

Serotype: A	Report date: 13/06/2007
WRL Ref No: LAO/6/2006	
Sender Ref: LAO 2/07	
Date collected: 25/12/2006	
Date received by WRLFMD: 27/05/2007	Topotype: ASIA
Date received for sequencing: 04/06/2007	Genotype/strain: none designated
Species: Cattle	Sequence filename: LAO06-06.SEQ
Material used: LK2 BHK1 BTy1	Date sequence last updated: 11/06/2007
Region sequenced: VP1	Total no. of comparisons: 868
RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 300
No. of Nt determined: 636	Total turn-around time: 17 days
No. of ambiguities: 0	Sequencing time: 9 days
Gene length: 636	

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/LAO/7/2006	LAO06-07	636	635	0	99.84	0.16
2	A/LAO/8/2006	LAO06-08	636	634	0	99.69	0.31
3	A/CAM/2/2006	CAM06-02	633	630	0	99.53	0.47
4	A/CAM/1/2006	CAM06-01	633	629	0	99.37	0.63
5	A/TAI/8/2003	TAI03-08	628	609	5	96.97	3.03
6	A/TAI/5/2003	TAI03-05	621	602	0	96.94	3.06
7	A/TAI/9/2003	TAI03-09	614	595	1	96.91	3.09
8	A/TAI/7/2003	TAI03-07	633	613	0	96.84	3.16
9	A/VIT/11/2004	VIT04-11	633	613	0	96.84	3.16
10	A/VIT/5/2004	VIT04-05	633	613	0	96.84	3.16

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/TAI/2/97 (EF208778)	TAI97-02	633	592	0	93.52	6.48
2	A/TAI/118/87* (EF208777)	TAI87-AD	633	571	0	90.21	9.79
3	A/IND/7/82 (1980)	IND82-07	636	546	0	85.85	14.15
4	A/SAU/41/91	SAU91-41	633	526	0	83.1	16.9
5	A/IRN/87	IRN87--M	631	524	2	83.04	16.96
6	A/SAU/23/86	SAU86-23	636	528	0	83.02	16.98
7	A22/IRQ/24/64 (AJ251474)	IRQ64-24	636	526	0	82.7	17.3
8	A/IRN/22/99 (EF208772)	IRN99-22	633	520	0	82.15	17.85
9	A/IRN/1/96 (EF208771)	IRN96-01	635	520	1	81.89	18.11
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	636	511	0	80.35	19.65

nt, nucleotides

*, not a WRLFMD reference number

Serotype: A
WRL Ref No: LAO/7/2006
Sender Ref: LAO 9/07
Date collected: 25/12/2006
Date received by WRLFMD: 27/05/2007
Date received for sequencing: 04/06/2007
Species: Cattle
Material used: LK2 BHK1 BTy1
Region sequenced: VP1
RT-PCR primers: A-1C562F/EUR-2B52R;
A-1C612F/EUR-2B52R
No. of Nt determined: 636
No. of ambiguities: 0
Gene length: 636

Report date: 13/06/2007
Topotype: ASIA
Genotype/strain: none designated
Sequence filename: LAO06-07.SEQ
Date sequence last updated: 11/06/2007
Total no. of comparisons: 868
Min. no. of nt for comparison: 300
Total turn-around time: 17 days
Sequencing time: 9 days

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/LAO/6/2006	LAO06-06	636	635	0	99.84	0.16
2	A/LAO/8/2006	LAO06-08	636	635	0	99.84	0.16
3	A/CAM/2/2006	CAM06-02	633	629	0	99.37	0.63
4	A/CAM/1/2006	CAM06-01	633	628	0	99.21	0.79
5	A/TAI/8/2003	TAI03-08	628	608	5	96.82	3.18
6	A/TAI/5/2003	TAI03-05	621	601	0	96.78	3.22
7	A/TAI/9/2003	TAI03-09	614	594	1	96.74	3.26
8	A/TAI/7/2003	TAI03-07	633	612	0	96.68	3.32
9	A/VIT/11/2004	VIT04-11	633	612	0	96.68	3.32
10	A/VIT/5/2004	VIT04-05	633	612	0	96.68	3.32

