

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

## Genotyping Report

Report Date for this Batch: 8 January 2014

FMDV type O

Country: Libya

Period: 2013

No. of samples: 2\*

BATCH: WRLFMD/2013/00030

\*, this batch of samples was submitted via [REDACTED] Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Brescia, Italy.



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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: 08/01/2014
WRLFMD Ref No: LIB/17/2013	Reported by: N.J. Knowles
Batch No: WRLFMD/2013/00030	Checked by: K. Bachanek-Bankowska
Sender Ref: W	
Location: not given, Libya	Topotype: ME-SA
Date collected: 01/10/2013	Genotype/strain: Ind-2001 <sup>KAR-13</sup>
Date received by WRLFMD: 16/12/2013	Sequence filename: LIB13-17.SEQ
Date received for sequencing: 07/01/2014	Date sequence last updated: 08/01/2014
Species: Cattle	No. of Nt determined: 639
Material used: BTy2 21/12/2013	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3753
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 23 days
	Sequencing time: 1 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/LIB/1/2013	LIB13-01	639	638	0	99.84	0.16	ME-SA	Ind-2001 <sup>KAR-13</sup>
2	O/LIB/4/2013	LIB13-04	639	638	0	99.84	0.16	ME-SA	Ind-2001 <sup>KAR-13</sup>
3	O/LIB/5/2013	LIB13-05	639	638	0	99.84	0.16	ME-SA	Ind-2001 <sup>KAR-13</sup>
4	O/LIB/7/2013	LIB13-07	639	638	0	99.84	0.16	ME-SA	Ind-2001 <sup>KAR-13</sup>
5	O/LIB/2/2013	LIB13-02	639	637	0	99.69	0.31	ME-SA	Ind-2001 <sup>KAR-13</sup>
6	O/LIB/22/2013	LIB13-22	639	637	0	99.69	0.31	ME-SA	Ind-2001 <sup>KAR-13</sup>
7	O/LIB/3/2013	LIB13-03	639	637	0	99.69	0.31	ME-SA	Ind-2001 <sup>KAR-13</sup>
8	O/LIB/6/2013	LIB13-06	639	637	0	99.69	0.31	ME-SA	Ind-2001 <sup>KAR-13</sup>
9	O/SAU/6/2013	SAU13-06	639	629	0	98.44	1.56	ME-SA	Ind-2001 <sup>KAR-13</sup>
10	O/SAU/7/2013	SAU13-07	639	629	0	98.44	1.56	ME-SA	Ind-2001 <sup>KAR-13</sup>
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/1/2013	BHU13-01	639	619	0	96.87	3.13	ME-SA	Ind-2001 <sup>KAR-13</sup>
2	O/BHU/3/2009	BHU09-03	639	614	0	96.09	3.91	ME-SA	Ind-2001d
3	O/OMN/7/2001 (DQ164941)	OMN01-07	639	585	0	91.55	8.45	ME-SA	Ind-2001b
4	O/KUW/3/97 (DQ164904)	KUW97-03	639	582	0	91.08	8.92	ME-SA	Ind-2001a
5	O/IRN/31/2009	IRN09-31	639	575	0	89.98	10.02	ME-SA	PanAsia-2 <sup>FAR-09</sup>
6	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
7	O/TUR/257/2008* (FMDI)	TUR08-AD	639	570	0	89.20	10.80	ME-SA	PanAsia-2 <sup>TER-08</sup>
8	O/IRN/8/2005	IRN05-08	639	569	0	89.05	10.95	ME-SA	PanAsia-2
9	O/PAK/16/2010	PAK10-16	639	568	0	88.89	11.11	ME-SA	PanAsia-2 <sup>PUN-10</sup>
10	O/UKG/35/2001 (AJ539141)	UKG01-35	639	568	0	88.89	11.11	ME-SA	PanAsia

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: O WRLFMD Ref No: LIB/22/2013 Batch No: WRLFMD/2013/00030 Sender Ref: Y3 Location: not given, Libya Date collected: 01/12/2013 Date received by WRLFMD: 16/12/2013 Date received for sequencing: 07/01/2014 Species: Cattle Material used: BTy1 18/12/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 08/01/2014 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska  Topotype: ME-SA Genotype/strain: Ind-2001 <sup>KAR-13</sup> Sequence filename: LIB13-22.SEQ Date sequence last updated: 08/01/2014 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3753 Min. no. of nt for comparison: 600 Total turn-around time: 23 days Sequencing time: 1 days
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nt, nucleotides

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# Report on FMDV O in Libya in 2013

Batch: WRLFMD/2013/00030

◆ indicates viruses in this batch

Software: MEGA 5.2

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

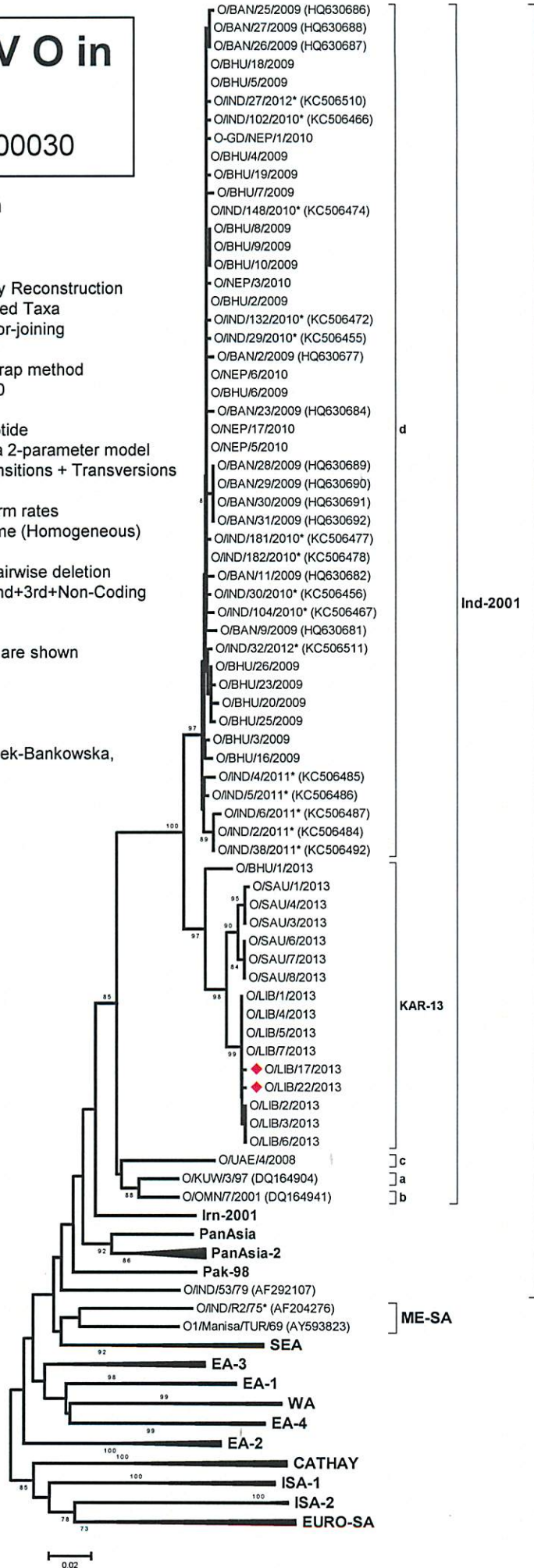
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,  
 08 January 2014

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Ind-2001

ME-SA

KAR-13

c  
a  
b

ME-SA

0.02