

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

Genotyping Report

Report Date for this Batch: 19 November 2013

FMDV type O

Country: Taiwan

Period: 2013

No. of samples: 1

BATCH: WRLFMD/2013/00022



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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: TAW/1/2013 Batch No: WRLFMD/2013/00022 Sender Ref: FMDV/O/TW/PH/2012 Location: Not given, Taiwan Date collected: 29/10/2013 Date received by WRLFMD: 06/11/2013 Date received for sequencing: 18/11/2013 Species: Pig Material used: RS1 08/11/2013 Region sequenced: VP1 RT-PCR primers: O-1C244F/EUR-2B52R O-1C272F/EUR-2B52R	Report date: 19/11/2013 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska Topotype: CATHAY Genotype/strain: unnamed Sequence filename: TAW13-01.SEQ Date sequence last updated: 19/11/2013 No. of Nt determined: 636 No. of ambiguities: 3 Gene length: 639 Total no. of comparisons: 3702 Min. no. of nt for comparison: 600 Total turn-around time: 13 days Sequencing time: 1 days
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Comments: The VP1 sequence contained three nucleotide (nt) ambiguities which were predicted to result in the amino acid (aa) substitutions. The ambiguities were at nt positions 248 (A/C), 328 (A/G) and 418 (A/G) resulting in Glu/Ala, Lys/Glu and Thr/Ala at aa residues 83, 110 and 140, respectively. All three aa residues are predicted to lie on the surface of the virus capsid, 83 and 110 close to the 5-fold axis of symmetry and 140 in the β G- β H loop (Figure 1); thus these could affect virus antigenicity. Additionally, at nt position 594 (C) a substantial proportion was U; however, this did not result in an aa substitution. Using this data, it is not possible to ascertain if this is a highly heterogeneous virus population or a mixture of two variants.

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TAW/1/2009	TAW09-01	636	616	0	96.86	3.14	CATHAY	unnamed
2	O/TAW/YLP/09* (AHRI)	TAW09-AC	636	616	0	96.86	3.14	CATHAY	unnamed
3	O-TW-258-2009 (GQ292740)	TAW09-AB	636	616	0	96.86	3.14	CATHAY	unnamed
4	O-TW-257-2009 (GQ292739)	TAW09-AA	636	615	0	96.70	3.30	CATHAY	unnamed
5	O/Yunlin/TAW/97 (AF308157)	TAW97--B	636	575	0	90.41	9.59	CATHAY	unnamed
6	O-TW-256-2001 (GQ292738)	TAW01-AA	636	575	0	90.41	9.59	CATHAY	unnamed
7	O/Chu-Pei/TAW/97	TAW97--A	636	574	0	90.25	9.75	CATHAY	unnamed
8	O/Penghu/TAI/99 (AY593833)	TAW99--B	636	574	0	90.25	9.75	CATHAY	unnamed
9	O/TAI/97 (AY593835)	TAW97--C	636	574	0	90.25	9.75	CATHAY	unnamed
10	O/TAW/Taoyuan-113/97 (AF095872)	TAW97-AL	636	574	0	90.25	9.75	CATHAY	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/Yunlin/TAW/97 (AF308157)	TAW97--B	636	575	0	90.41	9.59	CATHAY	unnamed
2	O/PHI/7/96 (AJ294926)	PHI96-07	636	557	0	87.58	12.42	CATHAY	unnamed
3	O/HKN/6/83 (AJ294919)	HKN83-06	634	535	2	84.38	15.62	CATHAY	unnamed
4	O/HKN/21/70 (AJ294911)	HKN70A21	634	520	2	82.02	17.98	CATHAY	unnamed
5	O/IND/53/79 (AF292107)	IND79A53	636	502	0	78.93	21.07	ME-SA	unnamed
6	O/PAK/16/2010	PAK10-16	636	502	0	78.93	21.07	ME-SA	PanAsia-2 ^{PUN-10}
7	O/IRN/8/2005	IRN05-08	636	501	0	78.77	21.23	ME-SA	PanAsia-2
8	O/UGA/3/2002 (DQ165077)	UGA02-03	636	500	0	78.62	21.38	EA-2	unnamed
9	O/KEN/5/2002 (DQ165073)	KEN02-05	636	498	0	78.30	21.70	EA-2	Unnamed
10	O/MAL/1/98 (DQ165074)	MAL98-01	636	496	0	77.99	22.01	EA-2	unnamed

