

FMD Detection And Serotyping Results

Lab Reference WRL batch Number: WRLFMD/2010/00044

Sender Details:



Date Received: 25/11/2010

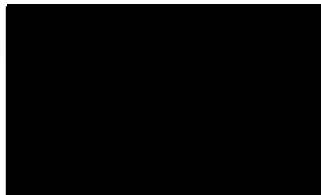
Country of Origin: MYANMAR

Dear Wilai Linchongsubongkoch,

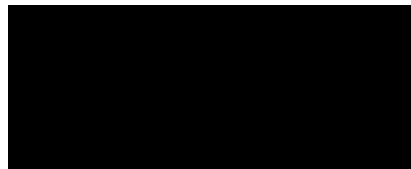
Diagnostics work has now been completed in respect of the samples you submitted and the details are as attached.

Please note that sample MYA 4/2010 (your reference MYA 1/10 (RNA)) was not tested by antigen ELISA. Sequencing results for this sample have been submitted in an earlier report.

Results Approved By:



Official Stamp:



Date:

10/1/11.

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: 8 December 2010

FMDV type A

Country: Myanmar

Period: 2010

No. of isolates: 1

BATCH: WRLFMD/2010/00044



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FAO World Reference Laboratory for FMD Genotyping Report

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

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Serotype: A WRLFMD Ref No: MYA/4/2010 Batch No: WRLFMD/2010/00044 Sender Ref: MYA 1/10 (RNA) Location: Taungpyoletwae Township, Maungtaw, Myanmar Date collected: 29/09/2010 Date received by WRLFMD: 25/11/2010 Date received for sequencing: 06/12/2010 Species: Cattle Material used: RNA Region sequenced: VP1 RT-PCR primers: A-1C562F/EUR-2B52R A-1C612F/EUR-2B52R	Report date: 08/12/2010 Reported by: N.J. Knowles Checked by: D.P. King Topotype: ASIA Genotype/strain: Unnamed Sequence filename: MYA10-04.SEQ Date sequence last updated: 08/12/2010 No. of Nt determined: 639 No. of ambiguities: 0 Gene length: 639 Total no. of comparisons: 1186 Min. no. of nt for comparison: 600 Total turn-around time: 13 days Sequencing time: 2 days
Comments: Amplified from RNA submitted by the OIE Regional Reference Laboratory for FMD in Southeast Asia, Pakchong, Thailand.	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	A/IND/104/2000* (AF390592)	IND00104	639	595	0	93.11	6.89	ASIA	Unnamed
2	A/IND/126/2000* (AF390599)	IND00126	639	595	0	93.11	6.89	ASIA	Unnamed
3	A/IND/40/2000* (AF390646)	IND00-40	639	595	0	93.11	6.89	ASIA	Unnamed
4	A/IND/128/2000* (AF390600)	IND00128	639	594	0	92.96	7.04	ASIA	Unnamed
5	A/IND/172/2000* (AF390614)	IND00172	639	594	0	92.96	7.04	ASIA	Unnamed
6	A/IND/38/2000* (AF390643)	IND00-38	639	594	0	92.96	7.04	ASIA	Unnamed
7	A/IND/42/2000* (AF390648)	IND00-42	639	594	0	92.96	7.04	ASIA	Unnamed
8	A/IND/80/2000* (AF390665)	IND00-80	639	594	0	92.96	7.04	ASIA	Unnamed
9	A/IND/81/2000* (AF390666)	IND00-81	639	594	0	92.96	7.04	ASIA	Unnamed
10	A/IND/17/2000* (AF390613)	IND00-17	624	580	5	92.95	7.05	ASIA	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	A/IRN/1/96 (EF208771)	IRN96-01	638	539	1	84.48	15.52	ASIA	Iran-96
2	A22/IRQ/64 (AY593763)	IRQ64--A	639	539	0	84.35	15.65	ASIA	A ₂₂
3	A/IRN/22/99 (EF208772)	IRN99-22	636	531	0	83.49	16.51	ASIA	Iran-99
4	A15/Bangkok/TAI/60 (AY593755)	TAI60--D	639	530	0	82.94	17.06	ASIA	A ₁₅
5	A12/UK/119/32 (M10975)	UKG32119	639	523	0	81.85	18.15	EURO-SA	A ₁₂
6	A/TAI/118/87* (EF208777)	TAI87-AD	636	520	0	81.76	18.24	ASIA	Thai-87
7	A/IRN/2/87 (EF208770)	IRN87-02	636	518	0	81.45	18.55	ASIA	Iran-87
8	A5/Allier/FRA/60 (AY593780)	FRA60--F	636	512	0	80.50	19.50	EURO-SA	A ₅
9	A/AFG/6/2007	AFG07-06	639	514	0	80.44	19.56	ASIA	Iran-05 ^{AFG-07}
10	A/NGR/2/73	NGR73-02	639	514	0	80.44	19.56	AFRICA	G-V

