

FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: O	Report date: 02/04/2024
WRLFMD Ref No: UGA04/2024	Reported by: N.J. Knowles
Batch No: WRLMEG/2024/000004	Checked by: D.P. King
Sender Ref: UGA04/2024	
Location: not known, Uganda	Topotype: EA-2
Date collected: 2024	Genotype/strain:
Date received by WRLFMD: 28/03/2024	Sequence filename: UGA24-AA.seq
Date received for sequencing:	Date sequence last updated: 02/04/2024
Species: Bovine	No. of Nt determined: 577
Material used:	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C272F/EUR-2B52R	Total no. of comparisons: 7418
	Min. no. of nt for comparison: 550
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/COD/76/2021	COD21-76	577	554	0	96.01	3.99	EA-2	unnamed
2	O/COD/80/2021	COD21-80	577	554	0	96.01	3.99	EA-2	unnamed
3	O/COD/82/2021	COD21-82	577	554	0	96.01	3.99	EA-2	unnamed
4	O/MBG/TZ/23/2021 (OQ615919)	TAN21-AF	576	553	1	96.01	3.99	EA-2	unnamed
5	O/UGA/19/2020	UGA20-19	577	554	0	96.01	3.99	EA-2	unnamed
6	O/UGA/20/2020	UGA20-20	577	554	0	96.01	3.99	EA-2	unnamed
7	O/UGA/25/2020	UGA20-25	577	554	0	96.01	3.99	EA-2	unnamed
8	O/MBG/TZ/07/2021 (OQ615920)	TAN21-AB	573	550	4	95.99	4.01	EA-2	unnamed
9	O/COD/12/2021	COD21-12	577	553	0	95.84	4.16	EA-2	unnamed
10	O/COD/19/2021	COD21-19	577	553	0	95.84	4.16	EA-2	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/TAN/2/2004 (KF561679)	TAN04-02	577	530	0	91.85	8.15	EA-2	unnamed
2	O/UGA/3/2002 (DQ165077)	UGA02-03	577	512	0	88.73	11.27	EA-2	unnamed
3	O/KEN/5/2002 (DQ165073)	KEN02-05	577	507	0	87.87	12.13	EA-2	unnamed
4	O/MAL/1/98 (DQ165074)	MAL98-01	577	506	0	87.69	12.31	EA-2	unnamed
5	O/K40/84* (KY091280)	KEN84-40	577	482	0	83.54	16.46	EA-1	unnamed
6	O/OMN/7/2001 (DQ164941)	OMN01-07	577	481	0	83.36	16.64	ME-SA	Ind-2001b
7	O/UAE/4/2008 (KM921876)	UAE08-04	574	478	0	83.28	16.72	ME-SA	Ind-2001c
8	O/BHU/3/2009 (KM921814)	BHU09-03	577	480	0	83.19	16.81	ME-SA	Ind-2001d
9	O/KUW/3/97 (DQ164904)	KUW97-03	577	479	0	83.02	16.98	ME-SA	Ind-2001a
10	O/SRL/2/97 (AJ303531)	SRL97-02	577	479	0	83.02	16.98	ME-SA	Srl-97

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.5

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Report on FMDV O in Uganda in 2024

Batch: WRLMEG/2024/00004

◆ indicates viruses in this batch

Software: MEGA 7.0.21

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

----- Gamma Distributed (G)

Gamma Parameter ----- 1

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 648

No Of Bootstrap Reps = 1000

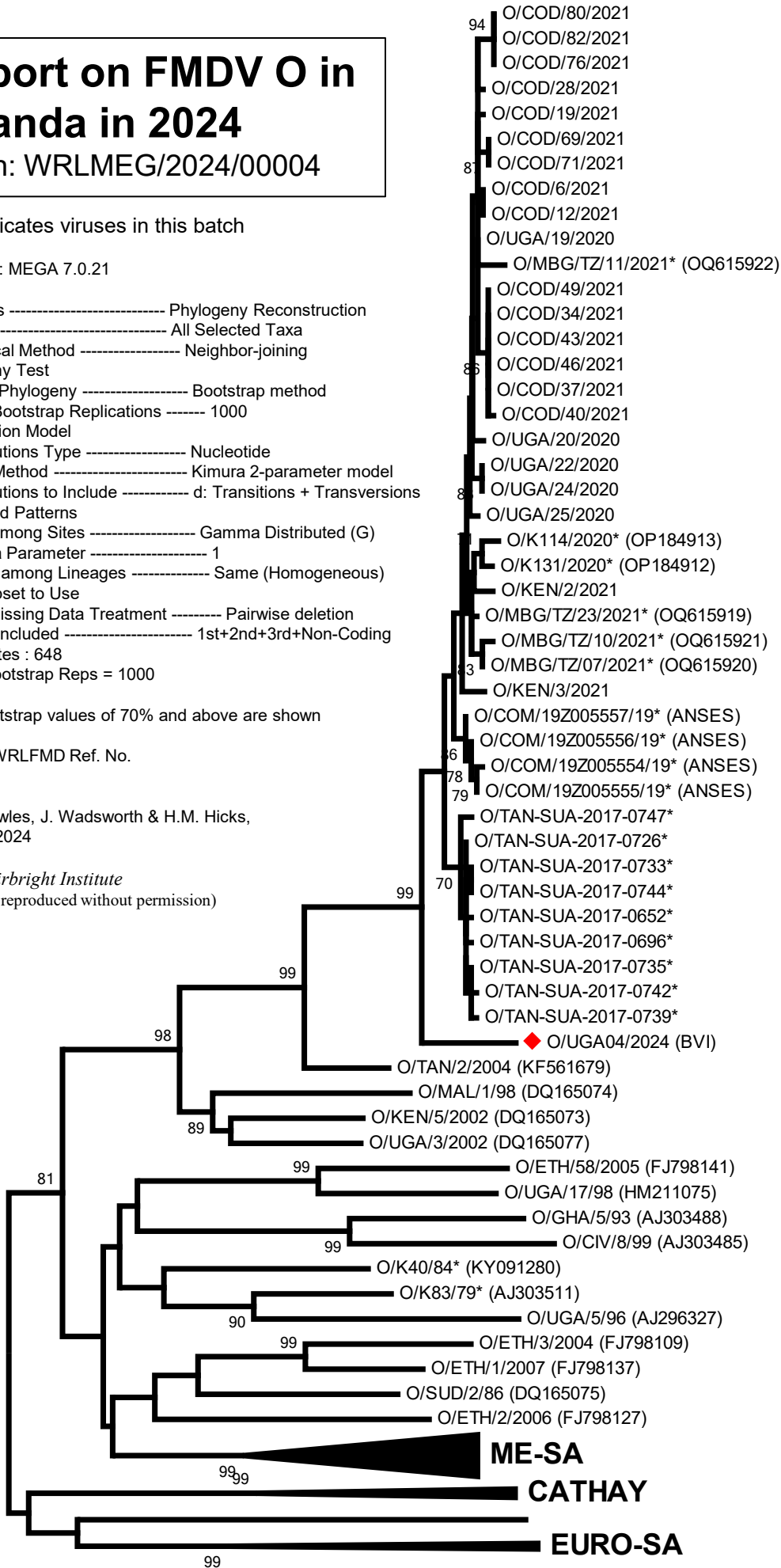
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & H.M. Hicks,
03 April 2024

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EA-2

EA-4

WA

EA-1

EA-3

ME-SA

CATHAY

EURO-SA

0.02