

Serotype: O  
WRL Ref No: none  
Sender Ref: O/TUR/285/2007  
Date collected: 2007  
Date received by WRLFMD: 15/03/2007 (seq only)  
Species: unknown  
Material used: unknown  
Region sequenced: VP1  
RT-PCR primers: unknown  
No. of Nt determined: 639  
No. of ambiguities: 0  
Gene length: 639

Report date: 22/03/2007  
Topotype: ME-SA  
Genotype/strain: PanAsia  
Sequence filename: TUR07-AA.SEQ  
Date sequence last updated: 21/03/2007  
Total no. of comparisons: 1558  
Min. no. of nt for comparison: 300

Comments:

### Ten Most Closely Related Viruses

| Pos. | Virus name    | Filename | No. nt compared | No. nt matched | No. of ambiguities | % Identity | % Difference |
|------|---------------|----------|-----------------|----------------|--------------------|------------|--------------|
| 1    | O/JOR/6/2006  | JOR06-06 | 639             | 633            | 0                  | 99.06      | 0.94         |
| 2    | O/IRN/39/2006 | IRN06-39 | 639             | 631            | 0                  | 98.75      | 1.25         |
| 3    | O/ISR/3/2007  | ISR07-03 | 639             | 631            | 0                  | 98.75      | 1.25         |
| 4    | O/JOR/7/2006  | JOR06-07 | 639             | 631            | 0                  | 98.75      | 1.25         |
| 5    | O/IRN/12/2006 | IRN06-12 | 639             | 630            | 0                  | 98.59      | 1.41         |
| 6    | O/IRN/14/2006 | IRN06-14 | 639             | 630            | 0                  | 98.59      | 1.41         |
| 7    | O/ISR/1/2007  | ISR07-01 | 639             | 630            | 0                  | 98.59      | 1.41         |
| 8    | O/IRN/10/2006 | IRN06-10 | 639             | 629            | 0                  | 98.44      | 1.56         |
| 9    | O/IRN/17/2006 | IRN06-17 | 639             | 629            | 0                  | 98.44      | 1.56         |
| 10   | O/IRN/19/2006 | IRN06-19 | 639             | 629            | 0                  | 98.44      | 1.56         |

### Relationships to Reference Virus Strains

| Pos. | Virus name                  | Filename | No. nt compared | No. nt matched | No. of ambiguities | % Identity | % Difference |
|------|-----------------------------|----------|-----------------|----------------|--------------------|------------|--------------|
| 1    | O/TAW/2/99                  | TAW99-02 | 639             | 598            | 0                  | 93.58      | 6.42         |
| 2    | O/IND/53/79 [AF292107]      | IND79A53 | 639             | 565            | 0                  | 88.42      | 11.58        |
| 3    | O/IND/R2/75* [AF204276]     | IND75--A | 639             | 565            | 0                  | 88.42      | 11.58        |
| 4    | O1/Manisa/TUR/69 (AJ251477) | TUR69--E | 639             | 557            | 0                  | 87.17      | 12.83        |
| 5    | O/TAI/189/87* [TRRL]        | TAI87-AC | 639             | 551            | 0                  | 86.23      | 13.77        |
| 6    | O/ISR/2/88 (DQ164899)       | ISR88-02 | 639             | 550            | 0                  | 86.07      | 13.93        |
| 7    | O/MOR/1/91                  | MOR91-01 | 639             | 546            | 0                  | 85.45      | 14.55        |
| 8    | O/PHI/5/95 (DQ164946)       | PHI95-05 | 639             | 517            | 0                  | 80.91      | 19.09        |
| 9    | O1/BFS 1860/UK/67           | UKG67--A | 639             | 510            | 0                  | 79.81      | 20.19        |
| 10   | O/HKN/6/83                  | HKN83-06 | 637             | 507            | 2                  | 79.59      | 20.41        |

