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## **FMD Genotyping Report**

Lab Reference WRL Batch Number: WRLFMD/2011/00042

Sender Details:



Date Received: 29<sup>th</sup> September 2011  
Country of Origin: Democratic Republic of Congo  
Date Reported: 18<sup>th</sup> October 2011

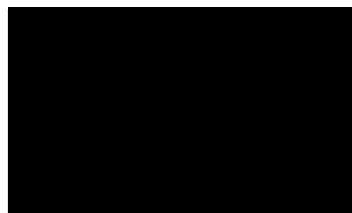
Dear Dr. Mulinda,

Sequencing work has now been completed in respect of the samples you submitted and the details are as attached. Please note that all of our phylogenetic trees can be accessed via the internet at: <http://www.wrlfmd.org/>

Results Approved By:



Official Stamp:



Date: 25/10/2011



A UKAS accredited testing laboratory No. 4025.

To help us improve the quality of our service, please send any suggestions or requests to the Reference Laboratory by fax (+44 (0) 1483 232621 or email: [elizabeth.wilson@bbsrc.ac.uk](mailto:elizabeth.wilson@bbsrc.ac.uk)). IAH actively seeks and appreciates feedback, if you would like to offer feedback please complete the WRLFMD survey here: <http://www.surveymonkey.com/s/WRLFMD>

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

## Genotyping Report

Report Date for this Batch: 25 October 2011

FMDV type O

Country: Democratic Republic of the Congo

Period: 2010

No. of samples: 4

BATCH: WRLFMD/2011/00042



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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 WRLFMD Ref No: COD/1/2010 Batch No: WRLFMD/2011/00042 Sender Ref: MUT 2 Location: Mutarule, Sud-Kivu, Plaine de La Ruzizi, Dem.Rep.Congo Date collected: 05/10/2010 Date received by WRLFMD: 29/09/2011 Date received for sequencing: 18/10/2011 Species: Cattle Material used: 10% epithelium susp. Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 25/10/2011 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: unnamed Sequence filename: COD10-01.SEQ Date sequence last updated: 19/10/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3131 Min. no. of nt for comparison: 600 Total turn-around time: 26 days Sequencing time: 7 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/COD/2/2010	COD10-02	639	637	0	99.69	0.31	EA-2	unnamed
2	O/COD/4/2010	COD10-04	639	636	0	99.53	0.47	EA-2	unnamed
3	O/COD/3/2010	COD10-03	639	635	0	99.37	0.63	EA-2	unnamed
4	O/ZAM/1/2010	ZAM10-01	639	635	0	99.37	0.63	EA-2	Unnamed
5	O/ZAM/3/2010	ZAM10-03	639	635	0	99.37	0.63	EA-2	Unnamed
6	O/ZAM/4/2010	ZAM10-04	639	635	0	99.37	0.63	EA-2	Unnamed
7	O/COD/80/2006	COD06-80	639	621	0	97.18	2.82	EA-2	unnamed
8	O/COD/82/2006	COD06-82	639	621	0	97.18	2.82	EA-2	unnamed
9	O/U18/06* (HM756627)	UGA06-AB	639	621	0	97.18	2.82	EA-2	Unnamed
10	O/U312/06* (HM191257)	UGA06-AD	639	621	0	97.18	2.82	EA-2	Unnamed
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/UGA/3/2002 (DQ165077)	UGA02-03	639	591	0	92.49	7.51	EA-2	unnamed
2	O/KEN/5/2002 (DQ165073)	KEN02-05	639	589	0	92.18	7.82	EA-2	Unnamed
3	O/MAL/1/98 (DQ165074)	MAL98-01	639	567	0	88.73	11.27	EA-2	unnamed
4	O/TAN/2/2004	TAN04-02	639	563	0	88.11	11.89	EA-2	unnamed
5	O/K40/84*	KEN84-40	639	559	0	87.48	12.52	EA-1	unnamed
6	O/PAK/16/2003 (DQ165068)	PAK03-16	639	544	0	85.13	14.87	ME-SA	Pak-98
7	O/PAK/16/2010	PAK10-16	639	544	0	85.13	14.87	ME-SA	PanAsia-2 <sup>PUN-10</sup>
8	O/IRN/61/2001 (DQ164896)	IRN01-61	638	543	1	85.11	14.89	ME-SA	Irn-2001
9	O/IND/53/79 (AF292107)	IND79A53	639	542	0	84.82	15.18	ME-SA	unnamed
10	O/ETH/1/2007 (FJ798137)	ETH07-01	639	541	0	84.66	15.34	EA-3	unnamed

