7	O/ETH/4/2011	ETH11-04	639	614	0	96.09	3.91	EA-3	unnamed
8	O/ETH/42/2011	ETH11-42	639	614	0	96.09	3.91	EA-3	unnamed
9	O/ETH/5/2011	ETH11-05	639	614	0	96.09	3.91	EA-3	unnamed
10	O/ETH/11/2011	ETH11-11	639	613	0	95.93	4.07	EA-3	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	O/ETH/1/2007 (FJ798137)	ETH07-01	639	595	0	93.11	6.89	EA-3	unnamed
2	O/ETH/3/2004 (FJ798109)	ETH04-03	639	582	0	91.08	8.92	EA-3	unnamed
3	O/SUD/2/86 (DQ165075)	SUD86-02	639	564	0	88.26	11.74	EA-3	unnamed
4	O/IND/53/79 (AF292107)	IND79A53	639	548	0	85.76	14.24	ME-SA	unnamed
5	O/IND/R2/75* (AF204276)	IND75--A	639	548	0	85.76	14.24	ME-SA	unnamed
6	O/ETH/2/2006 (FJ798127)	ETH06-02	639	546	0	85.45	14.55	EA-3	unnamed
7	O/K83/79* (AJ303511)	KEN79B83	638	544	1	85.27	14.73	EA-1	unnamed
8	O/BHU/3/2009 (KM921814)	BHU09-03	639	542	0	84.82	15.18	ME-SA	Ind-2001d
9	O/IRN/31/2009	IRN09-31	639	542	0	84.82	15.18	ME-SA	PanAsia-2$^{\text{FAR-09}}$
10	O/UGA/3/2002 (DQ165077)	UGA02-03	639	542	0	84.82	15.18	EA-2	unnamed

nt, nucleotides
*, not a WRLFMD reference number

Assembled with Report Generator v4.3

Report on FMDV O in Ethiopia in 2014

Batch: WRLFMD/2014/00038

◆ 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,
18 December 2014