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v3.11

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Report on FMDV A in Myanmar in 2010

Batch: WRLFMD/2010/00044

Software: MEGA 4.0

No. of Taxa : 84

Data File : n:\evd\meg\db\fmv\A\MYA2010a.meg

Data Title : A Myanmar 2010

Data Type : Nucleotide (Coding)

Analysis : Phylogeny reconstruction

Tree Inference : =====

->Method : Neighbor-Joining

->Phylogeny Test and options : Bootstrap (1000 replicates; seed=24054)

Include Sites : =====

->Gaps/Missing Data : Pairwise Deletion

->Codon Positions : 1st+2nd+3rd+Noncoding

Substitution Model : =====

->Model : Nucleotide: Kimura 2-parameter

->Substitutions to Include : d: Transitions + Transversions

->Pattern among Lineages : Same (Homogeneous)

->Rates among sites : Uniform rates

No. of Sites : 639

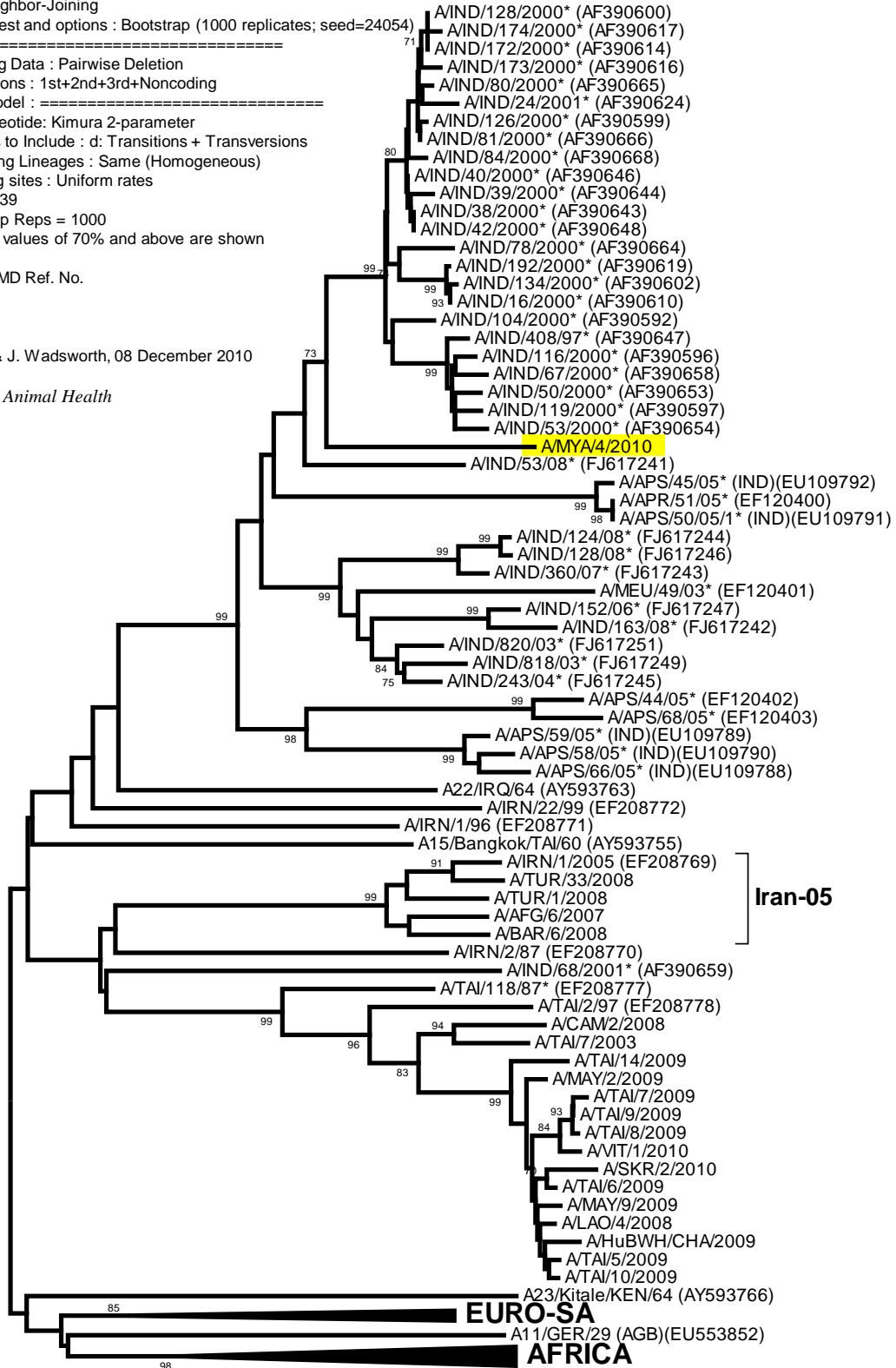
No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles & J. Wadsworth, 08 December 2010

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ASIA

Iran-05

EURO-SA

AFRICA

0.02