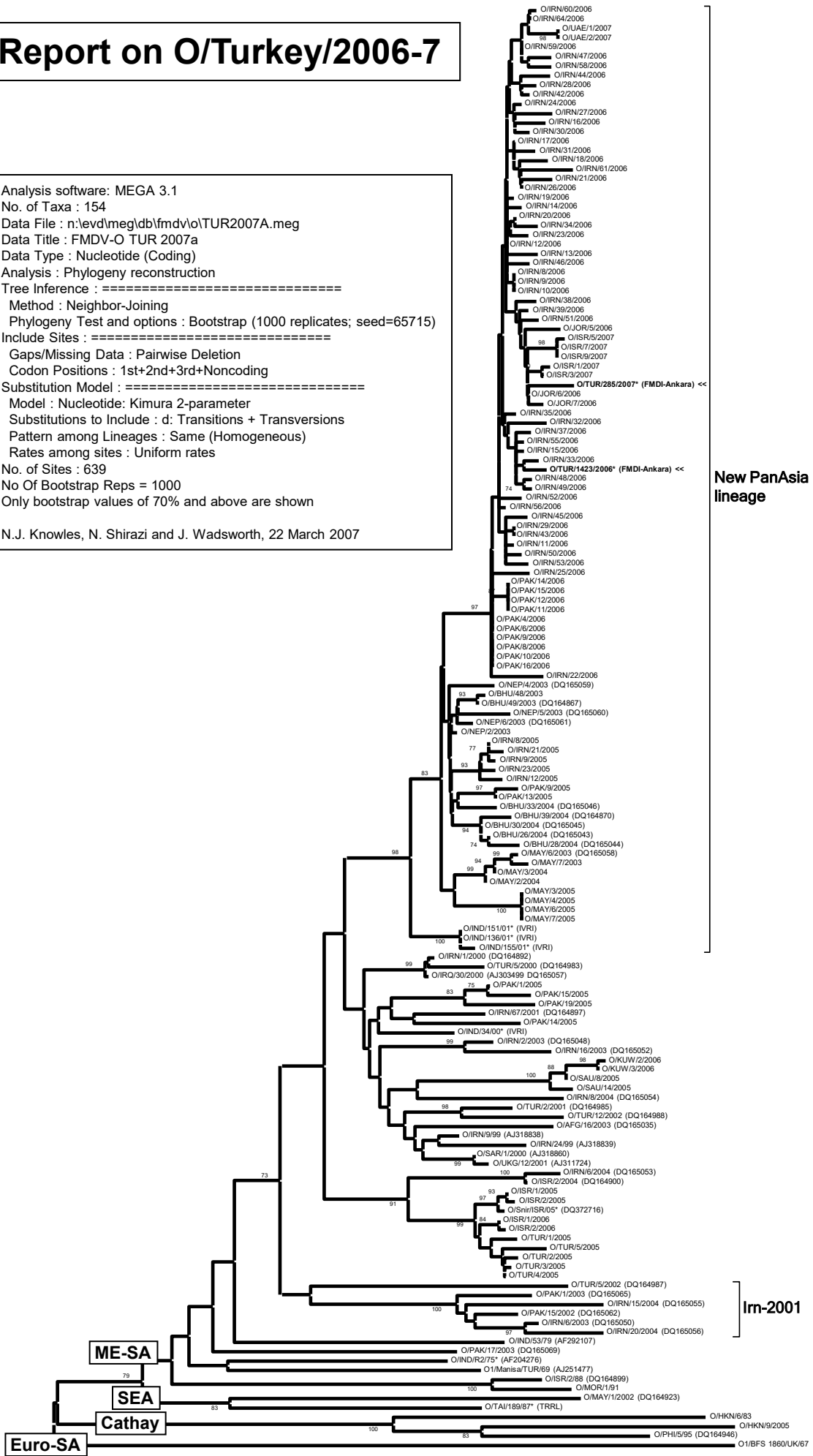
nt, nucleotides

\*, not a WRLFMD reference number

# Report on O/Turkey/2006-7

Analysis software: MEGA 3.1  
 No. of Taxa : 154  
 Data File : n:\evd\meg\db\fmvd\o\tur2007A.meg  
 Data Title : FMDV-O TUR 2007a  
 Data Type : Nucleotide (Coding)  
 Analysis : Phylogeny reconstruction  
 Tree Inference : =====  
 Method : Neighbor-Joining  
 Phylogeny Test and options : Bootstrap (1000 replicates; seed=65715)  
 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

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



New PanAsia lineage

PanAsia

Irn-2001

ME-SA

SEA

Cathay

Euro-SA

0.02

O/HKN/6/83  
 O/HKN/9/2005  
 O/PHI/5/95 (DQ164946)  
 O1/BFS 1860/UK/67