



INSTITUTE FOR ANIMAL HEALTH

Acting Director: Professor David Paton MA, VetMB, PhD, MRCVS

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Surrey,

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FMD Sequencing Report

Lab Reference WRL Batch Number: WRLFMD/2011/00016

Sender Details:



Date Received: 23rd March 2011

Country of Origin: Israel

Date Reported: 31st March 2011

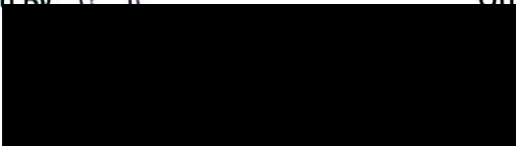
Dear Dr. Boris Gelman,

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:

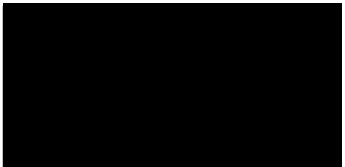
<http://www.wrlfmd.org/>

Please note that further work is in progress to further clarify the relationships identified in this report.

Results Approved By: *ll ll*



Official Stamp:



Date:

31/3/11



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)

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

Genotyping Report

Report Date for this Batch: 31 March 2011

FMDV type O

Country: Israel

Period: 2011

No. of samples: 2

BATCH: WRLFMD/2011/00016



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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: 31/03/2011
WRLFMD Ref No: ISR/1/2011	Reported by: N.J. Knowles
Batch No: WRLFMD/2011/00016	Checked by: V. Mioulet
Sender Ref: 99657	
Location: Kibbutz Bet Zera, Israel	Topotype: ME-SA
Date collected: 10/03/2011	Genotype/strain: PanAsia-2 ^{ANT-10}
Date received by WRLFMD: 23/03/2011	Sequence filename: ISR11-01.SEQ
Date received for sequencing: 25/03/2011	Date sequence last updated: 31/03/2011
Species: Cattle	No. of Nt determined: 639
Material used: BTy1	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 2697
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 8 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/ISR/2/2011	ISR11-02	639	639	0	100.00	0.00	ME-SA	PanAsia-2 ^{ANT-10}
2	O/BUL/1/2010	BUL10-01	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
3	O/BUL/10/2011	BUL11-10	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
4	O/BUL/11/2011	BUL11-11	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
5	O/BUL/13/2011	BUL11-13	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
6	O/BUL/14/2011	BUL11-14	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
7	O/BUL/15/2011	BUL11-15	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
8	O/TUR/153/2010* (FMDI)	TUR10-AR	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
9	O/TUR/154/2010* (FMDI)	TUR10-AS	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
10	O/TUR/39/2010	TUR10-39	639	630	0	98.59	1.41	ME-SA	PanAsia-2 ^{ANT-10}
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/IRN/88/2009	IRN09-88	639	622	0	97.34	2.66	ME-SA	PanAsia-2 ^{ANT-10}
2	O/IRN/31/2009	IRN09-31	639	595	0	93.11	6.89	ME-SA	PanAsia-2 ^{FAR-09}
3	O/IRN/8/2005	IRN05-08	639	595	0	93.11	6.89	ME-SA	PanAsia-2
4	O/TUR/257/2008* (FMDI)	TUR08-AD	639	593	0	92.80	7.20	ME-SA	PanAsia-2 ^{TER-08}
5	O/PAK/16/2010	PAK10-16	639	590	0	92.33	7.67	ME-SA	PanAsia-2 ^{PUN-10}
6	O/TUR/264/2009* (FMDI)	TUR09-AK	639	590	0	92.33	7.67	ME-SA	PanAsia-2 ^{SAN-09}
7	O/IRN/18/2010	IRN10-18	639	588	0	92.02	7.98	ME-SA	PanAsia-2 ^{BAL-09}
8	O/UKG/35/2001 (AJ539141)	UKG01-35	639	578	0	90.45	9.55	ME-SA	PanAsia
9	O/IRN/61/2001 (DQ164896)	IRN01-61	638	565	1	88.56	11.44	ME-SA	Im-2001
10	O/KUW/3/97 (DQ164904)	KUW97-03	639	565	0	88.42	11.58	ME-SA	Ind-2001a