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.1

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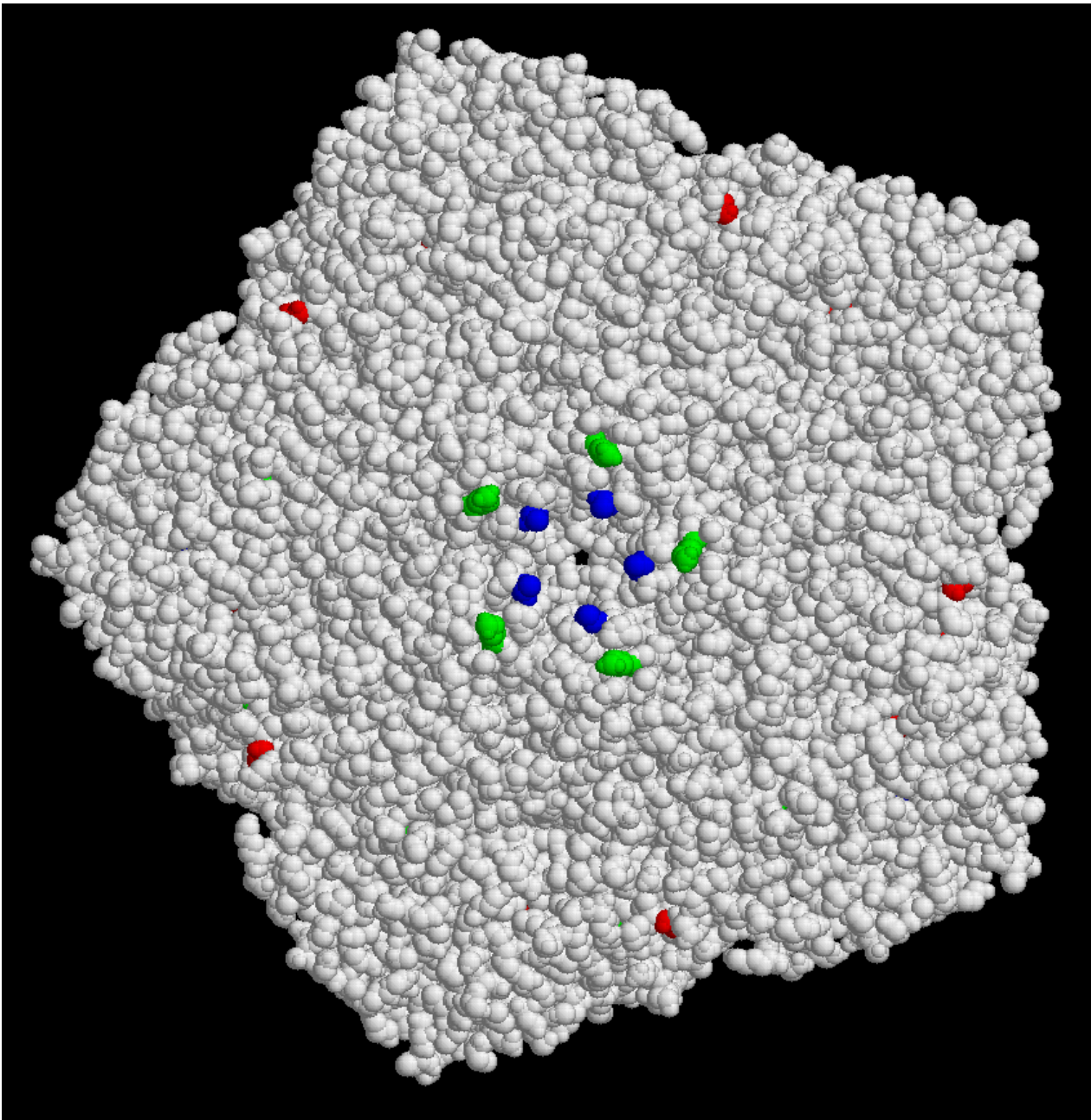


Figure 1. Possible amino acid substitutions on the O/TAW/1/2013 capsid pentamer subunit. VP1 amino acid residues 83 (green), 110 (blue) and 140 (red) are highlighted. The changes were mapped onto the surface of O₁ BFS 1860 (PDB accession 1FOD) using RasMol 2.7.2. In this structure the VP1 G-H loop is reduced and lies down on the virus surface covering part of VP2. In the unreduced virus the G-H loop may hold a different, more flexible, conformation possibly allowing a greater exposure of VP1 aa 140. The sequences of VP2 and VP3 were not determined and could possibly contain more changes.

