

Serotype: A
WRL Ref No: MAY/1/2007
Sender Ref: MVKKB 274/07
Date collected: 22/01/2007
Date received by WRLFMD: 30/11/2007
Date received for sequencing: 07/12/2007
Species: Pig
Material used: BTy2
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: 10/01/2008
Topotype: ASIA
Genotype/strain:
Sequence filename: MAY07-01.SEQ
Date sequence last updated: 12/12/2007
Total no. of comparisons: 916
Min. no. of nt for comparison: 300
Total turn-around time: 41 days
Sequencing time: 34 days

Comments:

Ten Most Closely Related Viruses

Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	A/TAI/8/2003	TAI03-08	631	607	5	96.2	3.8
2	A/MAY/3/2003	MAY03-03	636	611	0	96.07	3.93
3	A/TAI/5/2003	TAI03-05	624	599	0	95.99	4.01
4	A/TAI/9/2003	TAI03-09	617	592	1	95.95	4.05
5	A/MAY/1/2003	MAY03-01	636	610	0	95.91	4.09
6	A/TAI/7/2003	TAI03-07	636	610	0	95.91	4.09
7	A/MAY/4/2003	MAY03-04	636	609	0	95.75	4.25
8	A/TAI/10/2003	TAI03-10	636	609	0	95.75	4.25
9	A/TAI/2/04R2* [TRRL]	TAI04-AA	636	609	0	95.75	4.25
10	A/LAO/1/2006	LAO06-01	636	608	0	95.6	4.4

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	636	587	0	92.3	7.7
2	A/TAI/118/87* (EF208777)	TAI87-AD	636	565	0	88.84	11.16
3	A/IND/7/82 (1980)	IND82-07	636	533	0	83.81	16.19
4	A/SAU/23/86	SAU86-23	636	519	0	81.6	18.4
5	A/SAU/41/91	SAU91-41	633	516	0	81.52	18.48
6	A/IRN/87	IRN87--M	634	514	2	81.07	18.93
7	A22/IRQ/24/64 (AJ251474)	IRQ64-24	636	515	0	80.97	19.03
8	A/IRN/22/99 (EF208772)	IRN99-22	633	510	0	80.57	19.43
9	A/IRN/1/96 (EF208771)	IRN96-01	635	511	1	80.47	19.53
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	636	505	0	79.4	20.6

nt, nucleotides

*, not a WRLFMD reference number

Serotype: A	Report date: 10/01/2008						
WRL Ref No: MAY/3/2007							
Sender Ref: MVKKB 3664/07							
Date collected: 22/07/2007							
Date received by WRLFMD: 30/11/2007	Topotype: ASIA						
Date received for sequencing: 07/12/2007	Genotype/strain:						
Species: Cattle	Sequence filename: MAY07-03.SEQ						
Material used: BTy1	Date sequence last updated: 11/12/2007						
Region sequenced: VP1	Total no. of comparisons: 916						
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: 41 days						
No. of ambiguities: 0	Sequencing time: 34 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/TAI/4/2006	TAI06-04	636	622	0	97.8	2.2
2	A/TAI/2/2006	TAI06-02	636	621	0	97.64	2.36
3	A/TAI/22-2/06* (TRRL)	TAI06-AB	636	621	0	97.64	2.36
4	A/TAI/24-2/06* (TRRL)	TAI06-AC	636	621	0	97.64	2.36
5	A/TAI/29-2/06* (TRRL)	TAI06-AE	636	621	0	97.64	2.36
6	A/TAI/32-2/06* (TRRL)	TAI06-AF	636	621	0	97.64	2.36
7	A/TAI/38/06R1* (TRRL)	TAI06-AG	636	621	0	97.64	2.36
8	A/TAI/11/2006	TAI06-11	636	620	0	97.48	2.52
9	A/TAI/3/2006	TAI06-03	636	620	0	97.48	2.52
10	A/TAI/26/06* (TRRL)	TAI06-AD	636	619	0	97.33	2.67
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	636	586	0	92.14	7.86
2	A/TAI/118/87* (EF208777)	TAI87-AD	636	569	0	89.47	10.53
3	A/IND/7/82 (1980)	IND82-07	636	542	0	85.22	14.78
4	A/IRN/87	IRN87--M	634	526	2	82.97	17.03
5	A/SAU/41/91	SAU91-41	633	524	0	82.78	17.22
6	A/SAU/23/86	SAU86-23	636	525	0	82.55	17.45
7	A/IRN/1/96 (EF208771)	IRN96-01	635	519	1	81.73	18.27
8	A22/IRQ/24/64 (AJ251474)	IRQ64-24	636	519	0	81.6	18.4
9	A/IRN/22/99 (EF208772)	IRN99-22	633	509	0	80.41	19.59
10	A24/Cruzeiro/BRA/55 (AJ251476)	BRA55--C	636	501	0	78.77	21.23
nt, nucleotides							
*, not a WRLFMD reference number							

Report on FMDV A from Malaysia in 2007

Software: MEGA 3.1
 No. of Taxa : 120
 Data File : n:\levd\meg\db\fmvd\A\MAY2007a.meg
 Data Title : MAY/2007
 Data Type : Nucleotide (Coding)
 Analysis : Phylogeny reconstruction
 Tree Inference : =====
 Method : Neighbor-Joining
 Phylogeny Test and options : Bootstrap (1000 replicates; seed=64238)
 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, 10 January 2008

