

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

Genotyping Report

Report Date for this Batch: 8 June 2015

FMDV type O

Country: Ethiopia

Period: 2015

No. of samples: 3

BATCH: WRLFMD/2015/00009



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FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O	Report date: 08/06/2015
WRLFMD Ref No: ETH/3/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00009	Checked by: K. Bachanek-Bankowska
Sender Ref: ET-9997	
Location: Fafan, Fafan zone, Somali, Ethiopia	Topotype: EA-3
Date collected: 13/03/2015	Genotype/strain: unnamed
Date received by WRLFMD: 07/05/2015	Sequence filename: ETH15-03.SEQ
Date received for sequencing: 28/05/2015	Date sequence last updated: 04/06/2015
Species: Cattle (local Zebu)	No. of Nt determined: 639
Material used: BTY1 13/05/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4133
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 32 days
	Sequencing time: 11 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/4/2015	ETH15-04	639	637	0	99.69	0.31	EA-3	unnamed
2	O/ETH/13/2011	ETH11-13	639	620	0	97.03	2.97	EA-3	unnamed
3	O/ETH/17/2012	ETH12-17	639	620	0	97.03	2.97	EA-3	unnamed
4	O/ETH/24/2012	ETH12-24	639	620	0	97.03	2.97	EA-3	unnamed
5	O/ETH/25/2012	ETH12-25	639	620	0	97.03	2.97	EA-3	unnamed
6	O/ETH/11/2011	ETH11-11	639	619	0	96.87	3.13	EA-3	unnamed
7	O/ETH/12/2012	ETH12-12	639	619	0	96.87	3.13	EA-3	unnamed
8	O/ETH/16/2012	ETH12-16	639	619	0	96.87	3.13	EA-3	unnamed
9	O/ETH/18/2011	ETH11-18	639	619	0	96.87	3.13	EA-3	unnamed
10	O/ETH/22/2012	ETH12-22	639	619	0	96.87	3.13	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	591	0	92.49	7.51	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	556	0	87.01	12.99	EA-3	unnamed
4	O/IND/R2/75* (AF204276)	IND75--A	639	550	0	86.07	13.93	ME-SA	unnamed
5	O/K83/79* (AJ303511)	KEN79B83	638	543	1	85.11	14.89	EA-1	unnamed
6	O/BHU/3/2009 (KM921814)	BHU09-03	639	543	0	84.98	15.02	ME-SA	Ind-2001d
7	O/IND/53/79 (AF292107)	IND79A53	639	543	0	84.98	15.02	ME-SA	unnamed
8	O/TAN/2/2004 (KF561679)	TAN04-02	639	539	0	84.35	15.65	EA-2	unnamed
9	O/UGA/5/96 (AJ296327)	UGA96-05	639	538	0	84.19	15.81	EA-1	unnamed
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	537	0	84.04	15.96	ME-SA	Ind-2001a

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: ETH/4/2015 Batch No: WRLFMD/2015/00009 Sender Ref: ET-10434 Location: Tulo-Welenso, East Harerghe, Oromia, Ethiopia Date collected: 13/03/2015 Date received by WRLFMD: 07/05/2015 Date received for sequencing: 28/05/2015 Species: Bovine (local Breed) Material used: BTY1 13/05/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 08/06/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: EA-3 Genotype/strain: unnamed Sequence filename: ETH15-04.SEQ Date sequence last updated: 04/06/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4133 Min. no. of nt for comparison: 600 Total turn-around time: 32 days Sequencing time: 11 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/3/2015	ETH15-03	639	637	0	99.69	0.31	EA-3	unnamed
2	O/ETH/13/2011	ETH11-13	639	622	0	97.34	2.66	EA-3	unnamed
3	O/ETH/17/2012	ETH12-17	639	622	0	97.34	2.66	EA-3	unnamed
4	O/ETH/24/2012	ETH12-24	639	622	0	97.34	2.66	EA-3	unnamed
5	O/ETH/25/2012	ETH12-25	639	622	0	97.34	2.66	EA-3	unnamed
6	O/ETH/11/2011	ETH11-11	639	621	0	97.18	2.82	EA-3	unnamed
7	O/ETH/12/2012	ETH12-12	639	621	0	97.18	2.82	EA-3	unnamed
8	O/ETH/16/2012	ETH12-16	639	621	0	97.18	2.82	EA-3	unnamed
9	O/ETH/18/2011	ETH11-18	639	621	0	97.18	2.82	EA-3	unnamed
10	O/ETH/22/2012	ETH12-22	639	621	0	97.18	2.82	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	593	0	92.80	7.20	EA-3	unnamed
2	O/ETH/3/2004 (FJ798109)	ETH04-03	639	584	0	91.39	8.61	EA-3	unnamed
3	O/SUD/2/86 (DQ165075)	SUD86-02	639	558	0	87.32	12.68	EA-3	unnamed
4	O/IND/R2/75* (AF204276)	IND75--A	639	552	0	86.38	13.62	ME-SA	unnamed
5	O/K83/79* (AJ303511)	KEN79B83	638	545	1	85.42	14.58	EA-1	unnamed
6	O/IND/53/79 (AF292107)	IND79A53	639	545	0	85.29	14.71	ME-SA	unnamed
7	O/BHU/3/2009 (KM921814)	BHU09-03	639	543	0	84.98	15.02	ME-SA	Ind-2001d
8	O/KUW/3/97 (DQ164904)	KUW97-03	639	539	0	84.35	15.65	ME-SA	Ind-2001a
9	O/TAN/2/2004 (KF561679)	TAN04-02	639	539	0	84.35	15.65	EA-2	unnamed
10	O/CAM/3/98 (AJ294910)	CAM98-03	639	538	0	84.19	15.81	SEA	Cam-94