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.0

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Sender Ref: 99657	
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Batch: WRLFMD/2011/00016

◆ 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 : 639

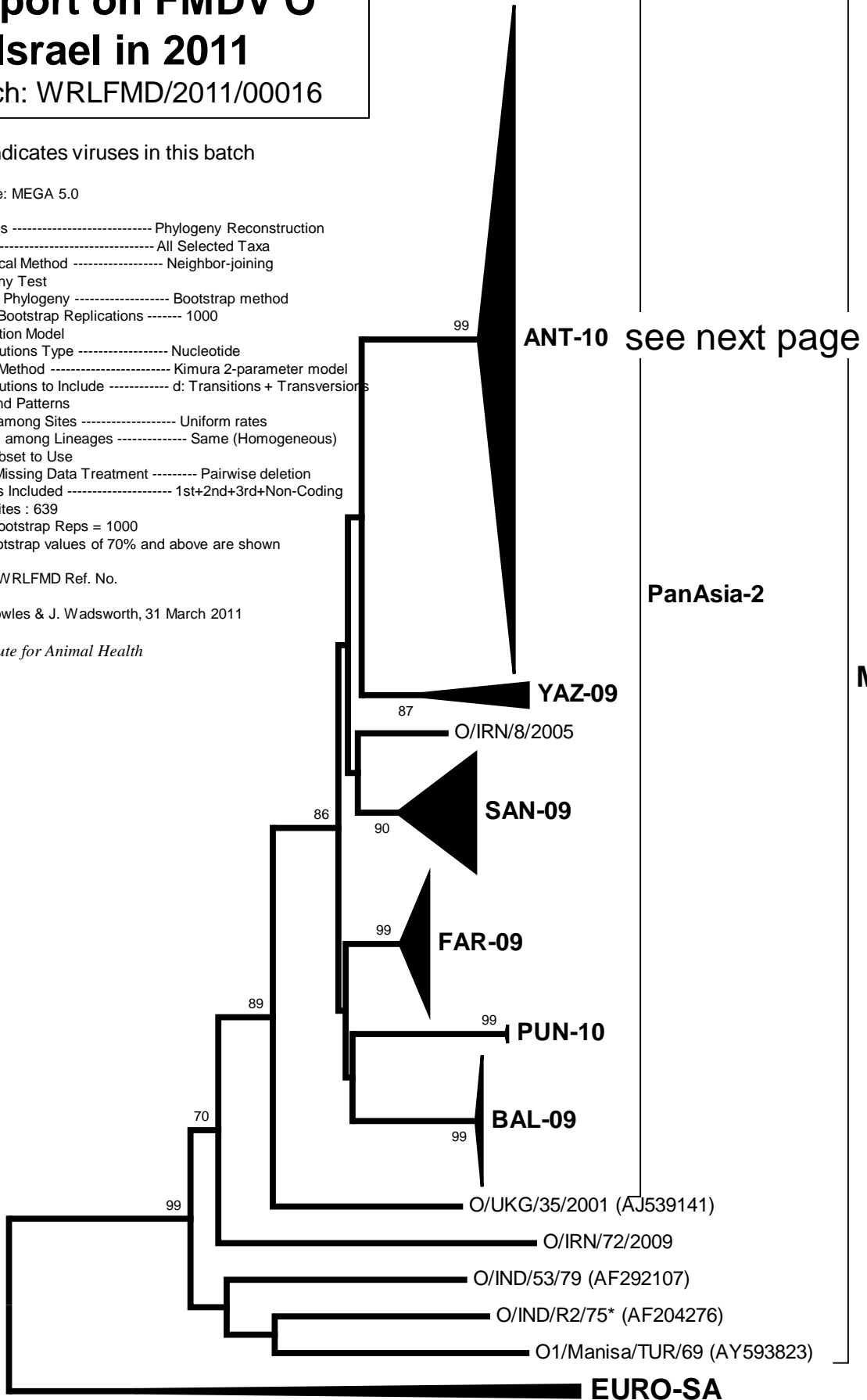
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 31 March 2011