Relationships to Reference Virus Strains

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/TAI/2/97 (EF208778)	TAI97-02	633	591	0	93.36	6.64
2	A/TAI/118/87* (EF208777)	TAI87-AD	633	572	0	90.36	9.64
3	A/IND/7/82 (1980)	IND82-07	636	545	0	85.69	14.31
4	A/SAU/41/91	SAU91-41	633	527	0	83.25	16.75
5	A/IRN/87	IRN87--M	631	523	2	82.88	17.12
6	A/SAU/23/86	SAU86-23	636	527	0	82.86	17.14
7	A22/IRQ/24/64 (AJ251474)	IRQ64-24	636	527	0	82.86	17.14
8	A/IRN/22/99 (EF208772)	IRN99-22	633	521	0	82.31	17.69
9	A/IRN/1/96 (EF208771)	IRN96-01	635	519	1	81.73	18.27
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	636	510	0	80.19	19.81

nt, nucleotides

*, not a WRLFMD reference number

Serotype: A	Report date: 13/06/2007						
WRL Ref No: LAO/8/2006							
Sender Ref: LAO 17/07							
Date collected: 25/12/2006							
Date received by WRLFMD: 27/05/2007	Topotype: ASIA						
Date received for sequencing: 04/06/2007	Genotype/strain: none designated						
Species: Cattle	Sequence filename: LAO06-08.SEQ						
Material used: LK2 BHK2 BTy1	Date sequence last updated: 11/06/2007						
Region sequenced: VP1	Total no. of comparisons: 868						
RT-PCR primers: A-1C562F/EUR-2B52R; A-1C612F/EUR-2B52R	Min. no. of nt for comparison: 300						
No. of Nt determined: 636	Total turn-around time: 17 days						
No. of ambiguities: 0	Sequencing time: 9 days						
Gene length: 636							
Comments:							
Ten Most Closely Related Viruses							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/LAO/7/2006	LAO06-07	636	635	0	99.84	0.16
2	A/LAO/6/2006	LAO06-06	636	634	0	99.69	0.31
3	A/CAM/2/2006	CAM06-02	633	628	0	99.21	0.79
4	A/CAM/1/2006	CAM06-01	633	627	0	99.05	0.95
5	A/TAI/8/2003	TAI03-08	628	608	5	96.82	3.18
6	A/TAI/5/2003	TAI03-05	621	600	0	96.62	3.38
7	A/TAI/9/2003	TAI03-09	614	593	1	96.58	3.42
8	A/TAI/7/2003	TAI03-07	633	611	0	96.52	3.48
9	A/VIT/11/2004	VIT04-11	633	611	0	96.52	3.48
10	A/VIT/5/2004	VIT04-05	633	611	0	96.52	3.48
Relationships to Reference Virus Strains							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/TAI/2/97 (EF208778)	TAI97-02	633	590	0	93.21	6.79
2	A/TAI/118/87* (EF208777)	TAI87-AD	633	571	0	90.21	9.79
3	A/IND/7/82 (1980)	IND82-07	636	546	0	85.85	14.15
4	A/SAU/41/91	SAU91-41	633	528	0	83.41	16.59
5	A/IRN/87	IRN87--M	631	524	2	83.04	16.96
6	A/SAU/23/86	SAU86-23	636	526	0	82.7	17.3
7	A22/IRQ/24/64 (AJ251474)	IRQ64-24	636	526	0	82.7	17.3
8	A/IRN/22/99 (EF208772)	IRN99-22	633	520	0	82.15	17.85
9	A/IRN/1/96 (EF208771)	IRN96-01	635	520	1	81.89	18.11
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	636	510	0	80.19	19.81
nt, nucleotides							
*, not a WRLFMD reference number							

Report on FMDV A from Laos in 2006

Software: MEGA 3.1
 No. of Taxa : 118
 Data File : n:\evd\meg\db\fmdv\A\TAI2006a.meg
 Data Title : Thailand/Cambodia/Laos 2006
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 Method : Neighbor-Joining
 Phylogeny Test and options : Bootstrap (1000 replicates; seed=64843)
 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 : 642
 No Of Bootstrap Reps = 1000
 Only bootstrap values of 70% and above are shown

N.J. Knowles & J. Wadsworth, 13 June 2007