nt, nucleotides

*, not a WRLFMD reference number

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Serotype: O WRLFMD Ref No: ETH/6/2015 Batch No: WRLFMD/2015/00009 Sender Ref: ET-9092 Location: Karsa Ala, Liyu zone, Oromia, Ethiopia Date collected: 18/03/2015 Date received by WRLFMD: 07/05/2015 Date received for sequencing: 28/05/2015 Species: Bovine (holstein-friesian Breed) Material used: BTY1 12/05/2015 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 08/06/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: EA-3 Genotype/strain: unnamed Sequence filename: ETH15-06.SEQ Date sequence last updated: 04/06/2015 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 4133 Min. no. of nt for comparison: 600 Total turn-around time: 32 days Sequencing time: 11 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/YEM/3/2006	YEM06-03	639	608	0	95.15	4.85	EA-3	unnamed
2	O/YEM/4/2006	YEM06-04	639	605	0	94.68	5.32	EA-3	unnamed
3	O/ETH/31/2008	ETH08-31	639	601	0	94.05	5.95	EA-3	unnamed
4	O/ETH/32/2008	ETH08-32	639	601	0	94.05	5.95	EA-3	unnamed
5	O/YEM/29/2006	YEM06-29	639	601	0	94.05	5.95	EA-3	unnamed
6	O/YEM/10/2008	YEM08-10	639	599	0	93.74	6.26	EA-3	unnamed
7	O/YEM/24/2009	YEM09-24	639	598	0	93.58	6.42	EA-3	unnamed
8	O/YEM/5/2008	YEM08-05	639	598	0	93.58	6.42	EA-3	unnamed
9	O/YEM/6/2008	YEM08-06	639	598	0	93.58	6.42	EA-3	unnamed
10	O/YEM/8/2008	YEM08-08	639	598	0	93.58	6.42	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	579	0	90.61	9.39	EA-3	unnamed
2	O/SUD/2/86 (DQ165075)	SUD86-02	639	574	0	89.83	10.17	EA-3	unnamed
3	O/ETH/3/2004 (FJ798109)	ETH04-03	639	569	0	89.05	10.95	EA-3	unnamed
4	O/IND/53/79 (AF292107)	IND79A53	639	554	0	86.70	13.30	ME-SA	unnamed
5	O/K83/79* (AJ303511)	KEN79B83	638	551	1	86.36	13.64	EA-1	unnamed
6	O/ETH/58/2005 (FJ798141)	ETH05-58	639	551	0	86.23	13.77	EA-4	unnamed
7	O/IND/R2/75* (AF204276)	IND75--A	639	551	0	86.23	13.77	ME-SA	unnamed
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	551	0	86.23	13.77	ME-SA	PanAsia
9	O/IRN/31/2009	IRN09-31	639	548	0	85.76	14.24	ME-SA	PanAsia-2 ^{FAR-09}
10	O/IRN/8/2005	IRN05-08	639	547	0	85.60	14.40	ME-SA	PanAsia-2

nt, nucleotides

*, not a WRLFMD reference number

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Report on FMDV O in Ethiopia in 2015

Batch: WRLFMD/2015/00009

◆ indicates viruses in this batch

Software: MEGA 6.06

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

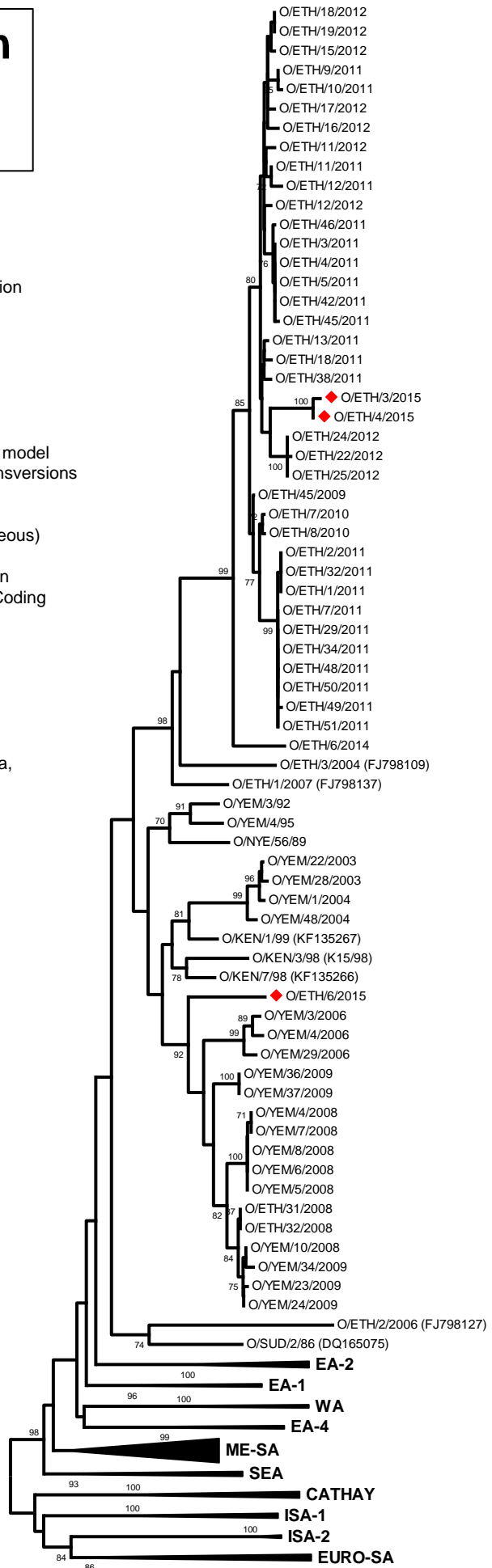
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
08 June 2015

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