Report on FMDV O in Taiwan in 2013

Batch: WRLFMD/2013/00022

◆ 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

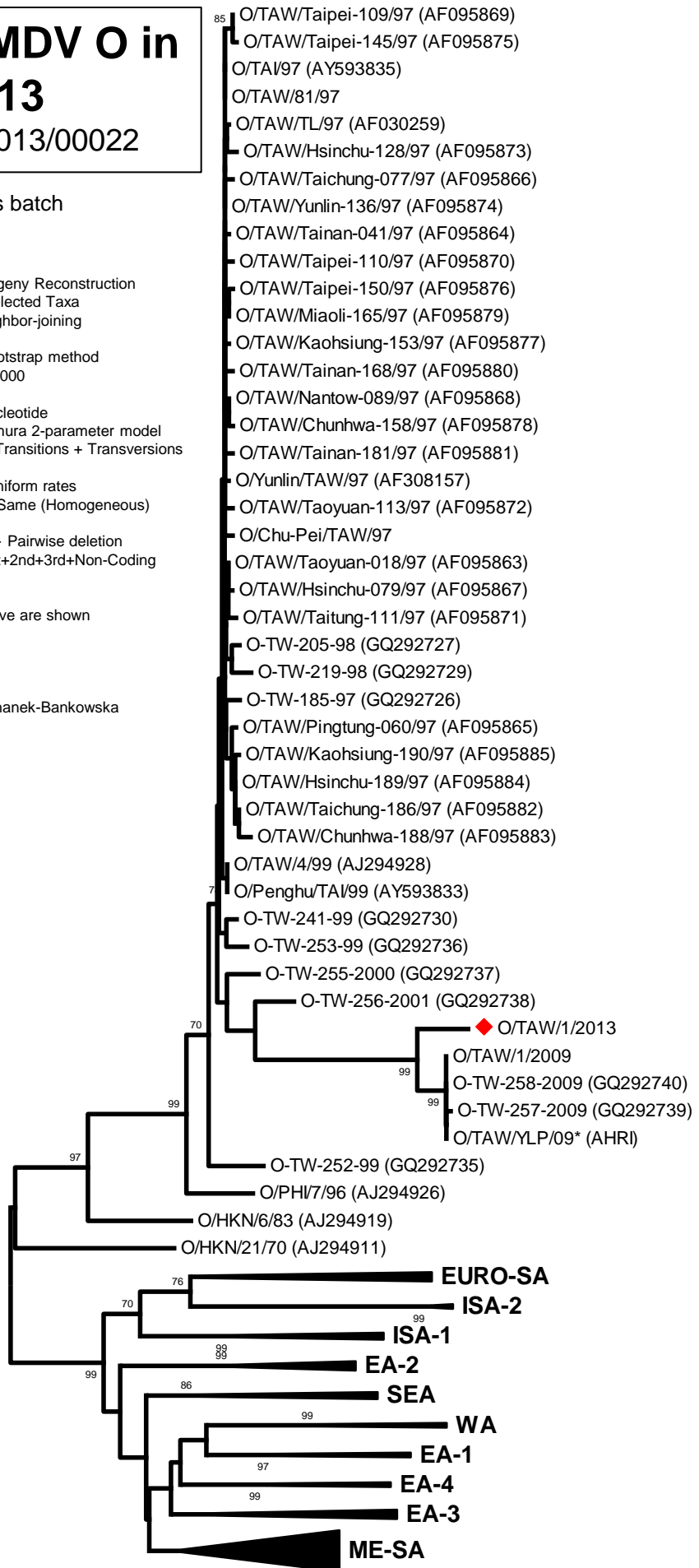
*, not a WRLFMD Ref. No.

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19 November 2013

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CATHAY

0.02