

| | |
|--|--|
| Serotype: A | Report date: 16/09/2008 |
| WRL Ref No: TAI/3/2007 | Reported by: N.J. Knowles |
| Sender Ref: 6/07 B2 | Checked by: D.P. King |
| Date collected: 02/06/2007 | |
| Date received by WRLFMD: 24/07/2008 | Topotype: ASIA |
| Date received for sequencing: 15/08/2008 | Genotype/strain: none designated |
| Species: Cattle | Sequence filename: TAI07-03.SEQ |
| Material used: BHK2 BTY1 | Date sequence last updated: 02/09/2008 |
| Region sequenced: VP1 | Total no. of comparisons: 959 |
| RT-PCR primers: A-1C562F/EUR-2B52R; | Min. no. of nt for comparison: 300 |
| A-1C612F/EUR-2B52R | Total turn-around time: 54 days |
| No. of Nt determined: 636 | Sequencing time: 32 days |
| No. of ambiguities: 0 | |
| 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/8/2003 | TAI03-08 | 631 | 611 | 5 | 96.83 | 3.17 |
| 2 | A/TAI/5/2003 | TAI03-05 | 624 | 603 | 0 | 96.63 | 3.37 |
| 3 | A/TAI/9/2003 | TAI03-09 | 617 | 596 | 1 | 96.6 | 3.4 |
| 4 | A/TAI/7/2003 | TAI03-07 | 636 | 614 | 0 | 96.54 | 3.46 |
| 5 | A/MAY/4/2003 | MAY03-04 | 636 | 613 | 0 | 96.38 | 3.62 |
| 6 | A/TAI/10/2003 | TAI03-10 | 636 | 613 | 0 | 96.38 | 3.62 |
| 7 | A/TAI/2/04R2* [TRRL] | TAI04-AA | 636 | 613 | 0 | 96.38 | 3.62 |
| 8 | A/LAO/1/2006 (2003)(EU667456) | LAO06-01 | 636 | 612 | 0 | 96.23 | 3.77 |
| 9 | A/LAO/36/2003 (EU667455) | LAO03-36 | 636 | 612 | 0 | 96.23 | 3.77 |
| 10 | A/MAY/3/2003 | MAY03-03 | 636 | 612 | 0 | 96.23 | 3.77 |

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 | 592 | 0 | 93.08 | 6.92 |
| 2 | A/TAI/118/87* (EF208777) | TAI87-AD | 636 | 570 | 0 | 89.62 | 10.38 |
| 3 | A/SAU/23/86 (EU414536) | SAU86-23 | 636 | 527 | 0 | 82.86 | 17.14 |
| 4 | A/IRN/2/87 (EF208770) | IRN87-02 | 636 | 525 | 0 | 82.55 | 17.45 |
| 5 | A22/IRQ/24/64 (AJ251474) | IRQ64-24 | 636 | 524 | 0 | 82.39 | 17.61 |
| 6 | A/SAU/41/91 | SAU91-41 | 633 | 521 | 0 | 82.31 | 17.69 |
| 7 | A/IRN/1/96 (EF208771) | IRN96-01 | 635 | 521 | 1 | 82.05 | 17.95 |
| 8 | A/IRN/22/99 (EF208772) | IRN99-22 | 633 | 516 | 0 | 81.52 | 18.48 |
| 9 | A/IRN/1/2005 (EF208769) | IRN05-01 | 636 | 517 | 0 | 81.29 | 18.71 |
| 10 | A24/Cruzeiro/BRA/55 (AJ251476) | BRA55--C | 636 | 504 | 0 | 79.25 | 20.75 |

nt, nucleotides

*, not a WRLFMD reference number

| | |
|--|--|
| Serotype: A | Report date: 16/09/2008 |
| WRL Ref No: TAI/11/2007 | Reported by: N.J. Knowles |
| Sender Ref: 26-1/07 B2 | Checked by: D.P. King |
| Date collected: 19/11/2007 | |
| Date received by WRLFMD: 24/07/2008 | Topotype: ASIA |
| Date received for sequencing: 15/08/2008 | Genotype/strain: none designated |
| Species: Cattle | Sequence filename: TAI07-11.SEQ |
| Material used: BHK2 BTY1 | Date sequence last updated: 02/09/2008 |
| Region sequenced: VP1 | Total no. of comparisons: 959 |
| RT-PCR primers: A-1C562F/EUR-2B52R; | Min. no. of nt for comparison: 300 |
| A-1C612F/EUR-2B52R | Total turn-around time: 54 days |
| No. of Nt determined: 636 | Sequencing time: 32 days |
| No. of ambiguities: 0 | |
| 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/MAY/3/2007 | MAY07-03 | 636 | 633 | 0 | 99.53 | 0.47 |
| 2 | A/SEN/7/2008 | SEN08-07 | 636 | 632 | 0 | 99.37 | 0.63 |
| 3 | A/SEN/3/2008 | SEN08-03 | 636 | 631 | 0 | 99.21 | 0.79 |
| 4 | A/TAI/4/2006 | TAI06-04 | 636 | 621 | 0 | 97.64 | 2.36 |
| 5 | A/TAI/2/2006 | TAI06-02 | 636 | 620 | 0 | 97.48 | 2.52 |
| 6 | A/TAI/22-2/06* (TRRL) | TAI06-AB | 636 | 620 | 0 | 97.48 | 2.52 |
| 7 | A/TAI/24-2/06* (TRRL) | TAI06-AC | 636 | 620 | 0 | 97.48 | 2.52 |
| 8 | A/TAI/29-2/06* (TRRL) | TAI06-AE | 636 | 620 | 0 | 97.48 | 2.52 |
| 9 | A/TAI/32-2/06* (TRRL) | TAI06-AF | 636 | 620 | 0 | 97.48 | 2.52 |
| 10 | A/TAI/38/06R1* (TRRL) | TAI06-AG | 636 | 620 | 0 | 97.48 | 2.52 |

