

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

Confidential Genotyping Report

Report Date for this Batch: 20 October 2015

FMDV type O

Country: Niger

Period: 2015

No. of samples: 1

BATCH: WRLFMD/2015/00024



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FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: O	Report date: 19/10/2015
WRLFMD Ref No: NGR/4/2015	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00024	Checked by: K. Bachanek-Bankowska
Sender Ref: NER 20/15	
Location: not known, Niger	Topotype: WA
Date collected: 26/05/2015	Genotype/strain: unnamed
Date received by WRLFMD: 13/08/2015	Sequence filename: NGR15-04.SEQ
Date received for sequencing: 13/10/2015	Date sequence last updated: 19/10/2015
Species: Bovine	No. of Nt determined: 639
Material used: BTy1 12/09/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 4168
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 67 days
	Sequencing time: 6 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/BEN/40/2010* (KC832986)	BEN10-AT	639	608	0	95.15	4.85	WA	unnamed
2	O/BEN/26/2010* (KC832981)	BEN10-AM	639	605	0	94.68	5.32	WA	unnamed
3	O/Lam/GHA/2012 (KF305227)	GHA12-AA	639	580	0	90.77	9.23	WA	unnamed
4	O/TOG/1/2004	TOG04-01	639	580	0	90.77	9.23	WA	unnamed
5	O/TOG/1/2005	TOG05-01	639	579	0	90.61	9.39	WA	unnamed
6	O/TOG/3/2005	TOG05-03	639	579	0	90.61	9.39	WA	unnamed
7	O/TOG/4/2005	TOG05-04	639	579	0	90.61	9.39	WA	unnamed
8	O/NIG/3/2011	NIG11-03	639	574	0	89.83	10.17	WA	unnamed
9	O/MOR/2/99	MOR99-02	639	573	0	89.67	10.33	WA	unnamed
10	O/BEN/1/2010* (KC832973)	BEN10-AA	639	572	0	89.51	10.49	WA	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/CIV/8/99 (AJ303485)	CIV99-08	639	571	0	89.36	10.64	WA	unnamed
2	O/GHA/5/93 (AJ303488)	GHA93-05	639	552	0	86.38	13.62	WA	unnamed
3	O/IND/R2/75* (AF204276)	IND75--A	639	538	0	84.19	15.81	ME-SA	unnamed
4	O/K83/79* (AJ303511)	KEN79B83	638	537	1	84.17	15.83	EA-1	unnamed
5	O/SUD/2/86 (DQ165075)	SUD86-02	639	537	0	84.04	15.96	EA-3	unnamed
6	O/UGA/17/98 (HM211075)	UGA98-17	639	536	0	83.88	16.12	EA-4	unnamed
7	O/IND/53/79 (AF292107)	IND79A53	639	535	0	83.72	16.28	ME-SA	unnamed
8	O1/Manisa/TUR/69 (AY593823)	TUR69--G	639	535	0	83.72	16.28	ME-SA	unnamed
9	O/UGA/5/96 (AJ296327)	UGA96-05	639	531	0	83.10	16.90	EA-1	unnamed
10	O/ETH/58/2005 (FJ798141)	ETH05-58	639	530	0	82.94	17.06	EA-4	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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Report on FMDV O in Niger in 2015

Batch: WRLFMD/2015/00024

◆ 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

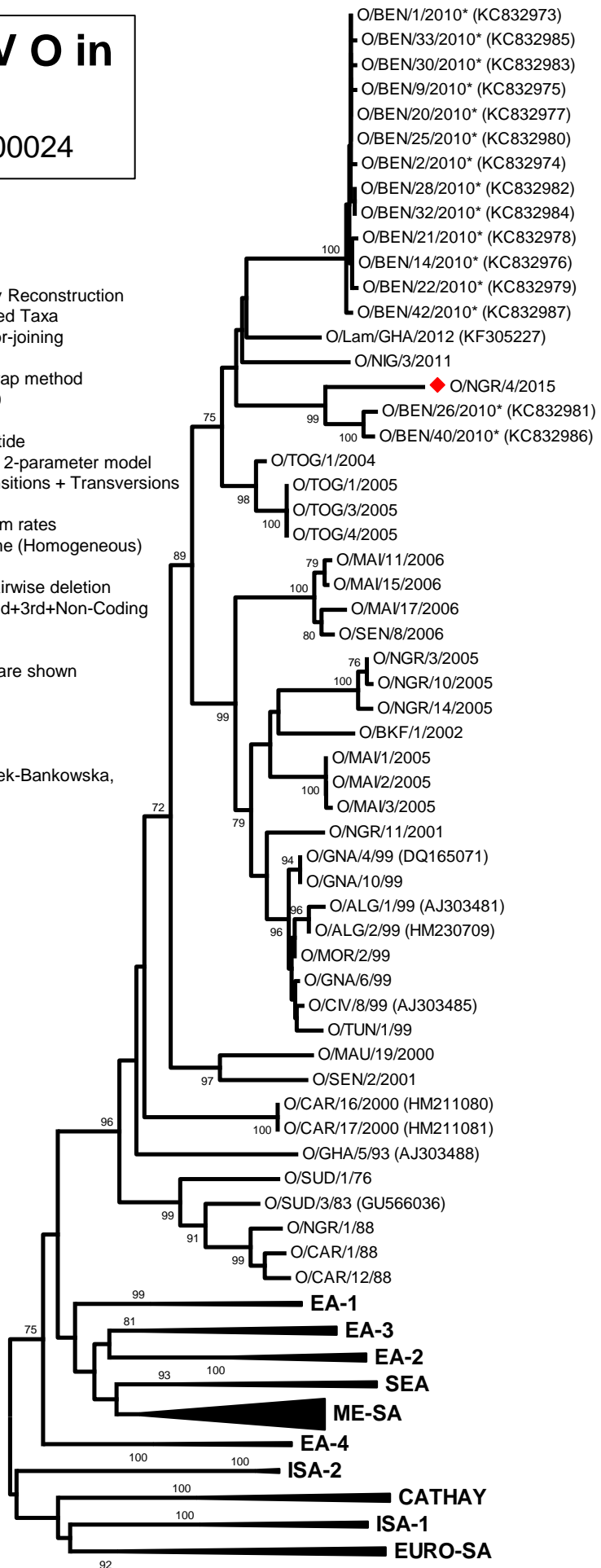
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
19 October 2015

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WA

0.02