

| Serotype: A | | Report date: 22/03/2007 | | | | | |
|---|--------------------------------|--|-----------------|-------------------------|--------------------|------------|--------------|
| WRL Ref No: none | | | | | | | |
| Sender Ref: A/TUR/324/2007 | | | | | | | |
| Date collected: 2007 | | | | | | | |
| Date received by WRLFMD: 15/03/2007 (seq only) | | Topotype: Asia | | Genotype/strain: Irn-05 | | | |
| Species: unknown | | Sequence filename: TUR07-AA.SEQ | | | | | |
| Material used: unknown | | Date sequence last updated: 21/03/2007 | | | | | |
| Region sequenced: VP1 | | Total no. of comparisons: 804 | | | | | |
| RT-PCR primers: unknown | | Min. no. of nt for comparison: 300 | | | | | |
| No. of Nt determined: 639 | | | | | | | |
| No. of ambiguities: 0 | | | | | | | |
| Gene length: 639 | | | | | | | |
| Comments: | | | | | | | |
| Ten Most Closely Related Viruses | | | | | | | |
| Pos. | Virus name | Filename | No. nt compared | No. nt matched | No. of ambiguities | % Identity | % Difference |
| 1 | A/SAU/41/91 | SAU91-41 | 636 | 540 | 0 | 84.91 | 15.09 |
| 2 | A/IND/7/82 (1980) | IND82-07 | 639 | 541 | 0 | 84.66 | 15.34 |
| 3 | A/IRN/87 | IRN87--M | 634 | 534 | 2 | 84.23 | 15.77 |
| 4 | A/IRN/22/99 (EF208772) | IRN99-22 | 636 | 532 | 0 | 83.65 | 16.35 |
| 5 | A/TAI/118/87* (EF208777) | TAI87-AD | 636 | 531 | 0 | 83.49 | 16.51 |
| 6 | A/TAI/2/97 (EF208778) | TAI97-02 | 636 | 527 | 0 | 82.86 | 17.14 |
| 7 | A/IRN/1/96 (EF208771) | IRN96-01 | 638 | 527 | 1 | 82.6 | 17.4 |
| 8 | A/SAU/23/86 | SAU86-23 | 639 | 527 | 0 | 82.47 | 17.53 |
| 9 | A22/IRQ/24/64 (AJ251474) | IRQ64-24 | 639 | 527 | 0 | 82.47 | 17.53 |
| 10 | A24/Cruzeiro/BRA/55 (AJ251476) | BRA55--C | 639 | 508 | 0 | 79.5 | 20.5 |
| Relationships to Reference Virus Strains | | | | | | | |
| Pos. | Virus name | Filename | No. nt compared | No. nt matched | No. of ambiguities | % Identity | % Difference |
| 1 | A/SAU/41/91 | SAU91-41 | 636 | 540 | 0 | 84.91 | 15.09 |
| 2 | A/IND/7/82 (1980) | IND82-07 | 639 | 541 | 0 | 84.66 | 15.34 |
| 3 | A/IRN/87 | IRN87--M | 634 | 534 | 2 | 84.23 | 15.77 |
| 4 | A/IRN/22/99 (EF208772) | IRN99-22 | 636 | 532 | 0 | 83.65 | 16.35 |
| 5 | A/TAI/118/87* (EF208777) | TAI87-AD | 636 | 531 | 0 | 83.49 | 16.51 |
| 6 | A/TAI/2/97 (EF208778) | TAI97-02 | 636 | 527 | 0 | 82.86 | 17.14 |
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| 8 | A/SAU/23/86 | SAU86-23 | 639 | 527 | 0 | 82.47 | 17.53 |
| 9 | A22/IRQ/24/64 (AJ251474) | IRQ64-24 | 639 | 527 | 0 | 82.47 | 17.53 |
| 10 | A24/Cruzeiro/BRA/55 (AJ251476) | BRA55--C | 639 | 508 | 0 | 79.5 | 20.5 |
| nt, nucleotides | | | | | | | |
| *, not a WRLFMD reference number | | | | | | | |

Report on FMDV A sequence from Turkey in 2007

Analysis software: MEGA 3.1
 No. of Taxa : 141
 Data File : n:\evd\megldb\fmdiva\tur2007a.meg
 Data Title : FMDV-A TUR2007a
 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

N.J. Knowles, N. Shirazi and J. Wadsworth, 22 March 2007