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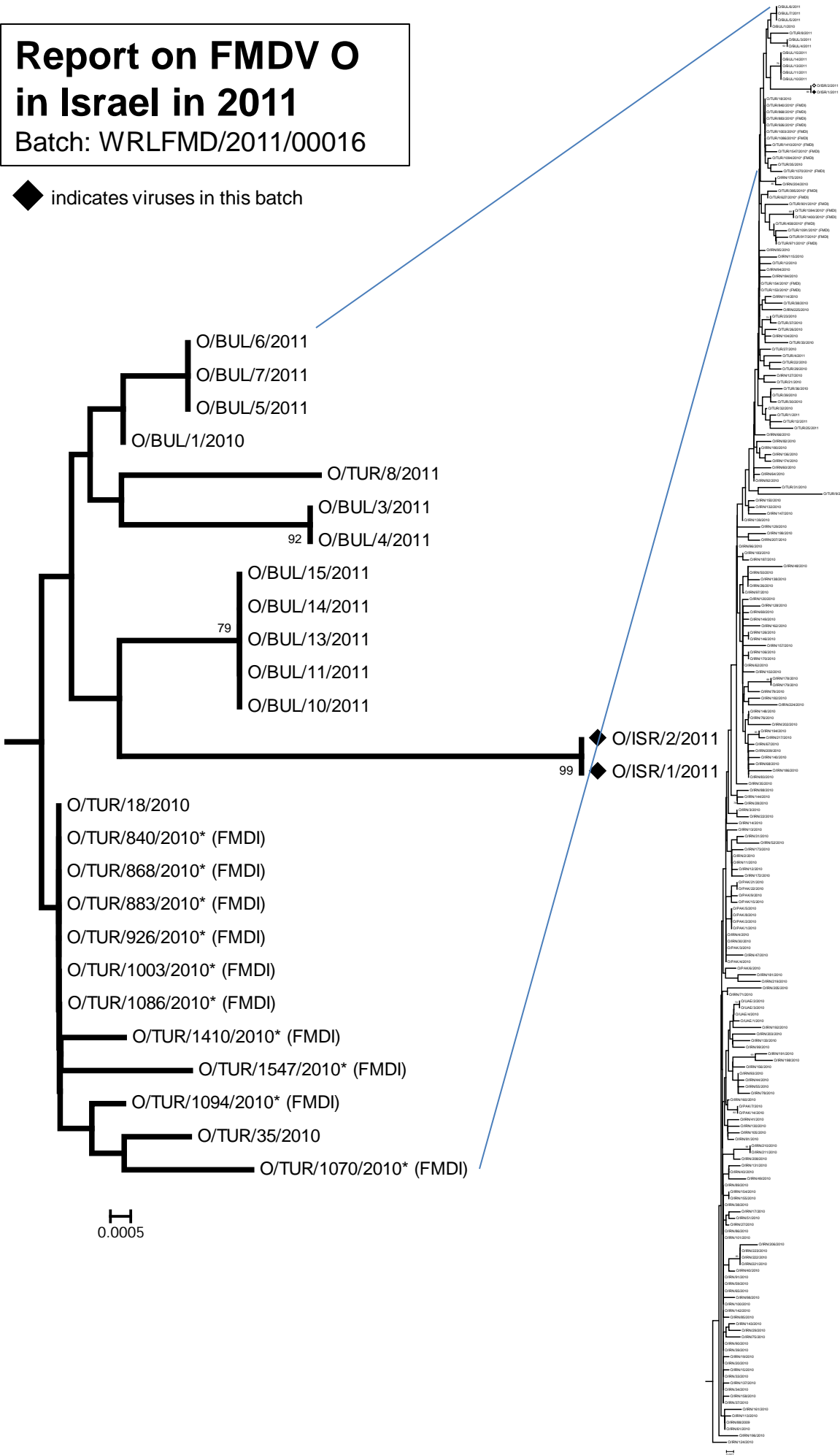


0.02

Report on FMDV O in Israel in 2011

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◆ indicates viruses in this batch



ME-SA/PanAsia-2ANT-10