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: COD/2/2010 Batch No: WRLFMD/2011/00042 Sender Ref: MUT 3 Location: Mutarule, Sud-Kivu, Plaine de la Ruzizi, Dem.Rep.Congo Date collected: 05/10/2010 Date received by WRLFMD: 29/09/2011 Date received for sequencing: 18/10/2011 Species: Cattle Material used: 10% epithelium susp. Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 25/10/2011 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: unnamed Sequence filename: COD10-02.SEQ Date sequence last updated: 19/10/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3131 Min. no. of nt for comparison: 600 Total turn-around time: 26 days Sequencing time: 7 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/COD/1/2010	COD10-01	639	637	0	99.69	0.31	EA-2	unnamed
2	O/COD/4/2010	COD10-04	639	636	0	99.53	0.47	EA-2	unnamed
3	O/COD/3/2010	COD10-03	639	635	0	99.37	0.63	EA-2	unnamed
4	O/ZAM/1/2010	ZAM10-01	639	635	0	99.37	0.63	EA-2	Unnamed
5	O/ZAM/3/2010	ZAM10-03	639	635	0	99.37	0.63	EA-2	Unnamed
6	O/ZAM/4/2010	ZAM10-04	639	635	0	99.37	0.63	EA-2	Unnamed
7	O/U312/06* (HM191257)	UGA06-AD	639	622	0	97.34	2.66	EA-2	Unnamed
8	O/COD/80/2006	COD06-80	639	621	0	97.18	2.82	EA-2	unnamed
9	O/COD/82/2006	COD06-82	639	621	0	97.18	2.82	EA-2	unnamed
10	O/U18/06* (HM756627)	UGA06-AB	639	621	0	97.18	2.82	EA-2	Unnamed
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/KEN/5/2002 (DQ165073)	KEN02-05	639	591	0	92.49	7.51	EA-2	Unnamed
2	O/UGA/3/2002 (DQ165077)	UGA02-03	639	591	0	92.49	7.51	EA-2	unnamed
3	O/MAL/1/98 (DQ165074)	MAL98-01	639	567	0	88.73	11.27	EA-2	unnamed
4	O/TAN/2/2004	TAN04-02	639	565	0	88.42	11.58	EA-2	unnamed
5	O/K40/84*	KEN84-40	639	560	0	87.64	12.36	EA-1	unnamed
6	O/PAK/16/2003 (DQ165068)	PAK03-16	639	545	0	85.29	14.71	ME-SA	Pak-98
7	O/PAK/16/2010	PAK10-16	639	545	0	85.29	14.71	ME-SA	PanAsia-2 <sup>PUN-10</sup>
8	O/IRN/61/2001 (DQ164896)	IRN01-61	638	544	1	85.27	14.73	ME-SA	Irn-2001
9	O/IND/53/79 (AF292107)	IND79A53	639	543	0	84.98	15.02	ME-SA	unnamed
10	O/ETH/1/2007 (FJ798137)	ETH07-01	639	542	0	84.82	15.18	EA-3	unnamed

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: COD/3/2010 Batch No: WRLFMD/2011/00042 Sender Ref: LUB 5 Location: Luberizi, Sud-Kivu, Plaine de La Ruzizi, Dem.Rep.Congo Date collected: 06/10/2010 Date received by WRLFMD: 29/09/2011 Date received for sequencing: 18/10/2011 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 25/10/2011 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: unnamed Sequence filename: COD10-03.SEQ Date sequence last updated: 19/10/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3131 Min. no. of nt for comparison: 600 Total turn-around time: 26 days Sequencing time: 7 days
Comments:	