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 | 585 | 0 | 91.98 | 8.02 |
| 2 | A/TAI/118/87* (EF208777) | TAI87-AD | 636 | 567 | 0 | 89.15 | 10.85 |
| 3 | A/IRN/2/87 (EF208770) | IRN87-02 | 636 | 529 | 0 | 83.18 | 16.82 |
| 4 | A/SAU/41/91 | SAU91-41 | 633 | 522 | 0 | 82.46 | 17.54 |
| 5 | A/SAU/23/86 (EU414536) | SAU86-23 | 636 | 522 | 0 | 82.08 | 17.92 |
| 6 | A/IRN/1/2005 (EF208769) | IRN05-01 | 636 | 520 | 0 | 81.76 | 18.24 |
| 7 | A/IRN/1/96 (EF208771) | IRN96-01 | 635 | 517 | 1 | 81.42 | 18.58 |
| 8 | A22/IRQ/24/64 (AJ251474) | IRQ64-24 | 636 | 516 | 0 | 81.13 | 18.87 |
| 9 | A/IRN/22/99 (EF208772) | IRN99-22 | 633 | 507 | 0 | 80.09 | 19.91 |
| 10 | A24/Cruzeiro/BRA/55 (AJ251476) | BRA55--C | 636 | 500 | 0 | 78.62 | 21.38 |

nt, nucleotides

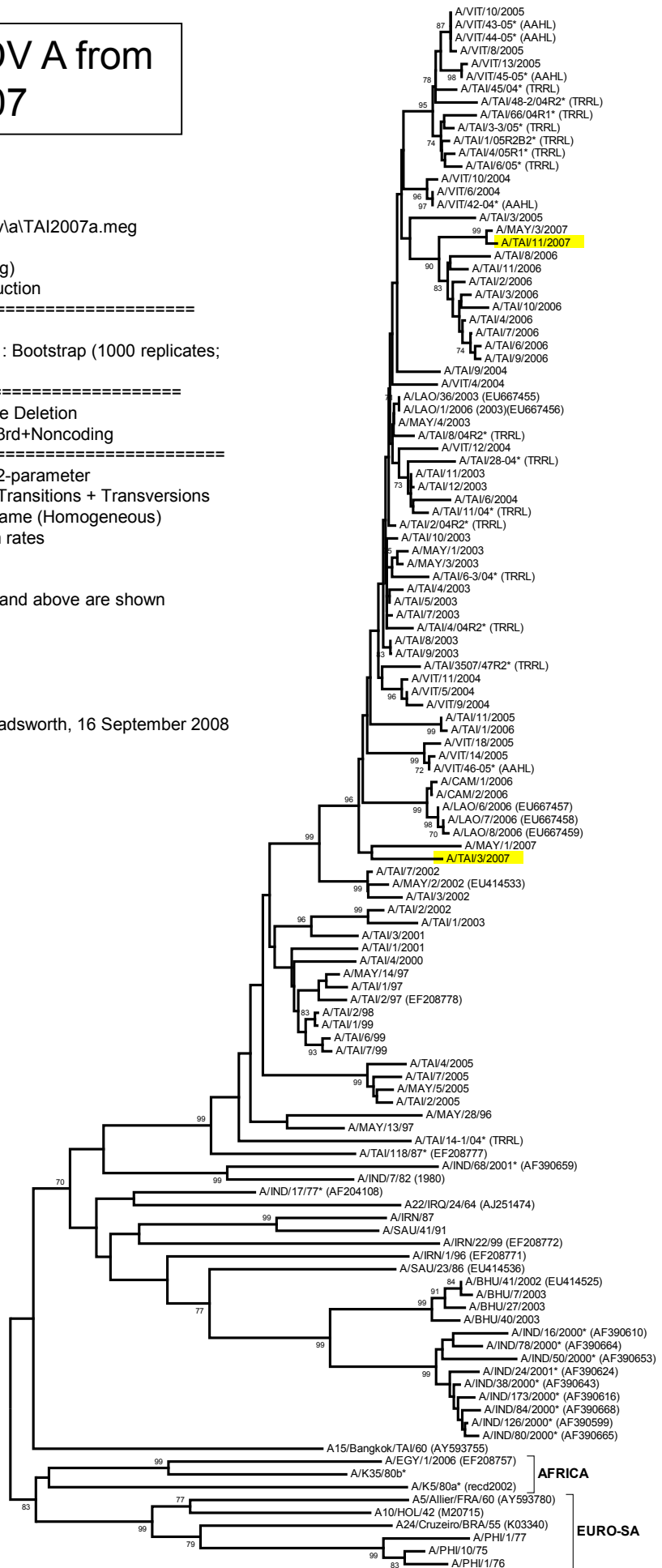
*, not a WRLFMD reference number

Report on FMDV A from Thailand in 2007

Software: MEGA 4.0
 No. of Taxa : 122
 Data File : n:\levd\meg\db\fmdiv\at\TAI2007a.meg
 Data Title : Thailand 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

*, not a WRLFMD Ref. No.

N.J. Knowles, K. Ebert & J. Wadsworth, 16 September 2008



ASIA

AFRICA

EURO-SA