<b>Most Closely Related Viruses</b>									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/COD/4/2010	COD10-04	639	638	0	99.84	0.16	EA-2	unnamed
2	O/COD/1/2010	COD10-01	639	635	0	99.37	0.63	EA-2	unnamed
3	O/COD/2/2010	COD10-02	639	635	0	99.37	0.63	EA-2	unnamed
4	O/ZAM/1/2010	ZAM10-01	639	633	0	99.06	0.94	EA-2	Unnamed
5	O/ZAM/3/2010	ZAM10-03	639	633	0	99.06	0.94	EA-2	Unnamed
6	O/ZAM/4/2010	ZAM10-04	639	633	0	99.06	0.94	EA-2	Unnamed
7	O/COD/80/2006	COD06-80	639	619	0	96.87	3.13	EA-2	unnamed
8	O/COD/82/2006	COD06-82	639	619	0	96.87	3.13	EA-2	unnamed
9	O/U18/06* (HM756627)	UGA06-AB	639	619	0	96.87	3.13	EA-2	Unnamed
10	O/U312/06* (HM191257)	UGA06-AD	639	619	0	96.87	3.13	EA-2	Unnamed
<b>Most Closely Related Reference Viruses</b>									
(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/UGA/3/2002 (DQ165077)	UGA02-03	639	589	0	92.18	7.82	EA-2	unnamed
2	O/KEN/5/2002 (DQ165073)	KEN02-05	639	587	0	91.86	8.14	EA-2	Unnamed
3	O/MAL/1/98 (DQ165074)	MAL98-01	639	567	0	88.73	11.27	EA-2	unnamed
4	O/TAN/2/2004	TAN04-02	639	561	0	87.79	12.21	EA-2	unnamed
5	O/K40/84*	KEN84-40	639	559	0	87.48	12.52	EA-1	unnamed
6	O/PAK/16/2003 (DQ165068)	PAK03-16	639	544	0	85.13	14.87	ME-SA	Pak-98
7	O/PAK/16/2010	PAK10-16	639	544	0	85.13	14.87	ME-SA	PanAsia-2 <sup>PUN-10</sup>
8	O/IRN/61/2001 (DQ164896)	IRN01-61	638	543	1	85.11	14.89	ME-SA	Irn-2001
9	O/ETH/1/2007 (FJ798137)	ETH07-01	639	542	0	84.82	15.18	EA-3	unnamed
10	O/IND/53/79 (AF292107)	IND79A53	639	542	0	84.82	15.18	ME-SA	unnamed

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: COD/4/2010 Batch No: WRLFMD/2011/00042 Sender Ref: LUB 8 Location: Luberizi, Sud-Kivu, Plaine De La Ruzizi, Dem.Rep.Congo Date collected: 06/10/2010 Date received by WRLFMD: 29/09/2011 Date received for sequencing: 18/10/2011 Species: Cattle Material used: BTy1 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 25/10/2011 Reported by: N.J. Knowles Checked by: D.P. King Topotype: EA-2 Genotype/strain: unnamed Sequence filename: COD10-04.SEQ Date sequence last updated: 19/10/2011 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 3131 Min. no. of nt for comparison: 600 Total turn-around time: 26 days Sequencing time: 7 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/COD/3/2010	COD10-03	639	638	0	99.84	0.16	EA-2	unnamed
2	O/COD/1/2010	COD10-01	639	636	0	99.53	0.47	EA-2	unnamed
3	O/COD/2/2010	COD10-02	639	636	0	99.53	0.47	EA-2	unnamed
4	O/ZAM/1/2010	ZAM10-01	639	634	0	99.22	0.78	EA-2	Unnamed
5	O/ZAM/3/2010	ZAM10-03	639	634	0	99.22	0.78	EA-2	Unnamed
6	O/ZAM/4/2010	ZAM10-04	639	634	0	99.22	0.78	EA-2	Unnamed
7	O/COD/80/2006	COD06-80	639	620	0	97.03	2.97	EA-2	unnamed
8	O/COD/82/2006	COD06-82	639	620	0	97.03	2.97	EA-2	unnamed
9	O/U18/06* (HM756627)	UGA06-AB	639	620	0	97.03	2.97	EA-2	Unnamed
10	O/U312/06* (HM191257)	UGA06-AD	639	620	0	97.03	2.97	EA-2	Unnamed
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/UGA/3/2002 (DQ165077)	UGA02-03	639	590	0	92.33	7.67	EA-2	unnamed
2	O/KEN/5/2002 (DQ165073)	KEN02-05	639	588	0	92.02	7.98	EA-2	Unnamed
3	O/MAL/1/98 (DQ165074)	MAL98-01	639	566	0	88.58	11.42	EA-2	unnamed
4	O/TAN/2/2004	TAN04-02	639	562	0	87.95	12.05	EA-2	unnamed
5	O/K40/84*	KEN84-40	639	558	0	87.32	12.68	EA-1	unnamed
6	O/IND/53/79 (AF292107)	IND79A53	639	543	0	84.98	15.02	ME-SA	unnamed
7	O/PAK/16/2003 (DQ165068)	PAK03-16	639	543	0	84.98	15.02	ME-SA	Pak-98
8	O/PAK/16/2010	PAK10-16	639	543	0	84.98	15.02	ME-SA	PanAsia-2 <sup>PUN-10</sup>
9	O/SUD/2/86 (DQ165075)	SUD86-02	639	543	0	84.98	15.02	EA-3	unnamed
10	O/IRN/61/2001 (DQ164896)	IRN01-61	638	542	1	84.95	15.05	ME-SA	Iran-2001

nt, nucleotides

\*, not a WRLFMD reference number

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# Report on FMDV O in the Democratic Republic of the Congo in 2010

Batch: WRLFMD/2011/00042

◆ indicates viruses in this batch

Software: MEGA 5.0

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

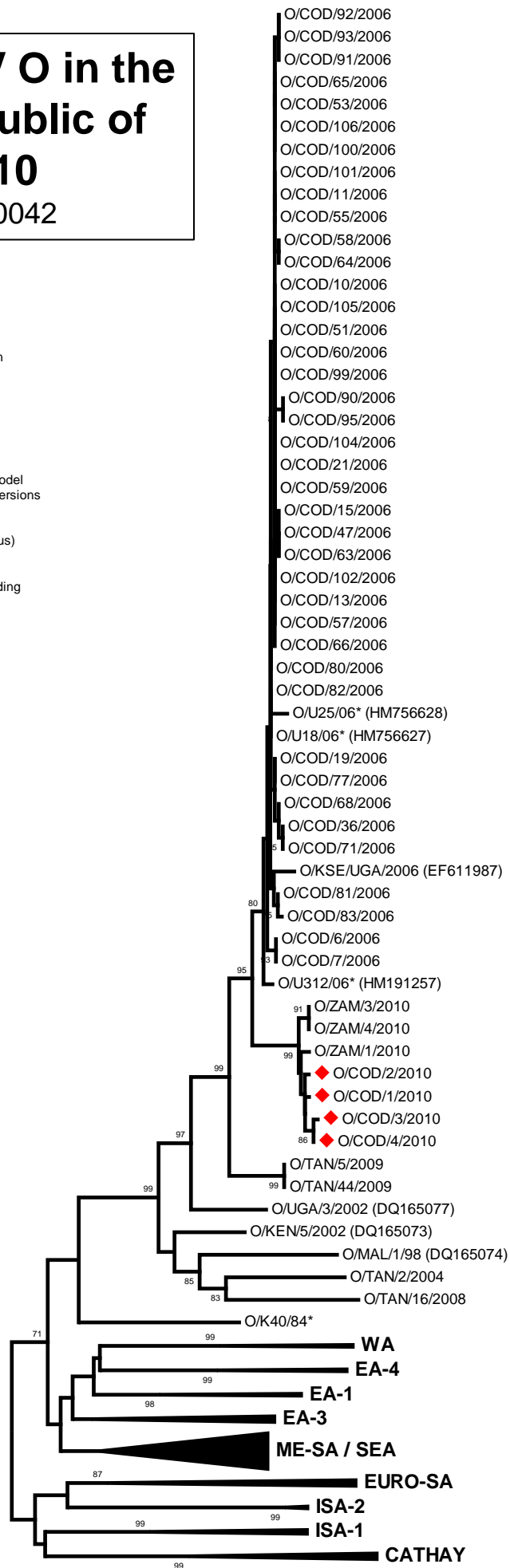
Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 25 October 2011

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EA-2

0.02